

This Page Is Inserted by IFW Operations
and is not a part of the Official Record

BEST AVAILABLE IMAGES

Defective images within this document are accurate representations of the original documents submitted by the applicant.

Defects in the images may include (but are not limited to):

- BLACK BORDERS
- TEXT CUT OFF AT TOP, BOTTOM OR SIDES
- FADED TEXT
- ILLEGIBLE TEXT
- SKEWED/SLANTED IMAGES
- COLORED PHOTOS
- BLACK OR VERY BLACK AND WHITE DARK PHOTOS
- GRAY SCALE DOCUMENTS

IMAGES ARE BEST AVAILABLE COPY.

**As rescanning documents *will not* correct images,
please do not report the images to the
Image Problem Mailbox.**

THIS PAGE BLANK (USPTO)

STIC-Biotech/ChemLib

108046

From: Chan, Christina
Sent: Wednesday, November 12, 2003 1:00 PM
To: Walicka, Malgorzata
Cc: STIC-Biotech/ChemLib
Subject: RE:

RECEIVED

NOV 12 2003

STIC

Please rush. Thanks Chris

Chris Chan

TC 1600 New Hire Training Coordinator and SPE 1644
308-3973
CM-1, 9B19

-----Original Message-----

From: Walicka, Malgorzata
Sent: Tuesday, November 11, 2003 1:40 PM
T : Chan, Christina
Cc: STIC-Biotech/ChemLib
Subject:

Please search the polypeptide of SEQ ID NO: 112,
113,
114,
115,
116, and 117

in application No. 09/843,676. Please use the CFR of 08/854,050. Please, RUSH.

Thank you in advance.

Malgorzata A. Walicka, Ph.D.
Patent Examiner
Recombinant Enzymes-Art Unit 1652
USPTO
1911 S. Clark Street, Crystal Mall 1, Room 10D06
Mail Room 10D01
Arlington, VA 22202
(703) 305-7270
malgorzata.walicka@uspto.gov

Searcher: _____
Phone: _____
Location: _____
Date Picked Up: _____
Date Completed: 11/14/03
Searcher Prep/Review: _____
Clerical: _____
Online time: _____

TYPE OF SEARCH:
NA Sequences: _____
AA Sequences: _____
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST (where applic.)
STN: _____
DIALOG: _____
Questel/Orbit: _____
DRLink: _____
Lexis/Nexis: _____
Sequence Sys.: _____
WWW/Internet: _____
Other (specify): _____

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 12, 2003, 19:41:04 ; Search time 28.6415 Seconds
(without alignments)
127.462 Million cell updates/sec

Title: US-08-854-050-113

Perfect score: 114

Sequence: 1 RQHLKRVQLRDVSEAEVRQUREA 23

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.*
2: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
3: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*
4: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.*
5: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1984.DAT.*
6: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1985.DAT.*
7: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1986.DAT.*
8: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1987.DAT.*
9: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1988.DAT.*
10: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1989.DAT.*
11: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1990.DAT.*
12: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1991.DAT.*
13: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1992.DAT.*
14: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1993.DAT.*
15: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1994.DAT.*
16: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1995.DAT.*
17: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1996.DAT.*
18: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1997.DAT.*
19: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.*
20: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*
21: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
22: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*
24: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	114	100.0	23	19 AAW57392	Human telomerase r
2	114	100.0	23	19 AAW57388	Human telomerase r
3	114	100.0	131	20 AAW97385	Amino acid sequenc
4	107	93.9	100	23 ABG71627	hTERT fragment wit
5	107	93.9	259	19 AAW46998	Human telomerase r
6	107	93.9	283	20 AAY43128	Human telomerase r
7	107	93.9	437	20 AAY25461	Human CRT-1 protei
8	107	93.9	438	20 AAY25462	Human CRT-1 protei
9	107	93.9	531	19 AAW47002	Glutathione-S-tran

10	107	93.9	564	19 AAW56109	Human telomerase r
11	107	93.9	591	20 AAW97384	A catalytic telome
12	107	93.9	617	20 AAY00636	N-terminal truncat
13	107	93.9	622	20 AAY25463	Human CRT-1 protei
14	107	93.9	807	19 AAW46997	Human telomerase r
15	107	93.9	807	20 AAY00637	N-terminal truncat
16	107	93.9	807	20 AAY00646	Truncated telomera
17	107	93.9	936	20 AAY00642	Truncated telomera
18	107	93.9	936	20 AAY00651	Truncated telomera
19	107	93.9	948	20 AAY00639	N-terminal truncat
20	107	93.9	948	20 AAY00648	Truncated telomera
21	107	93.9	949	19 AAW61349	Human telomerase p
22	107	93.9	1041	20 AAY00643	Altered C-terminus
23	107	93.9	1041	20 AAY00652	Altered C-terminus
24	107	93.9	1053	20 AAY00640	Altered C-terminus
25	107	93.9	1053	20 AAY00649	Altered C-terminus
26	107	93.9	1120	20 AAY00641	Telomerase protein
27	107	93.9	1120	20 AAY00650	Telomerase (ver. 2
28	107	93.9	1132	19 AAW71376	Human telomerase c
29	107	93.9	1132	19 AAW46957	Human telomerase r
30	107	93.9	1132	19 AAW56113	Human telomerase r
31	107	93.9	1132	20 AAY43621	A human telomerase
32	107	93.9	1132	20 AAY28881	Human telomerase r
33	107	93.9	1132	20 AAY32090	Human telomerase r
34	107	93.9	1132	20 AAY28401	Human EST2 protein
35	107	93.9	1132	20 AAY26580	Human telomerase r
36	107	93.9	1132	20 AAY00627	Human telomerase p
37	107	93.9	1132	20 AAY00638	Truncated telomera
38	107	93.9	1132	20 AAW90251	Human catalytic te
39	107	93.9	1132	21 AAY96566	hEST2, a human tel
40	107	93.9	1132	22 AAB82765	Human telomerase r
41	107	93.9	1132	22 AAB99930	Human telomerase p
42	107	93.9	1132	22 AAG64329	Human protein #2.
43	107	93.9	1132	22 AAG64859	Heart muscle cell
44	107	93.9	1132	23 AAE29226	Human telomerase r
45	107	93.9	1132	23 AAU72735	Human telomerase r

ALIGNMENTS

RESULT 1

AAW57392

ID AAW57392 standard; peptide; 23 AA.

XX AC AAW57392;

XX DT

XX DT 13-AUG-1998 (first entry)

XX DE Human telomerase reverse transcriptase antigenic peptide S-2.

XX DE Human telomerase reverse transcriptase; hTERT; TRT; diagnosis;

XX DE Human; telomerase reverse transcriptase; hTERT; TRT; diagnosis;

XX DE prognosis; cell proliferation; cancer; ageing; ribonucleoprotein.

XX OS Synthetic.

XX OS Homo sapiens.

XX PN GB2317891-A.

XX PD 08-APR-1998.

XX PF 01-OCT-1997; 97GB-0020890.

XX PR 14-AUG-1997; 97US-0915503.

XX PR 01-OCT-1996; 96US-0724643.

XX PR 18-APR-1997; 97US-0844419.

XX PR 25-APR-1997; 97US-0846017.

XX PR 06-MAY-1997; 97US-0851843.

XX PR 09-MAY-1997; 97US-0854050.

XX PR 14-AUG-1997; 97US-0911312.

XX PR 14-AUG-1997; 97US-0912951.

XX PA (GERO-) GERON CORP.

us-08-854-050-113.rag

Thu Nov 13 12:06:58 2003

```

PR 09-MAY-1997; 97US-0854050.
PR 14-AUG-1997; 97US-0911312.
PR 14-AUG-1997; 97US-0912951.
XX
XX (GERO-) GERON CORP.
XX (UYTE-) UNIV TECHNOLOGY CORP.
XX
XX Andrews WH, Cech TR, Chapman KB, Harley C, Lingner J;
XX Morin GB, Nakamura T, Harley CB;
XX WPI; 1998-171633/16.
XX
XX Pure and recombinant human Telomerase Reverse Transcriptase and its
XX variants - are useful in the diagnosis, prognosis and treatment of
XX cell proliferation conditions especially cancer and ageing
XX
XX Example 8; Fig 54; 387pp; English.
XX
XX The present sequence represents an antigenic peptide from human
XX telomerase reverse transcriptase (hTERT), from the present invention. The
XX present invention also describes the following methods: (A) determining
XX whether a test compound is a modulator of hTERT, by detecting the change
XX in hTERT recombinant protein or polynucleotide, on administration of the
XX compound; (B) preparation of recombinant telomerase by contacting a
XX protein preparation of hTERT with a telomerase RNA component; (C)
XX detection of the hTERT RNA or protein in a sample by binding a relevant
XX probe to the sample and detecting the complex formed or in the case of
XX RNA detection, amplifying the product and correlating the presence of
XX complex or amplification product with presence of hTERT in the sample;
XX and (D) increasing the proliferation of a vertebrate cell by increasing
XX hTERT expression; and (E) the use of an agent that causes an increase in
XX cell vertebrate cell proliferation to create a medicament that inhibits
XX ageing. A protein preparation of hTERT and the polynucleotide encoding
XX hTERT can be used in the manufacture of medicaments for inhibiting the
XX effect of ageing or cancer. Inhibitors of telomerase activity can be
XX used to treat conditions that are associated with high telomerase
XX activity. A protein preparation of hTERT can also be used in the new
XX methods.
XX
XX SQ Sequence 23 AA;
XX
XX Query Match 100.0%; Score 114; DB 19; Length 23;
XX Best Local Similarity 100.0%; Pred. No. 3.4e-11;
XX Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 RQHLKRVQLRDVSEAEVROHREA 23
XX | | | | | | | | | | | | | | | | | | | | |
XX Db 1 RQHLKRVQLRDVSEAEVROHREA 23
XX
XX RESULT 3
XX AAW57388
XX ID AAW57388 standard; peptide; 23 AA.
XX
XX AC AAW57388;
XX
XX DT 13-AUG-1998 (first entry)
XX
XX DE Human telomerase reverse transcriptase antigenic peptide.
XX
XX KW Human; telomerase reverse transcriptase; hTERT; TRT; diagnosis;
XX prognosis; cell proliferation; cancer; ageing; ribonucleoprotein;
XX antigenic.
XX
XX OS Synthetic.
XX OS Homo sapiens.
XX
XX PN GB2317891-A.
XX
XX PD 08-APR-1998.
XX
XX PF 01-OCT-1997; 97GB-0020890.
XX
XX PR 01-AUG-1997; 97US-0915503.
XX PR 01-OCT-1996; 96US-0724643.
XX PR 18-APR-1997; 97US-0844419.
XX PR 25-APR-1997; 97US-0846017.
XX PR 06-MAY-1997; 97US-0851843.
XX
XX PA (MITU) MITSUBISHI CHEM CORP.

```

acids of hTERT. The polypeptides of the invention are useful in a pharmaceutical composition or in a vaccine for preventing or treating cancer in populations of individuals having varying HLA profiles. The polypeptides are also useful in a diagnostic kit for diagnosing cancers such as breast, pancreatic, colorectal, lung, ovarian or cervical cancer, malignant melanoma, leukaemia, lymphoma or biliary tract carcinoma. The polypeptides or encoding polynucleotide sequences are useful for performing identity, sequence homology and/or hybridisation studies, for predicting structure and/or function (e.g. anti-cancer activity), or for screening methods in drug development or drug screening procedures. The present sequence represents a hTERT fragment with the 20 amino acid HLA epitope containing polypeptide at its N-terminus.

Query Match 93.9%; Score 107; DB 23; Length 100;
Best Local Similarity 91.3%; Pred. No. 2.5e-09;
Matches 21; Conservative 2; Mismatches 0; Indels 0; Gaps

Oy 1 RQHLKRVQLRDVSEAEVROHREA 23
IIIIIIIIII::IIIIIIIIII
Db 54 RQHLKRVQLRELSAEAEVROHREA 76

RESULT 5
AAW46998
ID AAW46998 standard; Protein; 259 AA.
AC AAW46998;
XX
XX
DT 13-AUG-1998 (first entry)
XX
DE
XX
KW
XX
KW
XX
OS Homo sapiens.
XX
PN GB2317891-A.
PD 08-APR-1998.
XX
XX
PF 01-OCT-1997; 97GB-0020890.
XX
PR 14-AUG-1997; 97US-0915503.
PR 01-OCT-1996; 96US-0724643.
PR 18-APR-1997; 97US-0844419.
PR 25-APR-1997; 97US-0846017.
PR 06-MAY-1997; 97US-0851843.
PR 09-MAY-1997; 97US-0854050.
PR 14-AUG-1997; 97US-0911312.
PR 14-AUG-1997; 97US-0912951.
XX
XX (GERO-) GERON CORP.
XX (UYTE-) UNIV TECHNOLOGY CORP.
XX
XX Andrews WH, Cech TR, Chapman KB, Harley C, Lingner J;
PI Morin GB, Nakamura T, Harley CB;
XX
XX WPI; 1998-171633/16.
DR N-PSDB; AAW22379.
XX
XX Pure and recombinant human Telomerase Reverse Transcriptase and its
PT variants - are useful in the diagnosis, prognosis and treatment of
PT cell proliferation conditions especially cancer and ageing
XX
XX Example 1; Fig 19; 387pp; English.
XX
XX The present sequence represents a human telomerase reverse transcriptase
CCC (hTERT) protein from a cDNA clone from the present invention. The present
CCC invention also describes the following methods: (A) determining whether

us-08-854-050-113.rag

Thu Nov 13 12:06:58 2003

a test compound is a modulator of hTERT, by detecting the change in hTERT recombinant protein or polynucleotide, on administration of the compound; (B) preparation of recombinant telomerase by contacting a protein preparation of hTERT with a telomerase RNA component; (C) detection of the hTERT RNA or protein in a sample by binding a relevant probe to the sample and detecting the complex formed or in the case of RNA detection, amplifying the product and correlating the presence of complex or amplification product with presence of hTERT in the sample; and (D) increasing the proliferation of a vertebrate cell by increasing hTERT expression; and (E) the use of an agent that causes an increase in cell vertebrate cell proliferation to create a medicament that inhibits ageing. A protein preparation of hTERT and the polynucleotide encoding hTERT can be used in the manufacture of medicaments for inhibiting the effect of ageing or cancer. Inhibitors of telomerase activity can be used to treat conditions that are associated with high telomerase activity. A protein preparation of hTERT can also be used in the new methods.

XX SQ Sequence 259 AA;

Query Match 93.9%; Score 107; DB 19; Length 259;

Best Local Similarity 91.3%; Pred. No. 7.8e-09; Indels 0; Gaps 0;

Matches 21; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RQHLKRVQLRDVSEAEVROHREA 23
 |||||:|||||
 Db 42 RQHLKRVQLRELSEAEVROHREA 64

RESULT 6
 AAY43128
 ID AAY43128 standard; Protein; 283 AA.
 AC AAY43128;
 XX 20-DEC-1999 (first entry)
 DT Human telomerase reverse transcriptase.
 XX Human telomerase reverse transcriptase; hTERT; antibody; diagnosis;
 DE Human telomerase reverse transcriptase; hTERT; antibody; diagnosis;
 XX Human telomerase reverse transcriptase; hTERT; antibody; diagnosis;
 KW telomerase-related disease; cancer.
 XX Homo sapiens.
 OS WO9950407-A1.
 PN 07-OCT-1999.
 XX 26-MAR-1999; 99WO-JP01557.
 PF 26-MAR-1998; 98JP-0098486.
 PR (KYOW) KYOWA HAKKO KOGYO KK.
 XX Hanai N, Yamaeaki M, Shibata K, Furuya A, Mikuni O, Anazawa H;
 PI WPI; 1999-591316/50.
 XX New monoclonal antibody recognizing human telomerase catalytic subunit (hTERT) useful for treating and diagnosing cancer.
 XX Claim 2; Page 72-73; 78pp; Japanese.
 PS This sequence represents the human telomerase reverse transcriptase
 CC This invention relates to a monoclonal antibody recognising the
 CC hTERT. The invention relates to a monoclonal antibody recognising the
 CC hTERT. The antibody can be used for the investigation, diagnosis and
 CC treatment of telomerase-related diseases, especially diseases in which
 CC telomerase expression is up-regulated e.g. cancers.
 XX SQ Sequence 283 AA;

Query Match 93.9%; Score 107; DB 20; Length 283;

Best Local Similarity 91.3%; Pred. No. 8.7e-09;

Matches 21; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RQHLKRVQLRDVSEAEVROHREA 23
 |||||:|||||
 Db 42 RQHLKRVQLRELSEAEVROHREA 64

RESULT 7
 AAY25461
 ID AAY25461 standard; Protein; 437 AA.
 XX AAY25461;
 AC AAY25461;
 XX 22-SEP-1999 (first entry)
 DT Human CRT-1 protein #1.
 DE CRT-1; reverse transcriptase; telomerase; inhibitor; detection;
 XX telomerase activity; cancer cell; screening; human.
 KW Homo sapiens.
 OS WO9935261-A1.
 PN 15-JUL-1999.
 XX 08-JAN-1999; 99WO-JP000039.
 PF 06-MAY-1998; 98JP-0139177.
 PR 08-JAN-1998; 98JP-0013232.
 PR 30-JAN-1998; 98JP-0033584.
 XX (CHUS) CHUGAI SEIYAKU KK.
 XX Tauchiya M, Yoshida K;
 PI WPI; 1999-430393/36.
 DR N-PSDB; AAX88243.
 XX Novel gene, useful in detection of telomerase activity and cancer
 PT cells as well as screening telomerase inhibitors for treatment of
 PT cancers
 XX Claim 2; Page 31-32; 44pp; Japanese.
 PS This invention describes novel human CRT-1 genes and their encoded
 CC proteins containing a reverse transcriptase motif, which act as
 CC telomerase inhibitors. The gene, its encoded protein and derived
 CC antibodies can be used to provide base sequence information, detect
 CC telomerase activity and cancer cells, and to screen telomerase
 CC inhibitors. The detection method is simple and effective.
 XX SQ Sequence 437 AA;

Query Match 93.9%; Score 107; DB 20; Length 437;

Best Local Similarity 91.3%; Pred. No. 1.5e-08;

Matches 21; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RQHLKRVQLRDVSEAEVROHREA 23
 |||||:|||||
 Db 80 RQHLKRVQLRELSEAEVROHREA 102

RESULT 8
 AAY25462
 ID AAY25462 standard; Protein; 438 AA.
 XX AAY25462;
 AC AAY25462;

XX DT 22-SEP-1999 (first entry)
 XX DE Human CRT-1 protein #2.
 XX KW CRT-1; reverse transcriptase; telomerase; inhibitor; detection;
 XX OS telomerase activity; cancer cell; screening; human.
 XX
 XX FH Homo sapiens.
 XX
 XX FT Key Location/Qualifiers
 XX FT Protein 1..438
 XX FT /label= CRT-1
 XX FT /note= "Partial sequence, no stop codon given"
 XX
 XX PN WO9935261-A1.
 XX PD 15-JUL-1999.
 XX PF 08-JAN-1999; 99WO-JP00039.
 XX PR 06-MAY-1998; 98JP-0139177.
 XX PR 08-JAN-1998; 98JP-0013232.
 XX PR 30-JAN-1998; 98JP-0033584.
 XX PA (CHUS) CHUGAI SEIYAKU KK.
 XX PI Tsuchiya M, Yoshida K;
 XX DR WPI; 1999-430393/36.
 XX DR N-PSDB; AAX88250.
 XX
 XX FT Novel gene, useful in detection of telomerase activity and cancer
 XX FT cells as well as screening telomerase inhibitors for treatment of
 XX FT cancers
 XX
 XX PS Example 1; Page 35-36; 44pp; Japanese.
 XX
 XX CC This invention describes novel human CRT-1 genes and their encoded
 XX CC proteins containing a reverse transcriptase motif, which act as
 XX CC telomerase inhibitors. The gene, its encoded protein and derived
 XX CC antibodies can be used to provide base sequence information, detect
 XX CC telomerase activity and cancer cells, and to screen telomerase
 XX CC inhibitors. The detection method is simple and effective.
 XX
 XX SQ Sequence 438 AA;
 XX
 XX Query Match 93.9%; Score 107; DB 20; Length 438;
 XX Best Local Similarity 91.3%; Pred. No. 1.5e-08;
 XX Matches 21; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX QY 1 ROHLKRVQLRDVSEAEVRQHREA 23
 XX DB 80 ROHLKRVQLRSEAEVRQHREA 102
 XX
 XX RESULT 9
 XX AAW47002
 XX ID AAW47002 standard; Protein; 531 AA.
 XX AC AAW47002;
 XX DT 13-AUG-1998 (first entry)
 XX DE Glutathione-S-transferase and hTERT fusion protein 2.
 XX KW Human; telomerase reverse transcriptase; hTERT; TRT; diagnosis;
 XX OS prognosis; cell proliferation; cancer; ageing; ribonucleoprotein.
 XX OS Synthetic.
 XX OS Homo sapiens.
 XX FH Key Location/Qualifiers

FT Region 1..221
 FT /note= "glutathione-S-transferase fragment"
 FT 249..531
 FT /note= "hTERT protein fragment"
 XX GB2317891-A.
 XX 08-APR-1998.
 XX 01-OCT-1997; 97GB-0020890.
 XX 14-AUG-1997; 97US-0915503.
 XX 01-OCT-1996; 96US-0724643.
 XX 18-APR-1997; 97US-0844419.
 XX 25-APR-1997; 97US-0846017.
 XX 06-MAY-1997; 97US-0851843.
 XX 09-MAY-1997; 97US-0854050.
 XX 14-AUG-1997; 97US-0911312.
 XX 14-AUG-1997; 97US-0912951.
 XX (GERO-) GERON CORP.
 XX (UYTE-) UNIV TECHNOLOGY CORP.
 XX Andrews WH, Cech TR, Chapman KB, Harley C, Lingner J;
 XX Morin GB, Nakamura T, Harley CB;
 XX WPI; 1998-171633/16.
 XX
 XX PT Pure and recombinant human Telomerase Reverse Transcriptase and its
 XX PT variants - are useful in the diagnosis, prognosis and treatment of
 XX PT cell proliferation conditions especially cancer and ageing
 XX
 XX PS Example 6; Page 225; 387pp; English.
 XX
 XX CC The present sequence represents a fusion protein from an example
 XX CC of the present invention which describes human telomerase reverse
 XX CC transcriptase (hTERT). The present invention also describes the
 XX CC following methods: (A) determining whether a test compound is
 XX CC a modulator of hTERT, by detecting the change in hTERT recombinant
 XX CC protein or polynucleotide, on administration of the compound;
 XX CC (B) preparation of recombinant telomerase by contacting a protein
 XX CC preparation of hTERT with a telomerase RNA component; (C) detection
 XX CC of the hTERT RNA or protein in a sample by binding a relevant
 XX CC probe to the sample and detecting the complex formed or in the case of
 XX CC RNA detection, amplifying the product and correlating the presence of
 XX CC complex or amplification product with presence of hTERT in the sample;
 XX CC and (D) increasing the proliferation of a vertebrate cell by increasing
 XX CC hTERT expression; and (E) the use of an agent that causes an increase in
 XX CC cell vertebrate cell proliferation to create a medicament that inhibits
 XX CC ageing. A protein preparation of hTERT and the polynucleotide encoding
 XX CC hTERT can be used in the manufacture of medicaments for inhibiting the
 XX CC effect of ageing or cancer. Inhibitors of telomerase activity can be
 XX CC used to treat conditions that are associated with high telomerase
 XX CC activity. A protein preparation of hTERT can also be used in the new
 XX CC methods.
 XX
 XX SQ Sequence 531 AA;
 XX
 XX Query Match 93.9%; Score 107; DB 19; Length 531;
 XX Best Local Similarity 91.3%; Pred. No. 1.8e-08;
 XX Matches 21; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX QY 1 ROHLKRVQLRDVSEAEVRQHREA 23
 XX DB 290 ROHLKRVQLRSEAEVRQHREA 312
 XX
 XX RESULT 10
 XX AAW56109
 XX ID AAW56109 standard; Protein; 564 AA.
 XX AC AAW56109;
 XX FH Key

us-08-854-050-113.rag

Thu Nov 13 12:06:58 2003

42 RQHLKRVQLRDLSEAEVROHREA 64
 Db
 RESULT 11
 AAW97384
 ID AAW97384 standard; Protein; 591 AA.
 XX
 AC AAW97384;
 XX
 DT 14-MAY-1999 (first entry)
 XX
 DE A catalytic telomerase protein.
 XX
 DE Catalytic telomerase; diagnosis; disease; telomerase activity.
 XX
 KW Homo sapiens.
 OS
 PN JP11046768-A.
 XX
 PD 23-FEB-1999.
 XX
 PF 01-AUG-1997; 97JP-0207708.
 XX
 PR 01-AUG-1997; 97JP-0207708.
 XX
 PA (MITU) MITSUBISHI CHEM CORP.
 XX
 DR WPI; 1999-208111/18.
 DR N-PSDB; AAX15923.
 XX
 PT New catalytic protein of telomerase of a higher animal and a gene
 PT coding it - useful for diagnosis of diseases caused by the change in
 PT activity of a telomerase
 PS
 PS Claim 1; Page 11-14; 18pp; Japanese.
 XX
 CC The present sequence represents a catalytic telomerase protein.
 CC The products are useful in drug compositions for the diagnosis
 CC of diseases caused by the change in activity of telomerase.
 XX
 SQ Sequence 591 AA;
 Query Match 93.9%; Score 107; DB 20; Length 591;
 Best Local Similarity 91.3%; Pred. No. 2.1e-08;
 Matches 21; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RQHLKRVQLRDLSEAEVROHREA 23
 Db 49 RQHLKRVQLRDLSEAEVROHREA 71
 RESULT 12
 AAY00636
 ID AAY00636 standard; Protein; 617 AA.
 XX
 AC AAY00636;
 XX
 DT 26-JUL-1999 (first entry)
 XX
 DE N-terminal truncated telomerase protein sequence.
 XX
 DE Telomerase; human; cancer; diagnosis; melanoma; skin cancer; leukaemia;
 KW neuroblastoma; breast carcinoma; colon carcinoma; lymphoma; osteosarcoma;
 KW smooth muscle cell hyperplasia; stem cell proliferation; Wilms tumor;
 KW stem cell differentiation; organ regeneration; organ differentiation.
 XX
 KW Homo sapiens.
 OS
 OS Synthetic.
 XX
 PN WO9901560-A1.
 XX
 PD 14-JAN-1999.
 XX

13-AUG-1998 (first entry)
 Human telomerase reverse transcriptase 63 kDa clone 712562 protein.
 Human; telomerase reverse transcriptase; hTERT; TRT; diagnosis;
 prognosis; cell proliferation; cancer; ageing; ribonucleoprotein.
 Synthetic.
 Homo sapiens.
 Key Location/Qualifiers
 FT Misc-difference 102
 FT /label= encoded by ARG
 GB2317891-A.
 08-APR-1998.
 01-OCT-1997; 97GB-0020890.
 14-AUG-1997; 97US-0915503.
 01-OCT-1996; 96US-0724643.
 18-APR-1997; 97US-0844419.
 25-APR-1997; 97US-0846017.
 06-MAY-1997; 97US-0851843.
 09-MAY-1997; 97US-0854050.
 14-AUG-1997; 97US-0911312.
 14-AUG-1997; 97US-0912951.
 (GERO-) GERON CORP.
 (UYTE-) UNIV TECHNOLOGY CORP.
 Andrews WH, Cech TR, Chapman KB, Harley C, Lingner J;
 Morin GB, Nakamura T, Harley CB;
 WPI; 1998-171633/16.
 N-PSDB; AAV22426.
 Pure and recombinant human Telomerase Reverse Transcriptase and its
 variants - are useful in the diagnosis, prognosis and treatment of
 cell proliferation conditions especially cancer and ageing
 Example 1; Fig 68; 387pp; English.
 The present sequence is a human telomerase reverse transcriptase (hTERT)
 clone protein from the present invention. The present invention also
 describes the following methods: (A) determining whether a test compound
 is a modulator of hTERT, by detecting the change in hTERT recombinant
 protein or polynucleotide, on administration of the compound; (B)
 preparation of recombinant telomerase by contacting a protein
 preparation of hTERT with a telomerase RNA component; (C) detection of
 the hTERT RNA or protein in a sample by binding a relevant probe to the
 sample and detecting the complex formed or in the case of RNA detection,
 amplifying the product and correlating the presence of complex or
 amplification product with presence of hTERT in the sample; and (D)
 increasing the proliferation of a vertebrate cell by increasing hTERT
 expression; and (E) the use of an agent that causes an increase in cell
 vertebrate cell proliferation to create a medicament that inhibits
 ageing. A protein preparation of hTERT and the polynucleotide encoding
 hTERT can be used in the manufacture of medicaments for inhibiting the
 effect of ageing or cancer. Inhibitors of telomerase activity can be
 used to treat conditions that are associated with high telomerase
 activity. A protein preparation of hTERT can also be used in the new
 methods.
 XX
 SQ Sequence 564 AA;
 Query Match 93.9%; Score 107; DB 19; Length 564;
 Best Local Similarity 91.3%; Pred. No. 2e-08;
 Matches 21; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RQHLKRVQLRDLSEAEVROHREA 23

PF 01-JUL-1998; 98WO-US13835.
 XX
 PR 09-SEP-1997; 97US-0058287.
 PR 01-JUL-1997; 97US-0051410.
 PR 21-JUL-1997; 97US-0053018.
 PR 21-JUL-1997; 97US-0053329.
 PR 04-AUG-1997; 97US-0054642.
 XX
 PA (CAMB-) CAMBIA BIOSYSTEMS LLC.
 XX
 XX Bowtell D, Kilian A;
 XX WPI; 1999-106060/09.
 DR N-PSDB; AAX18264.
 DR
 XX
 PT New isolated vertebrate telomerase genes - used to develop products
 PT for treating cancers or for organ regeneration, nerve cell or brain
 PT cell growth following injury or bone marrow transplantation
 XX
 XX Claim 4; Fig 11b-c; 134pp; English.
 XX
 CC This sequence is a truncated human telomerase of the
 CC invention. Primers that amplify the telomerase coding sequence can be
 CC used in a method for diagnosing cancer in a patient. The telomerase can
 CC be used for detection, diagnosis and drug screening. Inhibitors of
 CC telomerase activity can be used to treat cancers such as melanomas,
 CC other skin cancers, neuroblastomas, breast carcinomas, colon carcinomas,
 CC leukaemias, lymphomas, osteosarcomas or smooth muscle cell hyperplasias
 CC or skin growths. Enhancers of telomerase may be used to stimulate stem
 CC cell proliferation and differentiation (expansion of haematopoietic stem
 CC cells could be administered in the bone marrow transplant context). As
 CC well, many tissues have stem cells. Proliferation of these cells may be
 CC useful in wound healing, hair growth, treatment of disease such as
 CC Wilms' tumour, organ regeneration or differentiation after injury or
 CC diseases, nerve cell or brain cell growth following injury.
 CC Note: The C-terminus of this sequence can be replaced by the sequence
 CC shown in AAY00653.
 XX
 SQ Sequence 617 AA;
 XX
 Query Match 93.9%; Score 107; DB 20; Length 617;
 Best Local Similarity 91.3%; Pred. No. 2.2e-08;
 Matches 21; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RQHLKRVQLRDVSEAEVRQHREA 23
 |||||:|||||
 Db 550 RQHLKRVQLRELSEAEVRQHREA 572
 |||||:|||||
 RESULT 13
 AAY25463
 ID AAY25463 standard; Protein; 622 AA.
 XX
 AC AAY25463;
 XX
 DT 22-SEP-1999 (first entry)
 XX
 DE Human CRT-1 protein #3.
 XX
 KW CRT-1; reverse transcriptase; telomerase; inhibitor; detection;
 KW telomerase activity; cancer cell; screening; human.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Protein 1..622
 FT /label= CRT-1
 FT /note= "Partial sequence, no stop codon given"
 FT
 XX W09935261-A1.
 PN
 XX 15-JUL-1999.
 PD
 XX

PF 08-JAN-1999; 99WO-JP00039.
 XX
 PR 06-MAY-1998; 98JP-0139177.
 PR 08-JAN-1998; 98JP-0013232.
 PR 30-JAN-1998; 98JP-0033584.
 XX
 PA (CHUS) CHUGAI SEIYAKU KK.
 XX
 XX Teuchiya M, Yoshida K;
 PI WPI; 1999-430393/36.
 XX DR N-PSDB; AAX88251.
 XX
 PT Novel Gene, useful in detection of telomerase activity and cancer
 PT cells as well as screening telomerase inhibitors for treatment of
 PT cancers
 XX
 PS Example 1; Page 37-39; 44pp; Japanese.
 XX
 CC This invention describes novel human CRT-1 genes and their encoded
 CC proteins containing a reverse transcriptase motif, which act as
 CC telomerase inhibitors. The gene, its encoded protein and derived
 CC antibodies can be used to provide base sequence information, detect
 CC telomerase activity and cancer cells, and to screen telomerase
 CC inhibitors. The detection method is simple and effective.
 XX
 SQ Sequence 622 AA;
 XX
 Query Match 93.9%; Score 107; DB 20; Length 622;
 Best Local Similarity 91.3%; Pred. No. 2.2e-08;
 Matches 21; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RQHLKRVQLRDVSEAEVRQHREA 23
 |||||:|||||
 Db 80 RQHLKRVQLRELSEAEVRQHREA 102
 |||||:|||||
 RESULT 14
 AAW46997
 ID AAW46997 standard; Protein; 807 AA.
 XX
 AC AAW46997;
 XX
 DT 13-AUG-1998 (first entry)
 XX
 DE Human telomerase reverse transcriptase Delta182 variant.
 XX
 KW Human; telomerase reverse transcriptase; hTERT; TRT; diagnosis;
 KW prognosis; cell proliferation; cancer; ageing; ribonucleoprotein.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN GB2317891-A.
 XX
 PD 08-APR-1998.
 XX
 PF 01-OCT-1997; 97GB-0020890.
 XX
 PR 14-AUG-1997; 97US-0915503.
 PR 01-OCT-1996; 96US-0724643.
 PR 18-APR-1997; 97US-0844419.
 PR 25-APR-1997; 97US-0846017.
 PR 06-MAY-1997; 97US-0851843.
 PR 09-MAY-1997; 97US-0854050.
 PR 14-AUG-1997; 97US-0911312.
 PR 14-AUG-1997; 97US-0912951.
 XX
 PA (GERO-) GERON CORP.
 PA (UYTE-) UNIV TECHNOLOGY CORP.
 XX
 XX Andrews WH, Cech TR, Chapman KB, Harley C, Lingner J;
 PI Morin GB, Nakamura T, Harley CB;

us-08-854-050-113.rag

Thu Nov 13 12:06:58 2003

XX Bowtell D, Kilian A;
 PI WPI; 1999-106060/09.
 DR N-PSDB; AAX18265.
 XX New isolated vertebrate telomerase genes - used to develop products
 PT for treating cancers or for organ regeneration, nerve cell or brain
 PT cell growth following injury or bone marrow transplantation
 XX
 XX Claim 4; Fig 11d-e; 134pp; English.
 XX This sequence is a truncated human telomerase of the
 CC invention. Primers that amplify the telomerase coding sequence can be
 CC used in a method for diagnosing cancer in a patient. The telomerase can
 CC be used for detection, diagnosis and drug screening. Inhibitors of
 CC telomerase activity can be used to treat cancers such as melanomas, other
 CC skin cancers, neuroblastomas, breast carcinomas, colon carcinomas,
 CC leukaemias, lymphomas, osteosarcomas or smooth muscle cell hyperplasias
 CC or skin growths. Enhancers of telomerase may be used to stimulate stem
 CC cell proliferation and differentiation (expansion of haematopoietic stem
 CC cells could be administered in the bone marrow transplant context). As
 CC well, many tissues have stem cells. Proliferation of these cells may be
 CC useful in wound healing, hair growth, treatment of disease such as Wilm's
 CC tumour, organ regeneration or differentiation after injury or diseases,
 CC nerve cell or brain cell growth following injury.
 XX SQ Sequence 807 AA;
 Query Match 93.9%; Score 107; DB 20; Length 807;
 Best Local Similarity 91.3%; Pred. No. 3e-08; Indels 0; Gaps 0;
 Matches 21; Conservative 2; Mismatches 0;
 OY 1 RQHLKRVQLRDVSEAEVROHREA 23
 |||||:|||||
 Db 590 RQHLKRVQLRSEAEVROHREA 612

Search completed: November 12, 2003, 19:47:13
 Job time : 28.6415 secs

XX The present sequence represents a human telomerase reverse transcriptase
 DR (hTERT) variant from the present invention. The present invention also
 DR describes the following methods: (A) determining whether a test compound
 XX is a modulator of hTERT, by detecting the change in hTERT recombinant
 PT is a modulator of hTERT, on administration of the compound; (B)
 PT protein or polynucleotide, on administration of the compound; (C) detection of
 XX preparation of recombinant telomerase by contacting a protein
 XX the hTERT RNA or protein in a sample by binding a relevant probe to the
 XX sample and detecting the complex formed or in the case of RNA detection,
 XX amplifying the product and correlating the presence of complex or
 XX amplification product with presence of hTERT in the sample; and (D)
 XX increasing the proliferation of a vertebrate cell by increasing hTERT
 XX expression; and (E) the use of an agent that causes an increase in cell
 XX vertebrate cell proliferation to create a medicament that inhibits
 XX ageing. A protein preparation of hTERT and the polynucleotide encoding
 XX hTERT can be used in the manufacture of medicaments for inhibiting the
 XX effect of ageing or cancer. Inhibitors of telomerase activity can be
 XX used to treat conditions that are associated with high telomerase
 XX activity. A protein preparation of hTERT can also be used in the new
 XX methods.
 XX SQ Sequence 807 AA;
 Query Match 93.9%; Score 107; DB 19; Length 807;
 Best Local Similarity 91.3%; Pred. No. 3e-08; Indels 0; Gaps 0;
 Matches 21; Conservative 2; Mismatches 0;
 OY 1 RQHLKRVQLRDVSEAEVROHREA 23
 |||||:|||||
 Db 590 RQHLKRVQLRSEAEVROHREA 612

RESULT 15
 AAY00637
 ID AAY00637 standard; Protein; 807 AA.
 XX AC AAY00637;
 XX DT 26-JUL-1999 (first entry)
 XX DE N-terminal truncated telomerase protein sequence.
 XX Telomerase; human; cancer; diagnosis; melanoma; skin cancer; leukaemia;
 KW neuroblastoma; breast carcinoma; colon carcinoma; lymphoma; osteosarcoma;
 KW smooth muscle cell hyperplasia; stem cell proliferation; Wilm's tumour;
 KW stem cell differentiation; organ regeneration; organ differentiation.
 XX Homo sapiens.
 OS Synthetic.
 PN WO9901560-A1.
 XX PD 14-JAN-1999.
 XX PF 01-JUL-1998; 98WO-US13835.
 XX PR 09-SEP-1997; 97US-0058287.
 XX PR 01-JUL-1997; 97US-0051410.
 XX PR 21-JUL-1997; 97US-0053018.
 XX PR 21-JUL-1997; 97US-0053329.
 XX PR 04-JUG-1997; 97US-0054642.
 XX PR (CAMP-) CAMBIA BIOSYSTEMS LLC.

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 12, 2003, 19:43:50 ; Search time 10.7044 Seconds
(without alignments)
90.911 Million cell updates/sec

Title: US-08-854-050-113

Perfect score: 114

Sequence: 1 RQHLKRVQLRDVSEAEVRQHREA 23

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*

1: /cgn2_6/ptodata/1/iaa/5A COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/5B COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/6A COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PTUS COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Match	Length	DB ID	Description
1	114	100.0	23	3	US-08-851-843A-113	Sequence 113, App
2	114	100.0	23	3	US-08-851-843A-233	Sequence 233, App
3	114	100.0	23	3	US-08-854-050-113	Sequence 113, App
4	114	100.0	23	4	US-09-430-323-113	Sequence 113, App
5	114	100.0	23	4	US-08-912-951-114	Sequence 114, App
6	107	93.9	129	3	US-08-851-843A-67	Sequence 67, App
7	107	93.9	129	3	US-08-851-843A-13	Sequence 13, App
8	107	93.9	129	3	US-08-854-050-67	Sequence 67, App
9	107	93.9	129	4	US-09-430-323-67	Sequence 67, App
10	107	93.9	129	4	US-08-912-951-13	Sequence 13, App
11	107	93.9	259	3	US-08-974-549A-10	Sequence 10, App
12	107	93.9	259	3	US-08-912-951-10	Sequence 10, App
13	107	93.9	515	3	US-08-974-549A-604	Sequence 604, App
14	107	93.9	515	4	US-08-912-951-318	Sequence 318, App
15	107	93.9	530	3	US-08-974-549A-603	Sequence 603, App
16	107	93.9	530	4	US-08-912-951-317	Sequence 317, App
17	107	93.9	564	3	US-08-851-843A-101	Sequence 101, App
18	107	93.9	564	3	US-08-974-549A-267	Sequence 267, App
19	107	93.9	564	3	US-08-854-050-101	Sequence 101, App
20	107	93.9	564	4	US-09-430-323-101	Sequence 101, App
21	107	93.9	807	3	US-08-974-549A-5	Sequence 5, App
22	107	93.9	807	4	US-08-912-951-5	Sequence 5, App
23	107	93.9	1003	3	US-08-851-843A-217	Sequence 217, App
24	107	93.9	1003	3	US-08-974-549A-336	Sequence 336, App
25	107	93.9	1003	3	US-08-854-050-217	Sequence 217, App
26	107	93.9	1003	4	US-09-430-323-217	Sequence 217, App
27	107	93.9	1132	3	US-08-851-843A-225	Sequence 225, App

Sequence 2, Appli
Sequence 344, App
Sequence 225, App
Sequence 225, App
Sequence 2, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 611, App
Sequence 323, App
Sequence 613, App
Sequence 325, App
Sequence 612, App
Sequence 324, App
Sequence 600, App
Sequence 314, App
Sequence 628, App
Sequence 334, App

28 107 93.9 1132 3 US-08-974-549A-2
29 107 93.9 1132 3 US-08-974-549A-144
30 107 93.9 1132 3 US-08-854-050-225
31 107 93.9 1132 4 US-09-430-323-225
32 107 93.9 1132 4 US-09-128-354-2
33 107 93.9 1132 4 US-09-675-321-2
34 107 93.9 1132 4 US-09-052-919-2
35 107 93.9 1132 4 US-08-912-951-2
36 107 93.9 1154 3 US-08-974-549A-611
37 107 93.9 1189 3 US-08-912-951-323
38 107 93.9 1189 3 US-08-974-549A-613
39 107 93.9 1189 4 US-08-912-951-325
40 107 93.9 1200 3 US-08-974-549A-612
41 107 93.9 1200 4 US-08-912-951-324
42 107 93.9 1285 3 US-08-974-549A-600
43 107 93.9 1285 4 US-08-912-951-314
44 107 93.9 1407 3 US-08-974-549A-628
45 107 93.9 1407 4 US-08-912-951-334

ALIGNMENTS

RESULT 1

US-08-851-843A-113
; Sequence 113, Application US/08851843A
; Patent No. 6093809
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: No. 6093809el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/851,843A
; FILING DATE: 06-MAY-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002930US
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 113:

Page 2

```

; FILING DATE: 01-OCT-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-0029300S
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 113:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 23 amino acids
; TYPE: amino acid
; STRANDEDNESS: linear
; MOLECULE TYPE: peptide
; US-08-854-050-113
;
; Query Match 100.0%; Score 114; DB 3; Length 23;
; Best Local Similarity 100.0%; Pred. No. 1e-11;
; Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; Qy 1 ROHLKRVQLRDVSEAEVROHREA 23
; Db 1 ROHLKRVQLRDVSEAEVROHREA 23
;
; RESULT 4
; US-09-430-323-113
; Sequence 113, Application US/09430323
; Patent No. 6309867
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; LINGNER, JOACHIM
; NAKAMURA, TORU
; CHAPMAN, KAREN B.
; MORIN, GREGG B.
; HARLEY, CALVIN
; ANDREWS, WILLIAM H.
; TITLE OF INVENTION: NO. 6309867el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/430,323
; FILING DATE: 29-Oct-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-0029300S
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 113:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 23 amino acids
; TYPE: amino acid
; STRANDEDNESS: linear
; MOLECULE TYPE: peptide
; US-08-854-050-113
;
; Query Match 100.0%; Score 114; DB 3; Length 23;
; Best Local Similarity 100.0%; Pred. No. 1e-11;
; Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; Qy 1 ROHLKRVQLRDVSEAEVROHREA 23
; Db 1 ROHLKRVQLRDVSEAEVROHREA 23
;
; RESULT 5
; US-08-912-951-114
; Sequence 114, Application US/08912951
; Patent No. 6475789
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; LINGNER, JOACHIM
; NAKAMURA, TORU
; CHAPMAN, KAREN B.
; MORIN, GREGG B.
; HARLEY, CALVIN
; ANDREWS, WILLIAM H.
; TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT:
; NUMBER OF SEQUENCES: 335
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/912,951
; FILING DATE: 14-AUG-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; CLASSIFICATION: 435
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-0029300S
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 113:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 23 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; MOLECULE TYPE: peptide
; US-09-430-323-113
;
; Query Match 100.0%; Score 114; DB 4; Length 23;
; Best Local Similarity 100.0%; Pred. No. 1e-11;
; Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; Qy 1 ROHLKRVQLRDVSEAEVROHREA 23
; Db 1 ROHLKRVQLRDVSEAEVROHREA 23
;
; RESULT 5
; US-08-912-951-114
; Sequence 114, Application US/08912951
; Patent No. 6475789
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; LINGNER, JOACHIM
; NAKAMURA, TORU
; CHAPMAN, KAREN B.
; MORIN, GREGG B.
; HARLEY, CALVIN
; ANDREWS, WILLIAM H.
; TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT:
; NUMBER OF SEQUENCES: 335
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/912,951
; FILING DATE: 14-AUG-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; CLASSIFICATION: 435
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-0029300S
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 113:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 23 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; MOLECULE TYPE: peptide
; US-09-430-323-113

```

us-08-854-050-113.rai

Thu Nov 13 12:06:59 2003

```
;
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-0026000S
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 114:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 23 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-912-951-114

Query Match 100.0%; Score 114; DB 4; Length 23;
Best Local Similarity 100.0%; Pred. No. 1e-11;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ROHLKRVQLRDVSEAEVROHREA 23
DB 1 ROHLKRVQLRDVSEAEVROHREA 23

RESULT 6
US-08-851-843A-67
; Sequence 67, Application US/08851843A
; Patent No. 6093809
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: No. 6093809el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/851,843A
; FILING DATE: 06-MAY-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-0029300S
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300

;
; INFORMATION FOR SEQ ID NO: 67:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 129 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..129
; OTHER INFORMATION: /note= "TFT motifs from human"
; US-08-851-843A-67

Query Match 93.9%; Score 107; DB 3; Length 129;
Best Local Similarity 91.3%; Pred. No. 1e-09;
Matches 21; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 ROHLKRVQLRDVSEAEVROHREA 23
DB 49 ROHLKRVQLRELSEAEVROHREA 71

RESULT 7
US-08-974-549A-13
; Sequence 13, Application US/08974549A
; Patent No. 6166178
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin B.
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 727
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,549A
; FILING DATE: 19-NOV-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/911,312
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/912,951
; FILING DATE: 14-AUG-1997
```


us-08-854-050-113.ra1

Thu Nov 13 12:06:59 2003

```

;
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002930US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0300
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 67:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 129 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..129
; OTHER INFORMATION: /note= "TRT motifs from human"
; SEQUENCE DESCRIPTION: SEQ ID NO: 67:
;
; US-09-430-323-67
;
; Query Match 93.9%; Score 107; DB 4; Length 129;
; Best Local Similarity 91.3%; Pred. No. 1e-09; 0; Indels 0; Gaps 0;
; Matches 21; Conservative 2; Mismatches 0;
;
; QY 1 RQHLKRVQLRDVSEAEVROHREA 23
; Db 49 RQHLKRVQLRSEAEVROHREA 71
;
; RESULT 10
; US-08-912-951-13
; Sequence 13, Application US/08912951
; Patent No. 6475789
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND
; TITLE OF INVENTION: THERAPEUTIC METHODS
; NUMBER OF SEQUENCES: 335
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/912,951
; FILING DATE: 14-AUG-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; CLASSIFICATION: 435
;
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002930US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0300
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 67:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 129 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..129
; OTHER INFORMATION: /note= "TRT motifs from human"
; SEQUENCE DESCRIPTION: SEQ ID NO: 67:
;
; US-08-912-951-13
;
; Query Match 93.9%; Score 107; DB 4; Length 129;
; Best Local Similarity 91.3%; Pred. No. 1e-09; 0; Indels 0; Gaps 0;
; Matches 21; Conservative 2; Mismatches 0;
;
; QY 1 RQHLKRVQLRDVSEAEVROHREA 23
; Db 49 RQHLKRVQLRSEAEVROHREA 71
;
; RESULT 11
; US-08-974-549A-10
; Sequence 10, Application US/08974549A
; Patent No. 6166178
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 727
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,549A
;

```

;; FILING DATE: 19-NOV-1997
;; CLASSIFICATION: 536
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/724,643
;; FILING DATE: 01-OCT-1996
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/844,419
;; FILING DATE: 18-APR-1997
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/846,017
;; FILING DATE: 25-APR-1997
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/851,843
;; FILING DATE: 06-MAY-1997
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/854,050
;; FILING DATE: 09-MAY-1997
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/911,312
;; FILING DATE: 14-AUG-1997
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/912,951
;; FILING DATE: 14-AUG-1997
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/915,503
;; FILING DATE: 14-AUG-1997
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: WO PCT/US97/17618
;; FILING DATE: 01-OCT-1997
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: WO PCT/US97/17885
;; FILING DATE: 01-OCT-1997
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Apple, Randolph Ted
;; REGISTRATION NUMBER: 36,429
;; REFERENCE/DOCKET NUMBER: 015389-002610US
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (415) 576-0200
;; TELEFAX: (415) 576-0300
;; INFORMATION FOR SEQ ID NO: 10:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 259 amino acids
;; TYPE: amino acid
;; STRANDEDNESS:
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; FEATURE:
;; NAME/KEY: Protein
;; LOCATION: 1..259
;; OTHER INFORMATION: /note= "protein encoded by clone 712562"
US-08-974-549A-10

Query Match 93.9%; Score 107; DB 3; Length 259;
Best Local Similarity 91.3%; Pred. No. 2.3e-09;
Matches 21; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 ROHLKRVQLRDVSEAEVRQHREA 23
Db 42 ROHLKRVQLRELSEAEVRQHREA 64

RESULT 12
US-08-912-951-10
; Sequence 10, Application US/08912951
; Patent No. 6475789
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin
; APPLICANT: Andrews, William H.

;; TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND
;; TITLE OF INVENTION: THERAPEUTIC METHODS
;; NUMBER OF SEQUENCES: 335
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Townsend and Townsend and Crew LLP
;; STREET: Two Embarcadero Center, 8th Floor
;; CITY: San Francisco
;; STATE: California
;; COUNTRY: United States of America
;; ZIP: 94111
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/912,951
;; FILING DATE: 14-AUG-1997
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/854,050
;; FILING DATE: 09-MAY-1997
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/851,843
;; FILING DATE: 06-MAY-1997
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/846,017
;; FILING DATE: 25-APR-1997
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/844,419
;; FILING DATE: 18-APR-1997
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/724,643
;; FILING DATE: 01-OCT-1996
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Apple, Randolph T.
;; REGISTRATION NUMBER: 36,429
;; REFERENCE/DOCKET NUMBER: 015389-002600US
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (415) 576-0200
;; TELEFAX: (415) 576-0300
;; INFORMATION FOR SEQ ID NO: 10:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 259 amino acids
;; TYPE: amino acid
;; STRANDEDNESS:
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; FEATURE:
;; NAME/KEY: Protein
;; LOCATION: 1..259
;; OTHER INFORMATION: /note= "protein encoded by clone 712562"
US-08-912-951-10

Query Match 93.9%; Score 107; DB 4; Length 259;
Best Local Similarity 91.3%; Pred. No. 2.3e-09;
Matches 21; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 ROHLKRVQLRDVSEAEVRQHREA 23
Db 42 ROHLKRVQLRELSEAEVRQHREA 64

RESULT 13
US-08-974-549A-604
; Sequence 604, Application US/08974549A
; Patent No. 6166178
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin
; APPLICANT: Andrews, William H.

OTHER INFORMATION: glutathione-S-transferase sequence,
OTHER INFORMATION: thrombin cleavage sequence, recognition
OTHER INFORMATION: sequence for heart muscle protein
OTHER INFORMATION: kinase, residues introduced by cloning
OTHER INFORMATION: and hTERT protein fragment"
US-08-974-549A-604

Query Match 93.9%; Score 107; DB 3; Length 515;
Best Local Similarity 91.3%; Pred. No. 5.2e-09;
Matches 21; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RQHLKRVQVLDVSEAEVQRHREA 23
Db 278 RQHLKRVQVLDVSEAEVQRHREA 300

RESULT 14
US-08-912-951-318
Sequence 318, Application US/08912951
Patent No. 6475789
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin
APPLICANT: Andrews, William H.
TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND
TITLE OF INVENTION: THERAPEUTIC METHODS
NUMBER OF SEQUENCES: 335
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/912,951
FILING DATE: 14-AUG-1997
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-00260005
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200

APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin B.
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,549A
FILING DATE: 19-NOV-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-00261005
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0300
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 604:
SEQUENCE CHARACTERISTICS:
LENGTH: 515 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..515
OTHER INFORMATION: /note= "fusion protein composed of


```
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 318:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 515 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-912-951-318

Query Match          93.9%; Score 107; DB 4; Length 515;
Best Local Similarity 91.3%; Pred. No. 5.2e-09;
Matches 21; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RQHLKRVQLRDVSEAEVQRHREA 23
   |||||:|||||
Db 278 RQHLKRVQLRELSEAEVQRHREA 300

RESULT 15
US-08-974-549A-603
; Sequence 603, Application US/08974549A
; Patent No. 6166178
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin B.
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 727
; CORRESPONDENCE ADDRESS:
; ADDRESS: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,549A
; FILING DATE: 19-NOV-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/911,312
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/912,951
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/915,503
; FILING DATE: 14-AUG-1997
```

```
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/17618
; FILING DATE: 01-OCT-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/17885
; FILING DATE: 01-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph Ted
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002610US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 603:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 530 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..530
; OTHER INFORMATION: /note= "fusion protein composed of
; glutathione-S-transferase sequence,
; thrombin cleavage sequence, recognition
; sequence for heart muscle protein
; kinase, residues introduced by cloning,
; eight consecutive His residues and hTBT
; protein fragment"
US-08-974-549A-603

Query Match          93.9%; Score 107; DB 3; Length 530;
Best Local Similarity 91.3%; Pred. No. 5.4e-09;
Matches 21; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RQHLKRVQLRDVSEAEVQRHREA 23
   |||||:|||||
Db 289 RQHLKRVQLRELSEAEVQRHREA 311
```

Search completed: November 12, 2003, 19:53:27
Job time : 11.7044 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 12, 2003, 19:47:20 ; Search time 18.3711 Seconds
(without alignments)
215.025 Million cell updates/sec

Title: US-08-854-050-113

Perfect score: 114
Sequence: 1 RQHLKRVQLRDVSEAEVRQHREA 23

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 644079 seqs, 171749292 residues

Total number of hits satisfying chosen parameters: 644079

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	114	100.0	23	10	US-09-843-676-113 Sequence 113, App
2	114	100.0	23	10	US-09-843-676-113 Sequence 113, App
3	114	100.0	23	11	US-09-438-486-113 Sequence 113, App
4	114	100.0	23	15	US-10-053-758-113 Sequence 113, App
5	114	100.0	23	15	US-10-054-295-113 Sequence 113, App
6	114	100.0	23	15	US-10-054-295-113 Sequence 113, App
7	114	100.0	23	15	US-10-044-692-114 Sequence 114, App
8	114	100.0	23	15	US-10-044-692-114 Sequence 114, App
9	107	93.9	129	10	US-09-843-676-67 Sequence 67, Appl
10	107	93.9	129	10	US-09-843-676-67 Sequence 67, Appl
11	107	93.9	129	11	US-09-438-486-67 Sequence 67, Appl
12	107	93.9	129	15	US-10-053-758-67 Sequence 67, Appl
13	107	93.9	129	15	US-10-054-295-67 Sequence 67, Appl
14	107	93.9	129	15	US-10-054-295-67 Sequence 67, Appl
15	107	93.9	129	15	US-10-044-692-13 Sequence 13, Appl

16	107	93.9	129	15	US-10-044-539-13	Sequence 13, Appl
17	107	93.9	259	15	US-10-044-692-10	Sequence 10, Appl
18	107	93.9	259	15	US-10-044-539-10	Sequence 10, Appl
19	107	93.9	291	12	US-10-282-960-3	Sequence 3, Appl
20	107	93.9	437	15	US-10-294-778-2	Sequence 2, Appl
21	107	93.9	438	15	US-10-294-778-10	Sequence 10, Appl
22	107	93.9	500	12	US-10-282-960-81	Sequence 81, Appl
23	107	93.9	515	15	US-10-044-692-318	Sequence 318, App
24	107	93.9	515	15	US-10-044-539-318	Sequence 318, App
25	107	93.9	530	15	US-10-044-692-317	Sequence 317, App
26	107	93.9	530	15	US-10-044-539-317	Sequence 317, App
27	107	93.9	564	10	US-09-843-676-101	Sequence 101, App
28	107	93.9	564	10	US-09-766-253-101	Sequence 101, App
29	107	93.9	564	11	US-09-438-486-101	Sequence 101, App
30	107	93.9	564	15	US-10-053-758-101	Sequence 101, App
31	107	93.9	564	15	US-10-054-295-101	Sequence 101, App
32	107	93.9	564	15	US-10-054-611-101	Sequence 101, App
33	107	93.9	622	15	US-10-294-778-12	Sequence 12, Appl
34	107	93.9	807	15	US-10-044-692-5	Sequence 5, Appl
35	107	93.9	807	15	US-10-044-539-5	Sequence 5, Appl
36	107	93.9	1003	10	US-09-843-676-217	Sequence 217, App
37	107	93.9	1003	11	US-09-438-486-217	Sequence 217, App
38	107	93.9	1003	15	US-10-053-758-217	Sequence 217, App
39	107	93.9	1003	15	US-10-054-295-217	Sequence 217, App
40	107	93.9	1003	15	US-10-054-611-217	Sequence 217, App
41	107	93.9	1132	10	US-09-990-080-2	Sequence 2, Appl
42	107	93.9	1132	10	US-09-749-728B-31	Sequence 31, Appl
43	107	93.9	1132	10	US-09-843-676-225	Sequence 225, App
44	107	93.9	1132	10	US-09-953-052-2	Sequence 2, Appl
45	107	93.9	1132	12	US-10-295-681-57	Sequence 57, Appl

ALIGNMENTS

RESULT 1
US-09-843-676-113
; Sequence 113, Application US/09843676
; Patent No. US20020164786A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin
; Andrews, William H.
; TITLE OF INVENTION: No. US20020164786A1el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/843,676
; FILING DATE: 26-Apr-2001
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/724,643

FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 113:
SEQUENCE CHARACTERISTICS:
LENGTH: 23 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 113:
S-09-843-676-113

Query Match 100.0%; Score 114; DB 10; Length 23;
Best Local Similarity 100.0%; Pred. No. 2.3e-10;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 RQHLKRVQLRDVSEAEVQHQREA 23
|||||
1 RQHLKRVQLRDVSEAEVQHQREA 23

RESULT 2
S-09-766-253-113
Sequence 113, Application US/09766253
Publication No. US2002018741A1
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: No. US2002018741A1el Telomerase
NUMBER OF SEQUENCES: 171
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
CURRENT APPLICATION NUMBER: US/09/766,253
FILING DATE: 19-Jan-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/846,017
FILING DATE: 1997-04-25
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002920US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 113:
SEQUENCE CHARACTERISTICS:
LENGTH: 23 amino acids

```

; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-438-486-113

Query Match      100.0%; Score 114; DB 11; Length 23;
Best Local Similarity 100.0%; Pred. No. 2.3e-10;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RQHLKRVQLRDVSEAEVROHREA 23
   |||||
Db 1 RQHLKRVQLRDVSEAEVROHREA 23
   |||||

RESULT 4
US-10-053-758-113
; Sequence 113, Application US/10053758
; Publication No. US20030032075A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
;   Lingner, Joachim
;   Nakamura, Toru
;   Chapman, Karen B.
;   Morin, Gregg B.
;   Harley, Calvin
;   Andrews, William H.
; TITLE OF INVENTION: NO. US20030032075A1el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/053,758
; FILING DATE: 18-Jan-2002
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002930US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 113:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 23 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 113:
US-10-053-758-113

Query Match      100.0%; Score 114; DB 15; Length 23;
Best Local Similarity 100.0%; Pred. No. 2.3e-10;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RQHLKRVQLRDVSEAEVROHREA 23
   |||||
Db 1 RQHLKRVQLRDVSEAEVROHREA 23
   |||||

RESULT 6
```

```

Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RQHLKRVQLRDVSEAEVROHREA 23
   |||||
Db 1 RQHLKRVQLRDVSEAEVROHREA 23
   |||||

RESULT 5
US-10-054-295-113
; Sequence 113, Application US/10054295
; Publication No. US20030044953A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
;   Lingner, Joachim
;   Nakamura, Toru
;   Chapman, Karen B.
;   Morin, Gregg B.
;   Harley, Calvin
;   Andrews, William H.
; TITLE OF INVENTION: NO. US20030044953A1el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/054,295
; FILING DATE: 18-Jan-2002
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/854,050
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002930US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 113:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 23 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 113:
US-10-054-295-113

Query Match      100.0%; Score 114; DB 15; Length 23;
Best Local Similarity 100.0%; Pred. No. 2.3e-10;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RQHLKRVQLRDVSEAEVROHREA 23
   |||||
Db 1 RQHLKRVQLRDVSEAEVROHREA 23
   |||||
```

us-08-854-050-113.rapb

Thu Nov 13 12:07:01 2003

```

US-10-054-611-113
; Sequence 113, Application US/10054611
; Publication No. US20030059787A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin
; Andrews, William H.
; TITLE OF INVENTION: NO. US20030059787A1el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/10/054,611
; FILING DATE: 18-Jan-2002
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/854,050
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-0029310US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 113:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 23 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 113:
US-10-054-611-113
Query Match 100.0%; Score 114; DB 15; Length 23;
Best Local Similarity 100.0%; Pred. No. 2.3e-10;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RQHLKRVQLRDVSEAEVRQHREA 23
DB 1 RQHLKRVQLRDVSEAEVRQHREA 23

RESULT 7
US-10-044-692-114
; Sequence 114, Application US/10044692
; Publication No. US20030096344A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin
; Andrews, William H.
; TITLE OF INVENTION: HUMAN TETRAHYDROCATALYTIC SUBUNIT: DIAGNOSTIC AND
; THERAPEUTIC METHODS
; NUMBER OF SEQUENCES: 335
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/10/044,692
; FILING DATE: 11-Jan-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/912,951
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-0026000US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 114:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 23 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 114:
US-10-044-692-114
Query Match 100.0%; Score 114; DB 15; Length 23;
Best Local Similarity 100.0%; Pred. No. 2.3e-10;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RQHLKRVQLRDVSEAEVRQHREA 23
DB 1 RQHLKRVQLRDVSEAEVRQHREA 23

RESULT 8
US-10-044-539-114
; Sequence 114, Application US/10044539
; Publication No. US2003010093A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin
; Andrews, William H.

```

```

; TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND
; THERAPEUTIC METHODS
; NUMBER OF SEQUENCES: 335
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/044,539
; FILING DATE: 11-Jan-2002
; CLASSIFICATION: 435
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/912,951
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-00260005
;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
;
; INFORMATION FOR SEQ ID NO: 114:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 23 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
;
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 114:
US-10-044-539-114
;
; Query Match 100.0%; Score 114; DB 15; Length 23;
; Best Local Similarity 100.0%; Pred. No. 2.3e-10;
; Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; Qy 1 RQHLKRVQLRDVSEAEVROHREA 23
; Db 1 RQHLKRVQLRDVSEAEVROHREA 23
;
; RESULT 9
; US-09-843-676-67
; Sequence 67, Application US/09843676
; Patent No. US20020164786A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin
; Andrews, William H.
;
; TITLE OF INVENTION: No. US20020164786A1el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:

```

```

; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/843,676
; FILING DATE: 26-Apr-2001
; CLASSIFICATION: 536
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-00293005
;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
;
; INFORMATION FOR SEQ ID NO: 67:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 129 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..129
; OTHER INFORMATION: /note= "TRT motifs from human"
; SEQUENCE DESCRIPTION: SEQ ID NO: 67:
US-09-843-676-67
;
; Query Match 93.9%; Score 107; DB 10; Length 129;
; Best Local Similarity 91.3%; Pred. No. 1.6e-08;
; Matches 21; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
;
; Qy 1 RQHLKRVQLRDVSEAEVROHREA 23
; Db 49 RQHLKRVQLRDVSEAEVROHREA 71
;
; RESULT 10
; US-09-766-253-67
; Sequence 67, Application US/09766253
; Publication No. US20020187471A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin
; Andrews, William H.
;
; TITLE OF INVENTION: No. US20020187471A1el Telomerase
; NUMBER OF SEQUENCES: 171
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California

```

us-08-854-050-113.rapb

Thu Nov 13 12:07:01 2003

COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/766,253
FILING DATE: 19-Jan-2001
CLASSIFICATION: <unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/846,017
FILING DATE: 1977-04-25
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002920US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 67:
SEQUENCE CHARACTERISTICS:
LENGTH: 129 amino acids
TYPE: amino acid
STRANDEDNESS: <unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..129
OTHER INFORMATION: /note= "TRT motifs from human"
SEQUENCE DESCRIPTION: SEQ ID NO: 67:
US-09-766-253-67
Query Match 93.9%; Score 107; DB 10; Length 129;
Best Local Similarity 91.3%; Pred. No. 1.6e-08;
Matches 21; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 RQHLKRVQLRDVSEAEVQRHREA 23
Db 49 RQHLKRVQLRELSEAEVQRHREA 71
RESULT 11
US-09-438-486-67
Sequence 67, Application US/09438486
Publication No. US20030009019A1
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin
APPLICANT: Andrews, William H.
TITLE OF INVENTION: NO. US20030009019A1el Telomerase
NUMBER OF SEQUENCES: 223
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/438,486
FILING DATE: 12-NOV-1999
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002931US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 67:
SEQUENCE CHARACTERISTICS:
LENGTH: 129 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..129
OTHER INFORMATION: /note= "TRT motifs from human"
US-09-438-486-67
Query Match 93.9%; Score 107; DB 11; Length 129;
Best Local Similarity 91.3%; Pred. No. 1.6e-08;
Matches 21; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 RQHLKRVQLRDVSEAEVQRHREA 23
Db 49 RQHLKRVQLRELSEAEVQRHREA 71
RESULT 12
US-10-053-758-67
Sequence 67, Application US/10053758
Publication No. US20030032075A1
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin
APPLICANT: Andrews, William H.
TITLE OF INVENTION: NO. US20030032075A1el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS


```

; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/10/053,758
; APPLICATION NUMBER: US/10/053,758
; FILING DATE: 18-Jan-2002
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002930US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 67:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 129 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..129
; OTHER INFORMATION: /note= "TRT motifs from hum
; SEQUENCE DESCRIPTION: SEQ ID NO: 67:
US-10-053-758-67

Query Match 93.9%; Score 107; DB 15; Length
Best Local Similarity 91.3%; Pred. No. 1.6e-08;
Matches 21; Conservative 2; Mismatches 0; Indels

QY 1 ROHLKRVQLRDVSEAEVQRHEA 23
DB 49 ROHLKRVQLRELSEAEVQRHEA 71

RESULT 13
US-10-054-295-67
; Sequence 67, Application US/10054295
; Publication NO. US20030044953A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin
; Andrews, William H.
; TITLE OF INVENTION: No. US20030044953A1el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:

```

```

: APPLICATION NUMBER: US/10/054,295
: FILING DATE: 18-Jan-2002
: CLASSIFICATION: 536
: PRIORITY INFORMATION DATA:
: APPLICATION NUMBER: 08/854,050
: FILING DATE: <Unknown>
: APPLICATION NUMBER: US 08/846,017
: FILING DATE: 25-APR-1997
: APPLICATION NUMBER: US 08/844,419
: FILING DATE: 18-APR-1997
: APPLICATION NUMBER: US 08/724,643
: FILING DATE: 01-OCT-1996
: ATTORNEY/AGENT INFORMATION:
: NAME: Apple, Randolph T.
: REGISTRATION NUMBER: 36,429
: REFERENCE/DOCKET NUMBER: 015389-0029330US
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (415) 576-0200
: TELEFAX: (415) 576-0300
: INFORMATION FOR SEQ ID NO: 67:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 129 amino acids
: TYPE: amino acid
: STRANDEDNESS: <Unknown>
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: FEATURE:
: NAME/KEY: Peptide
: LOCATION: 1..129
: OTHER INFORMATION: /note= "TRT motifs from human"
: SEQUENCE DESCRIPTION: SEQ ID NO: 67:
US-10-054-295-67

Query Match          93.9%   Score 107;   DB 15;   Length 129
Best Local Similarity 91.3%;   Pred. No. 1.6e-08;
Matches 21;   Conservative 2;   Mismatches 0;   Indels

Qy  1  ROHLKRVQLRDVSEAEVRQHREA 23
      |||||:|||||:|||||
Db  49  ROHLKRVQLRSEAEVRQHREA 71

RESULT 14
US-10-054-611-67
: Sequence 67, Application US/10054611
: Publication No. US20030059787A1
: GENERAL INFORMATION:
: APPLICANT: Cech, Thomas R.
:             Lingner, Joachim
:             Nakamura, Toru
:             Chapman, Karen B.
:             Morin, Gregg B.
:             Harley, Calvin
:             Andrews, William H.
: TITLE OF INVENTION: No. US20030059787A1el Telomerase
: NUMBER OF SEQUENCES: 225
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Townsend and Townsend and Crew LLP
: STREET: Two Embarcadero Center, 8th Floor
: CITY: San Francisco
: STATE: California
: COUNTRY: United States of America
: ZIP: 94111
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/10/054,611
: FILING DATE: 18-Jan-2002
: CLASSIFICATION: 536
: PRIOR APPLICATION DATA:

```

us-08-854-050-113.rapb

Thu Nov 13 12:07:01 2003

```

APPLICATION NUMBER: 08/854,050
FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/846,017
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 67:
SEQUENCE CHARACTERISTICS:
LENGTH: 129 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..129
OTHER INFORMATION: /note= "TRT motifs from human"
SEQUENCE DESCRIPTION: SEQ ID NO: 67:
US-10-054-611-67

Query Match          93.9%; Score 107; DB 15; Length 129;
Best Local Similarity 91.3%; Pred. NO. 1.6e-08;
Matches 21; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RQHLKRVQLRDVSEAEVQHQREA 23
   |||||:|||||
Db 49 RQHLKRVQLRELSEAEVQHQREA 71

FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002600US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 129 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..129
OTHER INFORMATION: /note= "TRT motifs from human"
SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-10-044-692-13

Query Match          93.9%; Score 107; DB 15; Length 129;
Best Local Similarity 91.3%; Pred. NO. 1.6e-08;
Matches 21; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RQHLKRVQLRDVSEAEVQHQREA 23
   |||||:|||||
Db 49 RQHLKRVQLRELSEAEVQHQREA 71

Search completed: November 12, 2003, 19:55:47
Job time : 19.3711 secs

```

```

APPLICATION NUMBER: 08/854,050
FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 67:
SEQUENCE CHARACTERISTICS:
LENGTH: 129 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..129
OTHER INFORMATION: /note= "TRT motifs from human"
SEQUENCE DESCRIPTION: SEQ ID NO: 67:
US-10-054-611-67

Query Match          93.9%; Score 107; DB 15; Length 129;
Best Local Similarity 91.3%; Pred. NO. 1.6e-08;
Matches 21; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RQHLKRVQLRDVSEAEVQHQREA 23
   |||||:|||||
Db 49 RQHLKRVQLRELSEAEVQHQREA 71

RESULT 15
US-10-044-692-13
Sequence 13, Application US/10044692
Publication No. US20030096344A1
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND
THERAPEUTIC METHODS
NUMBER OF SEQUENCES: 335
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/044,692
FILING DATE: 11-Jan-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/912,951
FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/854,050

```

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 12, 2003, 19:43:04 ; Search time 8.96855 Seconds
(without alignments)
246.626 Million cell updates/sec

Title: US-08-854-050-113
Perfect score: 114
Sequence: 1 RQHLKRVQLRDVSEAEVRQHREA 23

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 76:.*
1: PIR1.*
2: PIR2.*
3: PIR3.*
4: PIR4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	107	93.9	1132	2 T03844	telomerase catalyt
2	52.5	46.1	1071	2 F81979	carbamoyl-phosphat
3	52	45.6	1071	2 D81035	carbamoyl-phosphat
4	49.5	43.4	324	2 E85513	probable integrase
5	49.5	43.4	324	2 G90662	transcription elon
6	48	42.1	162	2 S26176	cobalamin adenosy
7	47	41.2	221	2 G97695	hypothetical prote
8	47	41.2	270	2 G71061	hypothetical prote
9	47	41.2	568	2 T25859	hypothetical prote
10	47	41.2	643	2 H87038	hypothetical prote
11	46.5	40.8	803	2 E82045	hypothetical prote
12	46	40.4	745	2 T12528	aspartokinase II/h
13	45.5	39.9	335	2 H81887	hypothetical prote
14	45.5	39.9	387	1 RSBPI2	probable transposa
15	45.5	39.9	387	2 A33457	integrase - phage
16	45.5	39.9	495	2 D70505	prophage DLP12 int
17	45.5	39.9	655	2 G87306	probable HflX - My
18	45	39.5	638	2 E70528	threonyl-tRNA synt
19	44	38.6	256	2 B82097	conserved hypotet
20	44	38.6	763	2 S46678	hypothetical prote
21	44	38.6	858	2 S15762	neurofilament trip
22	44	38.6	881	2 I84737	kinesin heavy chai
23	44	38.6	963	1 A41919	trichohyalin - she
24	43.5	38.2	1549	1 A40691	acetyltransferase
25	43	37.7	181	2 A12976	hypothetical prote
26	43	37.7	181	2 B98306	statamin gene fami
27	43	37.7	185	2 I51696	hypothetical prote
28	43	37.7	465	2 F71028	El protein - human
29	43	37.7	609	2 S36569	

30	43	37.7	688	2 S50580	hypothetical prote
31	43	37.7	844	2 C28667	DNA mismatch repai
32	43	37.7	857	2 E98107	DNA mismatch repai
33	43	37.7	913	2 A82587	translation initia
34	43	37.7	913	2 B97369	translation initia
35	43	37.7	1093	2 A47212	transcription fact
36	43	37.7	1302	2 T20767	hypothetical prote
37	43	37.7	1707	2 AH2085	two-component hybr
38	43	37.7	1767	2 T20766	hypothetical prote
39	42.5	37.3	288	2 S22628	hypothetical prote
40	42.5	37.3	335	2 F82016	probable transposa
41	42.5	37.3	488	2 G87033	probable ATP/GTP-b
42	42.5	37.3	497	2 T35116	hypothetical prote
43	42.5	37.3	518	2 S72938	hflX protein - Myc
44	42.5	37.3	814	2 A70399	conserved hypotet
45	42	36.8	191	2 E69495	conserved hypotet

ALIGNMENTS

RESULT 1

T03844
telomerase catalytic chain - human
N:Alternate names: telomerase reverse transcriptase
C:Species: Homo sapiens (man)
C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 08-Oct-1999
C:Accession: T03844
R:Nakamura, T.M.; Morin, G.B.; Chapman, K.B.; Weinrich, S.L.; Andrews, W.H.; Lingner, J.
Science 277, 955-959, 1997
A:Title: Telomerase catalytic subunit homologs from fission yeast and human.
A:Reference number: 215111; MUID:97400623; PMID:9252327
A:Accession: T03844
A>Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-1132 <NAK>
A:Cross-references: EMBL:AF015950; NID:g2330016; PIDN:AACS1672.1; PID:g2330017
A:Experimental source: Kidney
C:Genetics:
A:Gene: TRT
A:Map position: 5p

Query Match 93.9%; Score 107; DB 2; Length 1132;
Best Local Similarity 91.3%; Pred. No. 9.6e-08;
Matches 21; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RQHLKRVQLRDVSEAEVRQHREA 23
|||||||:|||||||
Db 590 RQHLKRVQLRSELSEAEVRQHREA 612

RESULT 2

F81979
carbamoyl-phosphate synthase (glutamine-hydrolyzing) (EC 6.3.5.5) large chain NMA0602 [1
C:Species: Neisseria meningitidis
C:Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001
C:Accession: F81979
R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel
; Holroyd, S.; Jagers, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,
Nature 404, 502-506, 2000
A:Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.
A:Reference number: A81775; MUID:20222556; PMID:10761919
A:Accession: F81979
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1071 <PAR>
A:Cross-references: GB:AL162753; GB:AL157959; NID:g7379120; PIDN:CAB83892.1; PID:g737933
A:Experimental source: serogroup A, strain Z2491
C:Genetics:
A:Gene: carb; NMA0602
C:Superfamily: carbamoyl-phosphate synthase (glutamine-hydrolyzing) large chain; biotin
C:Keywords: ligase

G90662
probable integrase [imported] - Escherichia coli (strain O157:H7, substrain RMD 0509952)
C:Species: Escherichia coli
C:Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 17-May-2002
C:Accession: G90662
R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G. Sasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genomic reference number: A99629; MUID:21156231; PMID:11258796
A:Accession: G90662
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-324 <HAY>
A:Cross-references: GB:BA000007; PIDN:BA833694.1; PID:G13359728; GSPDB:GN00154
A:Experimental source: strain O157:H7, substrain RMD 0509952
C:Genetics:
A:Gene: ECs0271
C:Superfamily: phage P22 integrase

Query Match 43.4%; Score 49.5; DB 2; Length 324;
Best Local Similarity 33.3%; Pred. No. 9;
Matches 10; Conservative 7; Mismatches 4; Indels 9; Gaps 1;

QY 2 QHLKRVQLRDVSEAEV-----RQHRE 22
DB 25 QHFAGMQLRDITESKIYSAMQKMTNRREE 54

RESULT 6
S26176
transcription elongation factor greA - Rickettsia prowazekii
N:Alternate names: RP861
C:Species: Rickettsia prowazekii
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 03-Nov-2000
C:Accession: S26176; E71648; S21472
R:Marka, G.L.; Wood, D.O.
Nucleic Acids Res. 20, 3785, 1992
A:Title: Nucleotide sequence of the Rickettsia prowazekii greA homolog.
A:Reference number: S26176; MUID:92350688; PMID:1641348
A:Accession: S26176
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-162 <MAR>
A:Cross-references: EMBL:Z12122; NID:G46345; PIDN:CAA78107.1; PID:G46346
R:Andersson, S.G.E.; Zomorodipour, A.; Andersson, J.O.; Sichertz-Fonten, T.; Alsmark, Nature 396, 133-140, 1998
A:Title: The genome sequence of Rickettsia prowazekii and the origin of mitochondria.
A:Reference number: A71630; MUID:99039499; PMID:9823893
A:Accession: E71648
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-162 <AND>
A:Cross-references: GB:AJ235273; GB:AJ235269; NID:G3861237; PIDN:CAA15285.1; PID:G38613
A:Experimental source: strain Madrid E
C:Genetics:
A:Gene: greA; RP861
C:Superfamily: transcription elongation factor greB
C:Keywords: DNA binding; transcription factor

Query Match 42.1%; Score 48; DB 2; Length 162;
Best Local Similarity 47.6%; Pred. No. 7.1; Indels 4; Gaps 1;
Matches 10; Conservative 5; Mismatches 2; Gaps 1;

QY 2 QHLKRVQLRDVSEAEV-----RQHRE 20
DB 20 QHLKRVQLRDVSEAEV-----RQHRE 40

RESULT 7
G97695
cobalamin adenosyltransferase (PAL272) [imported] - Agrobacterium tumefaciens (strain C:Species: Agrobacterium tumefaciens

```

C>Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 18-Nov-2002
C:Accession: G97695
R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,
A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.;
Science 294, 2323-2328, 2001
A>Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
A:Reference number: A97359; MUID:21608551; PMID:11743194
A:Accession: G97695
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-221 <KUR>
A:Cross-references: GB:AE007869; PIDN:AAK88520.1; PID:gl5158035; GSPDB:GN00169
C:Genetics:
A:Gene: AGR_C 5090
A:Map position: circular chromosome
C:Superfamily: Escherichia coli cob(I)alamin adenosyltransferase coba

Query Match 41.2%; Score 47; DB 2; Length 221;
Best Local Similarity 38.9%; Pred. No. 14;
Matches 7; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY 5 KRVQLRDVSEAEVRQHR 22
: ||| : ||| : |||
Db 14 ERAWTRDISAEERHQ 31

RESULT 8
G71061
hypothetical protein PH1189 - Pyrococcus horikoshii
C:Species: Pyrococcus horikoshii
C>Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 05-Nov-1999
C:Accession: G71061
R:Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Seki,
M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi
DNA Res. 5, 55-76, 1998
A>Title: Complete sequence and gene organization of the genome of a hyper-thermophilic a
A:Reference number: A71000; MUID:98344137; PMID:9679194
A:Accession: G71061
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-270 <KAW>
A:Cross-references: GB:AP000005; NID:G3236132; PIDN:BAA30289.1; PID:d1031232; PID:g32576
A:Experimental source: strain OR3
A:Note: this accession replaces an interim accession for a sequence replaced by GenBank
C:Genetics:
A:Gene: PH1189

Query Match 41.2%; Score 47; DB 2; Length 270;
Best Local Similarity 37.0%; Pred. No. 17;
Matches 10; Conservative 7; Mismatches 4; Indels 6; Gaps 1;

QY 2 QHLKRVQLRDVSEAEV-----ROHRE 22
: ||| : ||| : ||| : |||
Db 152 KHLKRAQDISELQVQINLTRENRE 178

RESULT 9
T25859
hypothetical protein T04C9.6 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T25859
R:Favell, A.
submitted to the EMBL Data Library, December 1996
A:Description: The sequence of C. elegans cosmid T04C9.
A:Reference number: Z20101
A:Accession: T25859
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-568 <FAV>
A:Cross-references: EMBL:U80955; PIDN:AA838104.1; GSPDB:GN00021; CESP:T04C9.6
A:Experimental source: strain Bristol N2; clone T04C9
C:Genetics:

```

```

A:Gene: CESP:T04C9.6
A:Map position: 3
A:Introns: 52/3; 87/3; 129/2; 162/1; 197/2; 280/3; 393/3; 538/3
Query Match 41.2%; Score 47; DB 2; Length 568;
Best Local Similarity 42.1%; Pred. No. 38;
Matches 8; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 1 ROHLKRVQLRDVSEAEVRQ 19
: ||| : ||| : |||
Db 374 QSHVTNAQIRDAKRAEMRQ 392

RESULT 10
H87038
hypothetical protein dxs [imported] - Mycobacterium leprae
C:Species: Mycobacterium leprae
C>Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 10-May-2001
C:Accession: H87038
R:Cole, S.T.; Biglmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; Ho
R.; Davies, R.M.; Devlin, K.; Duthoy, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; Holroyd,
eam, M.A.; Rutherford, K.M.
Nature 409, 1007-1011, 2001
A:Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; Sq
A>Title: Massive gene decay in the leprosy bacillus.
A:Reference number: A86909; MUID:21128732; PMID:11234002
A:Accession: H87038
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-643 <STO>
A:Cross-references: GB:AL450380; NID:gl3093053; PIDN:CAC31419.1; GSPDB:GN00147
C:Genetics:
A:Gene: dxs
C:Superfamily: hypothetical protein C2814

Query Match 41.2%; Score 47; DB 2; Length 643;
Best Local Similarity 48.0%; Pred. No. 44;
Matches 12; Conservative 6; Mismatches 3; Indels 4; Gaps 2;

QY 2 QHLKRVQLRDVSEAEVRQ---HREA 23
: ||| : ||| : ||| : |||
Db 12 QHLSSQQQLRDIA-AEIRELLVHKVA 35

RESULT 11
B82045
aspartokinase II/homoserine dehydrogenase, methionine-sensitive VC2684 [imported] - Vibr
C:Species: Vibrio cholerae
C>Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
C:Accession: B82045
R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;
chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, P
1, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A>Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A:Reference number: A82035; MUID:20406833; PMID:10952301
A:Accession: B82045
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-803 <HEI>
A:Cross-references: GB:AE004335; GB:AE003852; NID:g9657289; PIDN:AAF95925.1; GSPDB:GN001
A:Experimental source: serogroup O1; strain N16961; biotype El Tor
C:Genetics:
A:Gene: VC2684
A:Map position: 1
C:Superfamily: thrA bifunctional enzyme; aspartate kinase homology; homoserine dehydroge

```

```

Query Match 40.8%; Score 46.5; DB 2; Length 803;
Best Local Similarity 52.4%; Pred. No. 66;
Matches 11; Conservative 6; Mismatches 3; Indels 1; Gaps 1;

QY 2 QHLKRVQLRDVS-EAEVRQHR 21
: ||| : ||| : ||| : |||

```


GenCore version 5.1.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 12, 2003, 19:41:59 ; Search time 4.77358 Seconds
(without alignments)
226.583 Million cell updates/sec

Title: US-08-854-050-113
Perfect score: 114
Sequence: 1 RQHLKRVQLRDVSEAEVQRHREA 23

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	107	93.9	1132	1 TERT HUMAN	O14746 homo sapien
2	75	65.8	1122	1 TERT MOUSE	O70372 mus musculus
3	52.5	45.1	1071	1 CARB NEIMA	Q91w02 neisseria m
4	52	45.6	1071	1 CARB NEIMA	Q91xw8 neisseria m
5	48	42.1	162	1 GRE A RICPR	P27640 rickettsia
6	47	41.2	387	1 TTC4 HUMAN	O95801 homo sapien
7	47	41.2	643	1 DKS MYCLE	O50000 mycobacteri
8	45.5	39.9	387	1 INTD ECOLI	P24218 escherichia
9	45.5	39.9	387	1 VINT_BPP22	P04890 bacterioph
10	45.5	39.9	655	1 SYT CAUCR	Q9aa88 caulobacter
11	45.5	39.9	850	1 D7 DICDI	P54682 dictyosteli
12	45	39.5	638	1 DKS MYCTU	O07184 mycobacteri
13	44	38.6	763	1 YH27 YEAST	P38883 saccharomyc
14	44	38.6	857	1 NPM CHICK	P15053 gallus gall
15	44	38.6	957	1 KF5C HUMAN	O60282 homo sapien
16	44	38.6	963	1 KINH HUMAN	P33176 homo sapien
17	44	38.2	1549	1 TRHY SHEEP	Q61768 mus musculu
18	43.5	38.2	1549	1 TRHY SHEEP	P22793 ovis aries
19	43	37.7	185	1 STN4_XENLA	Q09004 xenopus lae
20	43	37.7	609	1 VEL_HPV49	P36729 human papil
21	43	37.7	688	1 Y5Q7 YEAST	P40050 saccharomyc
22	43	37.7	844	1 HEXA STREN	P10564 streptococc
23	43	37.7	956	1 KF5C MOUSE	P28738 mus musculu
24	43	37.7	1093	1 TMF1 HUMAN	P82094 homo sapien
25	42.5	37.3	288	1 TRA6 NEIMA	O08840 neisseria m
26	42.5	37.3	389	1 CD34 CANFA	Q28270 canis fami
27	42	36.8	162	1 GRE A RICCN	Q92f25 rickettsia
28	42	36.8	212	1 SODF AQUAE	O67470 aquifex aeo
29	42	36.8	212	1 SODF AQUAE	Q9x6w9 aquifex pyr
30	42	36.8	386	1 TTC4 MOUSE	Q8x3b9 mus musculu
31	42	36.8	394	1 UXUA_SALTY	P43668 salmonella
32	42	36.8	637	1 FTSH_BACSU	P37476 bacillus su
33	42	36.8	735	1 YNTC_AZOCA	Q04855 azorhizobiu

ALIGNMENTS

RESULT 1

ID	TERT HUMAN	STANDARD;	PRT;	1132 AA.
AC	O14746; O14783;			
DT	30-MAY-2000 (Rel. 39, Created)			
DT	30-MAY-2000 (Rel. 39, Last sequence update)			
DT	28-FEB-2003 (Rel. 41, Last annotation update)			
DE	Telomerase reverse transcriptase (EC 2.7.7.-) (Telomerase catalytic subunit) (HEST2).			
GN	TERT OR TRT OR EST2 OR TCSI.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Kidney;			
RX	MEDLINE=97400623; PubMed=9252327;			
RA	Nakamura T.M., Morin G.B., Chapman K.B., Weinrich S.L., Andrews W.H., Lingner J., Harley C.B., Cech T.R.;			
RT	"Telomerase catalytic subunit homologs from fission yeast and human.";			
RL	Science 277:955-959(1997).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=97433088; PubMed=9288757;			
RA	Meyerson M., Counter C.M., Eaton E.N., Ellisen L.W., Steiner P., Caddle S.D., Ziaugra L., Beijersbergen R.L., Davidoff M.J., Liu Q., Bacchetti S., Haber D.A., Weinberg R.A.;			
RT	"hEST2, the putative human telomerase catalytic subunit gene, is up-regulated in tumor cells and during immortalization.";			
RL	Cell 90:785-795(1997).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=99267414; PubMed=10333526;			
RA	Wick M., Zubov D., Hagen G.;			
RT	"Genomic organization and promoter characterization of the gene encoding the human telomerase reverse transcriptase (hTERT).";			
RL	Gene 232:97-106(1999).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RA	Londono-Vallejo J.A.;			
RT	"Sequence of a BAC carrying the entire hTERT gene.";			
RL	Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.			
CC	-!- FUNCTION: TELOMERASE IS A RIBONUCLEOPROTEIN ENZYME ESSENTIAL FOR THE REPLICATION OF CHROMOSOME TERMINI IN MOST EUKARYOTES. IT ELONGATES TELOMERES. IT IS A REVERSE TRANSCRIPTASE THAT ADJS SIMPLE SEQUENCE REPEATS TO CHROMOSOME ENDS BY COPYING A TEMPLATE SEQUENCE WITHIN THE RNA COMPONENT OF THE ENZYME.			
CC	-!- SUBUNIT: Interacts with PINX1.			
CC	-!- SUBCELLULAR LOCATION: Nuclear.			
CC	-!- DISEASE: ACTIVATION OF TELOMERASE HAS BEEN IMPLICATED IN CELL IMMORTALIZATION AND CANCER CELL PATHOGENESIS.			
CC	-!- SIMILARITY: BELONGS TO THE REVERSE TRANSCRIPTASE FAMILY. TELOMERASE SUBFAMILY.			

This SWISS-PROT entry is copyright. It is produced through a collaboration

between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see <http://www.isb-sib.ch/announcement/> or send an email to license@isb-sib.ch).

```

CC      or send an email to licensee@sib.sib.ch).
CC      -----
CC      ENBL; AF015950; AAC51672.1; -
DR      ENBL; AF018167; AAC51724.1; -
DR      ENBL; AF018894; AAD30037.1; -
DR      ENBL; AF128893; AAD30037.1; JOINED.
DR      ENBL; AF007685; AAG32289.1; -
DR      ENBL; AF007685; AAG32289.1; -
DR      PIR; T03844; T03844.
DR      Genew; HGNC:11730; TERT.

```

DR Genew; HGNC:11730; TERT.
DR MIM; 187270; -.
DR GO; GO:0005696; C:telomere; TAS.
DR GO; GO:0003721; F:telomeric template RNA reverse transcripts. .; TAS.
DR GO; GO:0003721; F:telomeric template RNA reverse transcripts. .; TAS.

DR GO:0007003; P:telomere binding; TAS.
DR InterPro: IPR000477; RVTse.
DR InterPro: IPR003545; Telomerase_RT.
DR Pfam: PF000078; rvt: 1.
DR PRINIS: PR01365; TELOMERASERT.
DR Transbase; RNA-directed DNA polymerase; Nuclear protein;
KW DNA-binding.
FT CONFLICT 516 516 D -> G (IN REF. 2).
SO SEQUENCE 1132 AA; 126996 MW; 94E35459C4CA33A0 CRC64;

Query Match	93.9%	Score 107;	DB 1;	Length 1132;
Best Local Similarity	91.3%	Pred. No. 4e-08;		
		2 Mismatches		
			0: Indels	0: Gaps

	Matches	21; Conservative	2; mismatches	67; matches	94; mismatches
Qy	1	RHLLKRVQLRDVSEAEVRQHREA	23		
nq	590	ROHLKRVLRLSELSEAEVRQHREA	612		

RESULT 2
TERT MOUSE

ID	TERT MOUSE	STANDARD;	PRI; 1122 AA.
AC	O70372; O35432;		
DT	30-MAY-2000 (Rel. 39, Created)		
DT	30-MAY-2000 (Rel. 39, Last sequence update)		
DT	30-MAY-2000 (Rel. 41, Last annotation update)		

DE 28-FEB-2003 (ref. 41, *Macromolecules*)
DE Telomerase reverse transcriptase (EC 2.7.7.-) (Telomerase catalytic subunit).
DE TERT.
OS *Mus musculus* (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]

RP SEQUENCE FROM N.A.
RX MEDLINE-98241176; PubMed-9582020;
RA Greenberg R.A., Allsopp R.C., Chin L., Morin G.B., DePinho R.A.;
RT "Expression of mouse telomerase reverse transcriptase during
nt development: differentiation and proliferation";

K1
 RL
 RN
 RP
 RX
 SEQUENCE FROM N. A.
 MEDLINE=98393668; PubMed=9724727;
 [2]
 Oncogene 16:1723-1730(1998).

Martin-Rivera L., Herrera E., Albar J.P., Blasco M.A.;
 RA "Expression of mouse telomerase catalytic subunit in embryos and
 RT adult tissues."
 Proc. Natl. Acad. Sci. U.S.A. 95:10471-10476(1998).

RN [3]
RP SEQUENCE OF 550-616 FROM N.A.
RA Drissi R., Cleveland J.L.;
RT "Partial sequence of *Mus musculus* telomerase catalytic subunit
PR homolog.":
PT

Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
 FUNCTION: TELOMERASE IS A RIBONUCLEOPROTEIN ENZYME ESSENTIAL FOR
 THE REPLICATION OF CHROMOSOME TERMINI IN MOST EUKARYOTES. IT
 IS A REVERSE TRANSCRIPTASE THAT ADDS
 ELONGATES TELOMERES. IT IS A REVERSE TRANSCRIPTASE THAT ADDS


```

CC      -!- SIMILARITY: BELONGS TO THE CARB FAMILY.
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use by non-profit institutions as long as its content is in no way
CC      modified and this statement is not removed. Usage by and for commercial
CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC      or send an email to license@isb-sib.ch).
CC      -----
CC      EMBL; AL162753; CAB83892.1; --
CC      PIR; F81979; F81979.
CC      HSSP; P00968; 1A9X.
CC      HAMAP; MF_01210; --; 1.
CC      InterPro; IPR006275; CarA_L_glu.
CC      InterPro; IPR005483; CPase_L.
CC      InterPro; IPR005479; CPase_L_D2.
CC      InterPro; IPR005480; CPase_L_D3.
CC      InterPro; IPR005481; CPase_L_N.
CC      InterPro; IPR004362; MGS_Like.
CC      Pfam; PF00289; CPase_L_Chain; 2.
CC      Pfam; PF02786; CPase_L_D2; 2.
CC      Pfam; PF02787; CPase_L_D3; 1.
CC      Pfam; PF02142; MGS; 1.
CC      PRINTS; PR00098; CPASE.
CC      TIGRfams; TIGR01369; CPaseII_lrg; 1.
CC      PROSITE; PS00866; CPASE 1; 1.
CC      PROSITE; PS00867; CPASE 2; 2.
CC      Arginine biosynthesis; Pyrimidine biosynthesis; Ligase; Repeat;
CC      ATP-binding; Manganese; Complete proteome.
CC      DOMAIN 1 403
CC      CARBOXYPHOSPHATE SYNTHETIC DOMAIN.
CC      OLIGOMERIZATION DOMAIN.
CC      CARBAMOYL PHOSPHATE SYNTHETIC DOMAIN.
CC      ALLOSTERIC DOMAIN.
CC      REPEAT 1 548
CC      REPEAT 549 1071
CC      NP_BIND 153 210
CC      NP_BIND 303 354
CC      METAL 285 285
CC      METAL 299 299
CC      METAL 301 301
CC      METAL 823 823
CC      METAL 835 835
CC      SEQUENCE 1071 AA; 117419 MW; 73B39CBD06729974 CRC64;

Query Match 46.1%; Score 52.5; DB 1; Length 1071;
Best Local Similarity 66.7%; Pred. No. 4.9;
Matches 12; Conservative 2; Mismatches 3; Indels 1; Gaps 1;

QY 5 KRV-QLRDVSEAEVQHR 21
DB 495 KRIAQLLDVKEVREHR 512

RESULT 4
CARB_NEIMB
ID CARB_NEIMB STANDARD; PRT; 1071 AA.
AC Q9JXW8;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Carbamoyl-phosphate synthase large chain (EC 6.3.5.5) (Carbamoyl-
DE phosphate synthetase ammonia chain).
GN CARB OR NMB1855.
OS Neisseria meningitidis (serogroup B).
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=491;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MC58 / Serogroup B;
RX MEDLINE=2017555; PubMed=10710307;
RA Tetelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E.,

```

```

RA Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J.,
RA Nelson W.C., Gwinn M.L., DeBoy R., Peterson J.D., Hickey E.K.,
RA Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A.,
RA Mason T., Ciecko A., Parksey D.S., Blair E., Cittone H., Clark E.B.,
RA Cotton M.D., Utterback T.R., Khouri H., Qin H., Vamathevan J.,
RA Gill J., Scarlato V., Maignani V., Pizzi M., Grandi G., Sun L.,
RA Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C.;
RT "Complete genome sequence of Neisseria meningitidis serogroup B strain
RT MC58."
RL Science 287:1809-1815(2000).
CC -!- CATALYTIC ACTIVITY: 2 ATP + L-glutamine + CO(2) + H(2)O = 2 ADP +
CC phosphate + L-glutamate + carbamoyl phosphate.
CC -!- COFACTOR: Binds 3 manganese ions per subunit (By similarity).
CC -!- PATHWAY: Pyrimidine biosynthesis.
CC -!- SUBUNIT: Composed of two chains; the small (or glutamine) chain
CC promotes the hydrolysis of glutamine to ammonia, which is used by
CC the large (or ammonia) chain to synthesize carbamoyl phosphate (By
CC similarity).
CC -!- SIMILARITY: BELONGS TO THE CARB FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AE002535; AAF42189.1; --
CC PIR; D81035; D81035.
CC HSSP; P00968; 1A9X.
CC TIGR; NMB1855; --; 1.
CC HAMAP; MF_01210; --; 1.
CC InterPro; IPR006275; CarA_L_glu.
CC InterPro; IPR005483; CPase_L.
CC InterPro; IPR005479; CPase_L_D2.
CC InterPro; IPR005480; CPase_L_D3.
CC InterPro; IPR005481; CPase_L_N.
CC InterPro; IPR004362; MGS_Like.
CC Pfam; PF00289; CPase_L_Chain; 2.
CC Pfam; PF02786; CPase_L_D2; 2.
CC Pfam; PF02787; CPase_L_D3; 1.
CC Pfam; PF02142; MGS; 1.
CC PRINTS; PR00098; CPASE.
CC TIGRfams; TIGR01369; CPaseII_lrg; 1.
CC PROSITE; PS00866; CPASE 1; 1.
CC PROSITE; PS00867; CPASE 2; 2.
CC Arginine biosynthesis; Pyrimidine biosynthesis; Ligase; Repeat;
CC ATP-binding; Manganese; Complete proteome.
CC DOMAIN 1 403
CC CARBOXYPHOSPHATE SYNTHETIC DOMAIN.
CC OLIGOMERIZATION DOMAIN.
CC CARBAMOYL PHOSPHATE SYNTHETIC DOMAIN.
CC ALLOSTERIC DOMAIN.
CC REPEAT 1 548
CC REPEAT 549 1071
CC NP_BIND 153 210
CC NP_BIND 303 354
CC METAL 285 285
CC METAL 299 299
CC METAL 301 301
CC METAL 823 823
CC METAL 835 835
CC SEQUENCE 1071 AA; 117375 MW; 6BBE498935B974EE CRC64;

Query Match 45.6%; Score 52; DB 1; Length 1071;
Best Local Similarity 46.7%; Pred. No. 5.9;
Matches 14; Conservative 3; Mismatches 5; Indels 8; Gaps 1;

QY 2 QHLKR-----VOLRDVSEAEVQHR 23
DB 485 RRLKRGKFGSKRLAQLLNSEKVEVREHRYA 514

```

```

Db          20 KHLKHVERKKISEDIAAREH 40

RESULT 5
ID GREA RICPR STANDARD; PRT; 162 AA.
AC P27640;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DE 28-FEB-2003 (Rel. 41, Last annotation update)
DE Transcription elongation factor greA (Transcript cleavage factor greA).
GN GREA OR RP861.
OS Rickettsia prowazekii..
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
OC Rickettsiaceae; Rickettsieae; Rickettsia.
OX NCBI_TaxID=782;
[1]
RN SEQUENCE FROM N.A.
RP STRAIN=Madrid E;
RC MEDLINE=92350688; PubMed=1641349;
RX Marks G.L., Wood D.O.;
RT "Nucleotide sequence of the Rickettsia prowazekii greA homolog.";
RL Nucleic Acids Res. 20:3785-3785(1992).
[2]
RN SEQUENCE FROM N.A.
RP STRAIN=Madrid E;
RC MEDLINE=92350688; PubMed=9823893;
RX Andersson S.G.E., Zomorodipour A., Andersson J.O.,
RA Sicheritz-Ponten T., Almark U.C.M., Podowski R.M., Naeslund A.K.,
RA Eriksson A.-S., Winkler H.H., Kurland C.G.;
RT "The genome sequence of Rickettsia prowazekii and the origin of mitochondria.";
RL Nature 396:133-140(1998).
CC -!- FUNCTION: Necessary for efficient RNA polymerase transcription
CC elongation past template-encoded arresting sites. The arresting
CC sites in DNA have the property of trapping a certain fraction of
CC elongating RNA polymerases that pass through, resulting in locked
CC ternary complexes. Cleavage of the nascent transcript by cleavage
CC factors such as greA or greB allows the resumption of elongation
CC from the new 3' terminus. GreA releases sequences of 2 to 3
CC nucleotides (by similarity).
CC -!- SIMILARITY: BELONGS TO THE GREB/GREB FAMILY.
-----
This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
-----
EMBL; Z12122; CAA78107.1; -.
EMBL; U02878; AAB81401.1; -.
EMBL; AJ235273; CAA15285.1; -.
PIR; S26176; S26176.
HSP; P21346; 1GRJ.
HAMAP; MF_00105; -.
InterPro; IPR006359; GreA.
InterPro; IPR001437; GreA_Greb.
Pfam; PF01272; GreA_Greb; 1.
Pfam; PF03449; GreA_Greb_N; 1.
ProDom; PD004918; GreA_Greb; 1.
TIGRFAMs; TIGR01462; greA; 1.
PROSITE; PS00829; GREAB_1; 1.
PROSITE; PS00830; GREAB_2; 1.
KW Transcription regulation; DNA-binding; Coiled coil; Complete proteome.
FT DOMAIN 44 .. 75 COILED COIL (POTENTIAL).
SQ SEQUENCE 162 AA; 18230 MW; F6774DA35140BD2B CRC64;

Query Match 42.1%; Score 48; DB 1; Length 162;
Best Local Similarity 47.6%; Pred. No. 3;
Matches 10; Conservative 5; Mismatches 4; Indels 2; Gaps 1;

RESULT 6
ID TTC4 HUMAN STANDARD; PRT; 387 AA.
AC O95801; Q9H312;
DT 30-MAY-2000 (Rel. 39, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Tetra tricopeptide repeat protein 4 (My044 protein).
GN TTC4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
[1]
RN SEQUENCE FROM N.A.
RP TISSUE=Brain;
RC MEDLINE=99134293; PubMed=9933562;
RX Su G., Roberts T., Cowell J.K.;
RT "TTC4, a novel human gene containing the tetra tricopeptide repeat and mapping to the region of chromosome 1p31 that is frequently deleted in sporadic breast cancer.";
RL Genomics 55:157-163(1999).
[2]
RN SEQUENCE FROM N.A.
RP TISSUE=Fetal brain;
RC MAO Y.M., Xie Y., Zheng Z.H.;
RL Submitted (MAY-1998) to the EMBL/GenBank/DBSJ databases.
[3]
RN SEQUENCE FROM N.A.
RP TISSUE=Cervix;
RC MEDLINE=23388257; PubMed=12477932;
RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D., Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler N.K., Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J.J., Hsieh F., Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E., Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A., Whitting M., Madan A., Young A.C., Shevchenko V., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalley D.E., Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- SIMILARITY: Contains 3 TPR repeats.
-----
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
-----
EMBL; AF073887; AAD19853.1; -.
EMBL; AF063602; AAG43161.1; -.
EMBL; BC001276; AAH01276.1; -.
GeneW; HGNC:12394; TTC4.
MINI; 606753; -.
GO; GO:0008181; F:tumor suppressor; TAS.
GO; GO:0007048; P:oncogenesis; TAS.
InterPro; IPR001440; TPR.

```



```

or send an email to license@isb-sib.ch).
-----
EMBL; AE005719; AAK22451.1; -.
DR PIR; G87306; G87306.
DR HSSP; P00955; 1EVL.
DR TIGR; CC0464; -.
DR HAMAP; MF 00184; -.
DR InterPro; IPR004154; HGTP anticodon.
DR InterPro; IPR004095; TGS_dom.
DR InterPro; IPR002314; tRNA-synt 2b.
DR InterPro; IPR002320; tRNA-synt thr.
DR InterPro; IPR006195; tRNA ligase II.
DR Pfam; PF03129; HGTP anticodon; 1.
DR Pfam; PF02824; TGS; 1.
DR Pfam; PF00587; tRNA-synt 2b; 1.
DR PRINTS; PRO1047; TRNASYNTHTHR.
DR TIGRFAMs; TIGR00418; thrS; 1.
DR PROSITE; PS00862; AA tRNA LIGASE II; 1.
KW Aminocyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
KW Metal-binding; Zinc; Complete proteome.
FT DOMAIN 248 540
FT METAL 340 340 ZINC (CATALYTIC) (BY SIMILARITY).
FT METAL 391 391 ZINC (CATALYTIC) (BY SIMILARITY).
FT METAL 517 517 ZINC (CATALYTIC) (BY SIMILARITY).
SQ SEQUENCE 655 AA; 73719 MW; BB75D312CC887799 CRC64;

Query Match 39.9%; Score 45.5; DB 1; Length 655;
Best Local Similarity 50.0%; Pred. No. 32;
Matches 10; Conservative 3; Mismatches 2; Indels 5; Gaps 1;

QY 3 HLKRVQLRDVSEAEVQHQRE 22
DB 237 HLKRIE-----EAKRDHRK 251

RESULT 11
D7_DICDI
ID D7_DICDI STANDARD; PRT; 850 AA.
AC PS4682;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE cAMP-inducible prespore protein D7 precursor.
GN D7.
OS Dictyostelium discoideum (slime mold).
OC Eukaryota; Mycetozoa; Dictyostellida; Dictyostelium.
OX NCBI_TaxID=44689;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=AX3;
RX MEDLINE=95080502; PubMed=7988791;
RA Agarwal A., Sloger M.S., Oyama M., Blumberg D.D.;
RT "Analysis of a novel cyclic Amp inducible prespore gene in
RT Dictyostelium discoideum: evidence for different patterns of cAMP
RT regulation."
RL Differentiation 57:151-162(1994).
CC -!- DEVELOPMENTAL STAGE: EXPRESSED SPECIFICALLY IN THE PRESPORE CELLS.
CC -!- INDUCTION: BY CAMP.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
-----
EMBL; U25143; AAA73514.1; -.
DR Dictyob; DD02038; -.
KW Sporulation; Signal.
FT SIGNAL 1 24
FT CHAIN 25 475
FT DOMAIN 470 850
FT POTENTIAL.
FT CAMP-INDUCIBLE PRESPORE PROTEIN D7.
FT POLY-GLN.

```

```

FT DOMAIN 555 568 POLY-ASN.
FT DOMAIN 728 738 POLY-GLN.
SQ SEQUENCE 850 AA; 95343 MW; 13BA634CCE7AA502 CRC64;

Query Match 39.9%; Score 45.5; DB 1; Length 850;
Best Local Similarity 43.5%; Pred. No. 42;
Matches 10; Conservative 4; Mismatches 8; Indels 1; Gaps 1;

QY 2 QHLKRVQL-RDVSEAEVQHQREA 23
DB 661 QHLQRIENGEDIDEYEAQAQHEVA 683

RESULT 12
DXS_MYCTU
ID DXS_MYCTU STANDARD; PRT; 638 AA.
AC Q00T84;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE 1-deoxy-D-xylose 5-phosphate synthase (EC 2.2.1.7) (1-
DE deoxyxylulose-5-phosphate synthase) (DXP synthase) (DXPS).
GN DXS OR RV2682C OR MT2756 OR MTCY05A6.03C.
OS Mycobacterium tuberculosis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacteriaceae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1773;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=H37RV;
RX MEDLINE=98295987; PubMed=9634230;
RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
RA Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekala F.,
RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
RA Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
RA Sulston J.E., Taylor K., Whitehead S., Barrett B.G.;
RT "Deciphering the biology of Mycobacterium tuberculosis from the
RT complete genome sequence."
RL Nature 393:537-544(1998).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=CDC 1551 / Oshkosh;
RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
RA Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
RA Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
RA Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
RA Bishai W.;
RT "Whole genome comparison of Mycobacterium tuberculosis clinical and
RT laboratory strains."
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Catalyzes the acyloin condensation reaction between C
CC atoms 2 and 3 of pyruvate and glyceraldehyde 3-phosphate to yield
CC 1-deoxy-D-xylose-5-phosphate (DXP) (By similarity).
CC -!- CATALYTIC ACTIVITY: Pyruvate + D-glyceraldehyde 3-phosphate = 1-
CC deoxy-D-xylose 5-phosphate + CO(2).
CC -!- COFACTOR: Binds 1 thiamine pyrophosphate per subunit (By
CC similarity).
CC -!- PATHWAY: Nonaevulonate terpenoid biosynthesis pathway; first step.
CC -!- PATHWAY: Biosynthetic pathway to thiamine and pyridoxol; first
CC step.
CC -!- SUBUNIT: Homodimer (By similarity).
CC -!- SIMILARITY: Belongs to the transketolase family. DXPS subfamily.
-----
This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
-----

```



```

FT DOMAIN 407 857 TAIL.
FT DOMAIN 99 130 COIL 1A.
FT DOMAIN 131 143 LINKER 1.
FT DOMAIN 144 242 COIL 1B.
FT DOMAIN 243 259 LINKER 12.
FT DOMAIN 260 281 COIL 2A.
FT DOMAIN 282 285 LINKER 2.
FT DOMAIN 286 406 COIL 2B.
FT CARBOHYD 46 46 O-LINKED (GLCNAC) (BY SIMILARITY).
FT CARBOHYD 426 426 O-LINKED (GLCNAC) (BY SIMILARITY).
FT CONFLICT 546 546 G -> R (IN REF. 2).
SQ SEQUENCE 857 AA; 95704 MW; 4E2E0FC6AC64778B CRC64;

Query Match 38.6%; Score 44; DB 1; Length 857;
Best Local Similarity 43.5%; Pred. No. 72;
Matches 10; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

QY 1 RQHLKRVQVLDVSEAEVROHREA 23
DB 132 QKHAGRAQLGDAYEQLRELGA 154

RESULT 15
KF5C HUMAN STANDARD; PRT; 957 AA.
AC O60282; OS05079;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Kinesin heavy chain isoform 5C (Kinesin heavy chain neuron-specific
DE 2).
GN KIF5C OR NKHC2 OR KIAA0531.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA MEDLINE=98290545; PubMed=9628581;
RA Nagase T., Ishikawa K.-I., Miyajima N., Tanaka A., Kotani H.,
RA Nomura N., Ohara O.,
RA "Prediction of the coding sequences of unidentified human genes. IX.
RT The complete sequences of 100 new cDNA clones from brain which can
RT code for large proteins in vitro.";
RL DNA Res. 5:31-39(1998).
RN [2]
RP SEQUENCE OF 355-585 FROM N.A.
RA Engelender S., Sharp A.H., Colomer V., Tokito M.K., Lanahan A.,
RA Worley P., Holzbaur E.L.F., Ross C.A.;
RT "Huntingtin associated protein 1 (HAP1) interacts with the p150Glued
RT subunit of dynactin.";
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: KINESIN IS A MICROTUBULE-ASSOCIATED FORCE-PRODUCING
CC PROTEIN THAT MAY PLAY A ROLE IN ORGANELLE TRANSPORT.
CC -!- SUBUNIT: OLIGOMER COMPOSED OF TWO HEAVY CHAINS AND TWO LIGHT
CC CHAINS.
CC -!- TISSUE SPECIFICITY: HIGHEST EXPRESSION IN BRAIN, PROSTATE, AND
CC TESTIS, AND MODERATE EXPRESSION IN KIDNEY, SMALL INTESTINE, AND
CC OVARY.
CC -!- DOMAIN: COMPOSED OF THREE STRUCTURAL DOMAINS: A LARGE GLOBULAR N-
CC TERMINAL DOMAIN WHICH IS RESPONSIBLE FOR THE MOTOR ACTIVITY OF
CC KINESIN (IT HYDROLYSES ATP AND BINDS MICROTUBULE), A CENTRAL
CC ALPHA-HELICAL COILED COIL DOMAIN THAT MEDIATES THE HEAVY CHAIN
CC DIMERIZATION; AND A SMALL GLOBULAR C-TERMINAL DOMAIN WHICH
CC INTERACTS WITH OTHER PROTEINS (SUCH AS THE KINESIN LIGHT CHAINS),
CC VESICLES AND MEMBRANOUS ORGANELLES.
CC -!- SIMILARITY: BELONGS TO THE KINESIN-LIKE PROTEIN FAMILY. KINESIN
CC SUBFAMILY.
-----
This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its

```

use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

```

CC EMBL; AB011103; BAA25457.1; -
CC EMBL; AF010146; AAD01436.1; -
CC HSSP; P56536; 2KIN.
CC MIM; 604593; -
CC GO; GO:0005871; C:kinesin complex; TAS.
CC GO; GO:0003777; F:microtubule motor activity; TAS.
CC GO; GO:0006996; P:organelle organization and biogenesis; TAS.
CC InterPro; IPR001752; kinesin_motor.
CC Pfam; PF00225; kinesin; 1.
CC PRINTS; PR00380; KINESINHEAVY.
CC SMART; SM00129; KISC; 1.
CC PROSITE; PS00411; KINESIN_MOTOR_DOMAIN1; 1.
CC PROSITE; PS0067; KINESIN_MOTOR_DOMAIN2; 1.
CC Motor protein; Microtubules; ATP-binding; Coiled coil.
KW DOMAIN 1 386 KINESIN-MOTOR (BY SIMILARITY).
FT DOMAIN 406 923 COILED COIL.
FT DOMAIN 859 956 GLOBULAR.
FT DOMAIN 174 315 MICROTUBULE-BINDING.
FT NP_BIND 86 93 ATP (BY SIMILARITY).
FT CONFLICT 355 360 TLKNVI -> STHAVV (IN REF. 2).
FT CONFLICT 583 585 EFT -> DRV (IN REF. 2).
SQ SEQUENCE 957 AA; 109494 MW; A9F25BB1C994322A CRC64;

```

Query Match 38.6%; Score 44; DB 1; Length 957;
Best Local Similarity 33.3%; Pred. No. 81;
Matches 9; Conservative 7; Mismatches 7; Indels 4; Gaps 1;

```

QY 1 RQHLKRVQV-----LRDVSEAEVROHREA 23
DB 687 KEHLTRLQDAEMKMKALEQQMESHREA 713

```

Search completed: November 12, 2003, 19:48:00
Job time : 4.77358 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 12, 2003, 19:42:29 ; Search time 21.9874 Seconds
(without alignments)
269.937 Million cell updates/sec

Title: US-08-854-050-113
Perfect score: 114
Sequence: 1 RQHLKRVQLRDVSEAEVROHREA 23

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPTREMBL 23.*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phase.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_rvirus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	107	93.9	795	4 Q8NG38	Q8ng38 homo sapien
2	107	93.9	807	4 Q8N6C3	Q8n6c3 homo sapien
3	107	93.9	1069	4 Q8NG46	Q8ng46 homo sapien
4	75	65.8	52	11 Q9ROB3	Q9rob3 mus musculus
5	75	65.8	575	11 Q9JK99	Q9jk99 rattus norv
6	70	61.4	1128	11 Q9QXZ4	Q9qxz4 mesocricetu
7	51	44.7	356	16 Q8QJW4	Q8qjw4 rhizobium l
8	49.5	43.4	324	16 Q8X7N3	Q8x7n3 escherichia
9	49.5	43.4	387	9 Q22093	Q22093 bacterioph
10	49	43.0	1268	5 Q9GYD2	Q9gyd2 leishmania
11	49	43.0	1584	5 Q8WQ43	Q8wq43 leishmania
12	47	41.2	221	16 Q8UBP4	Q8ubp4 agrobacteri
13	47	41.2	270	17 Q58907	Q58907 pyrococcus
14	47	41.2	573	5 Q9GP93	Q9gp93 caenorhabdi
15	47	41.2	637	6 Q8WN08	Q8wnu8 macaca fasc
16	46.5	40.8	715	5 Q9VPL5	Q9vp15 drosophila

17	46.5	40.8	803	16 Q9KNP7	Q9knp7 vibrio chol
18	46	40.4	523	13 Q8AV90	Q8av90 petromyzon
19	46	40.4	745	4 Q9Y4Q6	Q9y4q6 homo sapien
20	46	40.4	761	5 Q8WPK0	Q8wpk0 oikopleura
21	46	40.4	829	3 Q8NJ06	Q8nj06 neurospora
22	46	40.4	889	16 Q92SW4	Q92sw4 rhizobium m
23	46	40.4	1537	5 Q9VAI2	Q9vai2 drosophila
24	46	40.4	2266	4 Q8WYP5	Q8wyp5 homo sapien
25	46	40.4	2302	4 Q81ZA4	Q81za4 homo sapien
26	45.5	39.9	222	2 Q8KW74	Q8kw74 ruegeria sp
27	45.5	39.9	335	16 Q9JUQ1	Q9juq1 neisseria m
28	45.5	39.9	387	9 Q8HA16	Q8ha16 salmonella
29	45.5	39.9	495	16 Q33230	Q33230 mycobacteri
30	45.5	39.9	556	16 Q8VJE2	Q8vje2 mycobacteri
31	45	39.5	244	2 Q05934	Q05934 pseudomonas
32	45	39.5	323	16 Q8EKV1	Q8ekv1 oceanobacil
33	45	39.5	605	5 Q9V7L8	Q9v7l8 drosophila
34	45	39.5	609	5 Q46117	Q46117 drosophila
35	45	39.5	610	5 Q8MKK9	Q8mkk9 drosophila
36	45	39.5	610	5 Q9UY99	Q9uy99 drosophila
37	45	39.5	744	5 Q9N8P5	Q9n8f5 trypanosoma
38	45	39.5	1191	13 Q9DE32	Q9de32 xenopus lae
39	44.5	39.0	360	5 Q9V8J4	Q9v8j4 drosophila
40	44.5	39.0	413	5 Q25004	Q25004 homarus ame
41	44.5	39.0	869	11 Q8R3F9	Q8r3f9 mus musculu
42	44	38.6	253	11 Q9WV65	Q9wv65 rattus norv
43	44	38.6	256	16 Q9KPS6	Q9kps6 vibrio chol
44	44	38.6	463	4 Q9H5F4	Q9h5f4 homo sapien
45	44	38.6	472	17 Q8PXE5	Q8pxe5 methanosarc

ALIGNMENTS

RESULT 1

Q8NG38 ID Q8NG38 PRELIMINARY; PRT; 795 AA.
AC Q8NG38;
DT 01-OCT-2002 (Tremblrel. 22, Created)
DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE ABG-directed variant of telomerase reverse transcriptase.
GN TERT.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Stomach;
RA Hisatomi H., Nagao K., Kanamaru T., Hirata H., Miyachi K., Hikiji H.;
RT "Exon 11 deleted variant of human reverse transcriptase.";
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB086950; BAC11015.1;
DR InterPro; IPR003545; Telomerase_RT.
DR PRINTS; PR01365; TELOMERASERT.
KW RNA-directed DNA polymerase.
SQ SEQUENCE 795 AA; 88965 MW; 6BEAC8A6D1A2E8CB CRC64;

Query Match 93.9%; Score 107; DB 4; Length 795;
Best Local Similarity 91.3%; Pred. No. 7.1e-08;
Matches 21; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RQHLKRVQLRDVSEAEVROHREA 23
|||
Db 590 RQHLKRVQLRSELSEAEVROHREA 612

RESULT 2

Q8N6C3 ID Q8N6C3 PRELIMINARY; PRT; 807 AA.
AC Q8N6C3;
DT 01-OCT-2002 (Tremblrel. 22, Created)

Thu Nov 13 12:07:03 2003

```

OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Drissi R., Cleveland J.L.;
RT "Sequence of a Mus musculus telomerase catalytic subunit intron.";
RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF090439; AAD54013.1;
FT NON_TER 1
FT NON_TER 52
SQ SEQUENCE 52 AA; 6479 MW; 41473425E44BDA9C CRC64;

Query Match 65.8%; Score 75; DB 11; Length 52;
Best Local Similarity 59.1%; Pred. No. 0.00035;
Matches 13; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

QY 1 ROHLKRVQLRDVSEAEVRQHRE 22
DB 24 ROHLERVRLRELSQSEVRHHQD 45

RESULT 5
QJJK99 PRELIMINARY; PRT; 575 AA.
AC QJJK99;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Telomerase catalytic subunit (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Wong S., Gao S., Xu X., Yu H.;
RT "Rat telomerase catalytic subunit, rTERT.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF247818; AAF62177.1;
DR InterPro: IPR000477; RVTse
DR InterPro: IPR003545; Telomerase_RT
DR Pfam: PF00078; rvt; 1.
DR PRINTS; PR01365; TELOMERASERT.
DR RNA-directed DNA polymerase; Transferase.
KW NON_TER 1
KW NON_TER 575
SQ SEQUENCE 575 AA; 65672 MW; F80C81BD7F6A91A3 CRC64;

Query Match 65.8%; Score 75; DB 11; Length 575;
Best Local Similarity 59.1%; Pred. No. 0.004;
Matches 13; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

QY 1 ROHLKRVQLRDVSEAEVRQHRE 22
DB 33 ROHLERVRLRELSQSEVRHHQD 54

RESULT 6
QJJK99 PRELIMINARY; PRT; 1128 AA.
AC QJJK99;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Telomerase catalytic subunit.
OS Mesocricetus auratus (Golden hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Mesocricetus.
OX NCBI_TaxID=10036;
RN [1]
RP SEQUENCE FROM N.A.

```

```

RX MEDLINE=21240330; PubMed=11342218;
RA Guo W., Okamoto M., Lee Y.M., Baluda M.A.; Park N.H.;
RT "Enhanced activity of cloned hamster TERT gene promoter in transformed
RL cells."
RL Biochim. Biophys. Acta 1517:398-409(2001).
DR EMBL; AF149012; AAF17334.1; -.
DR InterPro; IPR000477; RVTse.
DR InterPro; IPR003545; Telomerase_RT.
DR Pfam; PF00078; rvt; 1.
DR PRINTS; PR01365; TELOMERASERT.
KW RNA-directed DNA polymerase; Transferase.
SQ SEQUENCE 1128 AA; 128394 MW; 1D4F81249012174E CRC64;

Query Match 61.4%; Score 70; DB 11; Length 1128;
Best Local Similarity 56.5%; Pred. No. 0.047;
Matches 13; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

QY 1 RQHLKRVQLRDVSEAEVQRH 23
DB 584 RHLLERVLQSLQSEVQRQEA 606

RESULT 7
Q98JW4 PRELIMINARY; PRT; 356 AA.
AC Q98JW4
DT 01-OCT-2001 (TrEMBLrel. 18, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Sensory transduction regulatory protein.
GN MR1749.
OS Rhizobium loti (Mesorhizobium loti).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Phyllobacteriaceae; Mesorhizobium.
OX NCBI_TaxID=381;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MAFF303099;
RX MEDLINE=21082930; PubMed=11214968;
RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
RA Watanabe A., Igesawa K., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
RA Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,
RA Takeuchi C., Yamada M., Tabata S.;
RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium
RL Mesorhizobium loti."
RL DNA Res. 7:331-338(2000).
DR EMBL; AP002998; BAB49051.1; -.
DR InterPro; IPR003594; Arpbind_ATPase.
DR InterPro; IPR005467; His_kinase.
DR InterPro; IPR000014; PAS_domain.
DR Pfam; PF02518; HATPase_c7.1.
DR SMART; SM00387; HATPase_c7.1.
DR SMART; SM00091; PAS; 1_c; 1.
DR PROSITE; PS01019; HIS_KIN; 1.
KW Complete proteome.
SQ SEQUENCE 356 AA; 39277 MW; EA6C73E5B2BFC099 CRC64;

Query Match 44.7%; Score 51; DB 16; Length 356;
Best Local Similarity 55.0%; Pred. No. 12;
Matches 11; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 RQHLKRVQLRDVSEAEVQRH 20
DB 185 RQHLKDAHQVLSVAEVRH 204

RESULT 8
Q8X7N3 PRELIMINARY; PRT; 324 AA.
AC Q8X7N3
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)

```

```

DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Putative integrase for prophage CP-933H.
GN INTH OR 20307 OR ECS0271.
OS Escherichia coli O157:H7.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=83334;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=O157:H7 / EDL933 / ATCC 700927;
RX MEDLINE=21074935; PubMed=11206551;
RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
RA Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
RA Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamoukis K.,
RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
RA Welch R.A., Blattner F.R.;
RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7."
RL Nature 409:529-533(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=O157:H7 / RIMD 0509952;
RX MEDLINE=21156231; PubMed=11258796;
RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
RA Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
RA Kuhara S., Shiba T., Hattori M., Shinagawa H.;
RT "Complete genome sequence of enterohemorrhagic Escherichia coli
RT O157:H7 and genomic comparison with a laboratory strain K-12."
RL DNA Res. 8:11-22(2001).
DR EMBL; AE005202; AAG54569.1; -.
DR EMBL; AP002551; BAB33694.1; -.
DR InterPro; IPR002104; Phage_integrase.
DR Pfam; PF00589; Phage_integrase; 1.
KW Complete proteome.
SQ SEQUENCE 324 AA; 37388 MW; 8058F2C51836088A CRC64;

Query Match 43.4%; Score 49.5; DB 16; Length 324;
Best Local Similarity 33.3%; Pred. No. 18;
Matches 10; Conservative 7; Mismatches 4; Indels 9; Gaps 1;

QY 2 QHLKRVQLRDVSEAEV-----RQHRE 22
DB 25 QHPAGQLRDITSEKISYAMQKMTNRHEE 54

RESULT 9
O22009 PRELIMINARY; PRT; 387 AA.
AC O22009
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Integrase.
GN INT.
OS Bacteriophage SfV (Shigella flexneri bacteriophage V).
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Podoviridae.
OX NCBI_TaxID=55884;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=97449297; PubMed=9305766;
RA Huan P.T., Whittle B.L., Bastin D.A., Lindberg A.A., Verma N.K.;
RT "Shigella flexneri type-specific antigen V: cloning, sequencing and
RT characterization of the glucosyl transferase gene of temperate
RT bacteriophage SfV."
RL Gene 195:207-216(1997).
DR EMBL; U82619; AAB72135.1; -.
DR HSSP; P21442; 1A1H.
DR InterPro; IPR002104; Phage_integrase.
DR Pfam; PF00589; Phage_integrase; 1.
SQ SEQUENCE 387 AA; 44839 MW; EC245FAAC8007690 CRC64;

Query Match 43.4%; Score 49.5; DB 9; Length 387;

```

Thu Nov 13 12:07:03 2003

```

RL Genome Res. 8:135-145(1998).
DR EMBL: AL359716; CAD19413.1;
KW Transmembrane.
SQ SEQUENCE 1584 AA; 168226 MW; AB2A79A3B4E28E07 CRC64;

Query Match 43.0%; Score 49; DB 5; Length 1584;
Best Local Similarity 47.4%; Pred. No. 1.1e+02;
Matches 9; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 1 ROHLKRVOLRDVSEAEVRQ 19
Db 1381 REHKRLHQRDTQDAQVAQ 1399

RESULT 12
ID Q8UBP4 PRELIMINARY; PRT; 221 AA.
AC Q8UBP4;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE COB (I)alamin adenosyltransferase.
GN COB OR ATU2807 OR AGR_C_5090.
OS Agrobacterium tumefaciens (strain C58 / ATCC 33970).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Rhizobium.
OX NCBI_TaxID=176299;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21608550; PubMed=11743193;
RA Wood D.W., Setubal J.C., Kaul R., Monks D.E., Almeida N.F. Jr., Woo L.,
RA Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Bovee D. Sr.,
RA Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr., Grant C.,
RA Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,
RA Kutyavin T., Levy R., Li M.-J., McClelland E., Palmieri A.,
RA Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D.,
RA Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M.,
RA Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,
RA Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
RA Nester E.W.;
RT "The genome of the natural genetic engineer Agrobacterium tumefaciens
RT C58."
RL Science 294:2317-2323(2001).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=21608551; PubMed=11743194;
RA Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M., Mullin L.,
RA Qurollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Liu F.,
RA Houmlel K., Gordon J., Vaudin M., Tarchouk O., Epp A., Liu F.,
RA Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B.,
RA Flanagan C., Crowell C., Gurson J., Lomo C., Sear C., Strub G.,
RA Cielo C., Slater S.;
RT "Genome sequence of the plant pathogen and biotechnology agent
RT Agrobacterium tumefaciens C58."
RL Science 294:2323-2328(2001).
DR EMBL: AE009228; AAL43788.1; ALT_INIT.
DR EMBL: AE008194; AAK8520.1;
DR InterPro: IPR003724; CoBa_CoBa_BtuR.
DR Pfam: PF02572; CoBa_CoBa_BtuR; 1.
DR TIGRFAMs: TIGR00708; CoBa; 1.
KW Transferase; Complete proteome.
SQ SEQUENCE 221 AA; 24333 MW; 30C985FBED6511 CRC64;

Query Match 41.2%; Score 47; DB 16; Length 221;
Best Local Similarity 38.9%; Pred. No. 29;
Matches 7; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY 5 KRVOLRDVSEAEVRQHRE 22
Db 14 ERAMTRDISDSEAEHRQ 31

RESULT 13

```

```

RL Genome Res. 8:135-145(1998).
DR EMBL: AL359716; CAD19413.1;
KW Transmembrane.
SQ SEQUENCE 1584 AA; 168226 MW; AB2A79A3B4E28E07 CRC64;

Query Match 43.0%; Score 49; DB 5; Length 1584;
Best Local Similarity 47.4%; Pred. No. 1.1e+02;
Matches 9; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 1 ROHLKRVOLRDVSEAEVRQ 19
Db 1381 REHKRLHQRDTQDAQVAQ 1399

RESULT 12
ID Q8UBP4 PRELIMINARY; PRT; 221 AA.
AC Q8UBP4;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE COB (I)alamin adenosyltransferase.
GN COB OR ATU2807 OR AGR_C_5090.
OS Agrobacterium tumefaciens (strain C58 / ATCC 33970).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Rhizobium.
OX NCBI_TaxID=176299;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21608550; PubMed=11743193;
RA Wood D.W., Setubal J.C., Kaul R., Monks D.E., Almeida N.F. Jr., Woo L.,
RA Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Bovee D. Sr.,
RA Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr., Grant C.,
RA Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,
RA Kutyavin T., Levy R., Li M.-J., McClelland E., Palmieri A.,
RA Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D.,
RA Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M.,
RA Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,
RA Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
RA Nester E.W.;
RT "The genome of the natural genetic engineer Agrobacterium tumefaciens
RT C58."
RL Science 294:2317-2323(2001).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=21608551; PubMed=11743194;
RA Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M., Mullin L.,
RA Qurollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Liu F.,
RA Houmlel K., Gordon J., Vaudin M., Tarchouk O., Epp A., Liu F.,
RA Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B.,
RA Flanagan C., Crowell C., Gurson J., Lomo C., Sear C., Strub G.,
RA Cielo C., Slater S.;
RT "Genome sequence of the plant pathogen and biotechnology agent
RT Agrobacterium tumefaciens C58."
RL Science 294:2323-2328(2001).
DR EMBL: AE009228; AAL43788.1; ALT_INIT.
DR EMBL: AE008194; AAK8520.1;
DR InterPro: IPR003724; CoBa_CoBa_BtuR.
DR Pfam: PF02572; CoBa_CoBa_BtuR; 1.
DR TIGRFAMs: TIGR00708; CoBa; 1.
KW Transferase; Complete proteome.
SQ SEQUENCE 221 AA; 24333 MW; 30C985FBED6511 CRC64;

Query Match 41.2%; Score 47; DB 16; Length 221;
Best Local Similarity 38.9%; Pred. No. 29;
Matches 7; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY 5 KRVOLRDVSEAEVRQHRE 22
Db 14 ERAMTRDISDSEAEHRQ 31

RESULT 13

```

```

RL Genome Res. 8:135-145(1998).
DR EMBL: AL359716; CAD19413.1;
KW Transmembrane.
SQ SEQUENCE 1584 AA; 168226 MW; AB2A79A3B4E28E07 CRC64;

Query Match 43.0%; Score 49; DB 5; Length 1584;
Best Local Similarity 47.4%; Pred. No. 1.1e+02;
Matches 9; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 1 ROHLKRVOLRDVSEAEVRQ 19
Db 1381 REHKRLHQRDTQDAQVAQ 1399

RESULT 12
ID Q8UBP4 PRELIMINARY; PRT; 221 AA.
AC Q8UBP4;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE COB (I)alamin adenosyltransferase.
GN COB OR ATU2807 OR AGR_C_5090.
OS Agrobacterium tumefaciens (strain C58 / ATCC 33970).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Rhizobium.
OX NCBI_TaxID=176299;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21608550; PubMed=11743193;
RA Wood D.W., Setubal J.C., Kaul R., Monks D.E., Almeida N.F. Jr., Woo L.,
RA Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Bovee D. Sr.,
RA Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr., Grant C.,
RA Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,
RA Kutyavin T., Levy R., Li M.-J., McClelland E., Palmieri A.,
RA Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D.,
RA Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M.,
RA Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,
RA Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
RA Nester E.W.;
RT "The genome of the natural genetic engineer Agrobacterium tumefaciens
RT C58."
RL Science 294:2317-2323(2001).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=21608551; PubMed=11743194;
RA Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M., Mullin L.,
RA Qurollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Liu F.,
RA Houmlel K., Gordon J., Vaudin M., Tarchouk O., Epp A., Liu F.,
RA Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B.,
RA Flanagan C., Crowell C., Gurson J., Lomo C., Sear C., Strub G.,
RA Cielo C., Slater S.;
RT "Genome sequence of the plant pathogen and biotechnology agent
RT Agrobacterium tumefaciens C58."
RL Science 294:2323-2328(2001).
DR EMBL: AE009228; AAL43788.1; ALT_INIT.
DR EMBL: AE008194; AAK8520.1;
DR InterPro: IPR003724; CoBa_CoBa_BtuR.
DR Pfam: PF02572; CoBa_CoBa_BtuR; 1.
DR TIGRFAMs: TIGR00708; CoBa; 1.
KW Transferase; Complete proteome.
SQ SEQUENCE 221 AA; 24333 MW; 30C985FBED6511 CRC64;

Query Match 41.2%; Score 47; DB 16; Length 221;
Best Local Similarity 38.9%; Pred. No. 29;
Matches 7; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY 5 KRVOLRDVSEAEVRQHRE 22
Db 14 ERAMTRDISDSEAEHRQ 31

RESULT 13

```

```
OS8907
ID O58907 PRELIMINARY; PRT; 270 AA.
AC O58907;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hypothetical protein PH1189.
GN PH1189.
OS Pyrococcus horikoshii.
OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
OC Pyrococcus.
OX NCBI_TaxID=53953;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=OT3;
RX MEDLINE=98344137; PubMed=9679194;
RA Kawarabayashi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y.,
RA Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Nagai Y.,
RA Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Y.,
RA Funahashi T., Tanaka T., Kudo H., Yamazaki J., Kishida N., Oguchi A.,
RA Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K.,
RA Maeuchi Y., Shizuya H., Kikuchi H.;
RT "Complete sequence and gene organization of the genome of a hyper-
thermophilic archaeobacterium, Pyrococcus horikoshii OT3.";
RL DNA Res. 5:55-76(1998)
DR EMBL; AP000005; BAA30289.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 270 AA; 31019 MW; AA5A4C8E94FB1EFE CRC64;

Query Match 41.2%; Score 47; DB 17; Length 270;
Best Local Similarity 37.0%; Pred. No. 36;
Matches 10; Conservative 7; Mismatches 4; Indels 6; Gaps 1;

Oy 2 OHLKRVQLRDVSEAEV-----RQHRE 22
Db 152 KHLKEAQAQDISELQVQINNLTRNRE 178

RESULT 14
O9GP93
ID O9GP93 PRELIMINARY; PRT; 573 AA.
AC O9GP93;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical 65.7 kDa protein.
GN T04C9.6.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Pelodierinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RA None;
RT "Genome sequence of the nematode C. elegans: a platform for
investigating biology. The C. elegans Sequencing Consortium.";
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Favello A., Favello A.;
RT "The sequence of C. elegans cosmid T04C9.";
RN Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Waterston R.;
RT "Direct Submission.";
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; U80955; AAC01559.2; -.
DR WormPep; T04C9.6; CE29463.
```

```
DR InterPro; IPR000299; Band 4.1.
DR Pfam; PF00373; Band 41; 1.
DR PRINTS; PRO0935; BAND41.
DR PROSITE; PS00660; BAND_41_1; 1.
DR PROSITE; PS50057; BAND_41_3; 1.
KW Hypothetical protein.
SQ SEQUENCE 573 AA; 65747 MW; A45FE0A562AE05ED CRC64;

Query Match 41.2%; Score 47; DB 5; Length 573;
Best Local Similarity 42.1%; Pred. No. 78;
Matches 8; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

Oy 1 ROHLKRVQLRDVSEAEVRQ 19
Db 379 QSHVTNAQIRDAKRAEMRQ 397

RESULT 15
O8WN08
ID O8WN08 PRELIMINARY; PRT; 637 AA.
AC O8WN08;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE mRNA, similar to human hypothetical protein FLJ23495, complete
cde.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis.
RA Hashimoto K., Osada N., Hida M., Kusuda J., Tanuma R., Hirai M.,
RA Terao K., Suzuki Y., Sugano S.;
RT "Isolation of novel full-length cDNA clones from macaque testis cDNA
libraries.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL; AB064997; BAB83539.1; -.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR Pfam; PF00069; pkinase; 1.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TK; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 637 AA; 73337 MW; FA3A5C3CEESAD16F CRC64;

Query Match 41.2%; Score 47; DB 6; Length 637;
Best Local Similarity 45.0%; Pred. No. 86;
Matches 9; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

Oy 3 HLKRVQLRDVSEAEVRQHRE 22
Db 590 YLKRRARHQNASEAEIRERLE 609

Search completed: November 12, 2003, 19:50:44
Job time : 22.1541 secs
```

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 12, 2003, 19:41:04 ; Search time 33.6226 Seconds
(without alignments)
127.462 Million cell updates/sec

Title: US-08-854-050-114

Perfect score: 130

Sequence: 1 ARTFRREKRAERLTSRVKALPSVLNVE 27

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A. Geneseq 19Jun03.*
1: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.*
2: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
3: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*
4: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.*
5: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1984.DAT.*
6: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1985.DAT.*
7: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1986.DAT.*
8: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1987.DAT.*
9: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1988.DAT.*
10: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1989.DAT.*
11: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1990.DAT.*
12: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1991.DAT.*
13: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1992.DAT.*
14: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1993.DAT.*
15: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1994.DAT.*
16: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1995.DAT.*
17: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1996.DAT.*
18: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1997.DAT.*
19: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.*
20: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*
21: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
22: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*
24: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	130	100.0	27	19	AAW57393 Human telomerase r
2	130	100.0	27	19	AAW57389 Human telomerase r
3	130	100.0	108	24	ABB99682 Splice variant of
4	130	100.0	131	20	AAW97385 Amino acid sequenc
5	130	100.0	174	24	ABB99681 Splice variant of
6	130	100.0	259	19	AAW46998 Human telomerase r
7	130	100.0	283	20	AAV43128 Human telomerase r
8	130	100.0	436	24	ABB99680 Splice variant of
9	130	100.0	437	20	AAV25461 Human CRT-1 protei

10	130	100.0	438	20	AAV25462 Human CRT-1 protei
11	130	100.0	463	24	ABB99679 Splice variant of
12	130	100.0	499	24	ABB99678 Amino acid sequenc
13	130	100.0	531	19	AAW47002 Glutathione-S-tran
14	130	100.0	591	20	AAW97384 A catalytic telome
15	130	100.0	622	20	AAV25463 Human CRT-1 protei
16	130	100.0	807	19	AAW46997 Human telomerase r
17	130	100.0	807	20	AAV00637 N-terminal truncat
18	130	100.0	807	20	AAV00646 Truncated telomera
19	130	100.0	936	20	AAV00642 Truncated telomera
20	130	100.0	936	20	AAV00651 Truncated telomera
21	130	100.0	948	20	AAV00639 N-terminal truncat
22	130	100.0	948	20	AAV00648 Truncated telomera
23	130	100.0	949	19	AAW61349 Human telomerase p
24	130	100.0	1041	20	AAV00643 Altered C-terminus
25	130	100.0	1041	20	AAV00652 Altered C-terminus
26	130	100.0	1053	20	AAV00640 Altered C-terminus
27	130	100.0	1093	20	AAV00649 Altered C-terminus
28	130	100.0	1120	20	AAV00641 Telomerase protein
29	130	100.0	1120	20	AAV00650 Telomerase (ver. 2
30	130	100.0	1132	19	AAW71376 Human telomerase c
31	130	100.0	1132	19	AAW46957 Human telomerase r
32	130	100.0	1132	19	AAW56113 Human telomerase r
33	130	100.0	1132	20	AAV43621 A human telomerase
34	130	100.0	1132	20	AAV28881 Human telomerase r
35	130	100.0	1132	20	AAV32090 Human telomerase r
36	130	100.0	1132	20	AAV28401 Human EST2 protein
37	130	100.0	1132	20	AAV26580 Human telomerase r
38	130	100.0	1132	20	AAV00627 Human telomerase p
39	130	100.0	1132	20	AAV00638 Truncated telomera
40	130	100.0	1132	20	AAW90251 Human catalytic te
41	130	100.0	1132	21	AAW96566 hEST2, a human tel
42	130	100.0	1132	22	ABB82765 Human telomerase r
43	130	100.0	1132	22	ABB99930 Human telomerase p
44	130	100.0	1132	22	AAW64329 Human protein #2.
45	130	100.0	1132	22	AAW64859 Heart muscle cell

ALIGNMENTS

RESULT 1
AAW57393
ID AAW57393 standard; peptide; 27 AA.
XX
AC AAW57393;
XX
DT 13-AUG-1998 (first entry)
XX Human telomerase reverse transcriptase antigenic peptide S-3.
DE
DE Human; telomerase reverse transcriptase; hTERT; TRT; diagnosis;
KW prognosis; cell proliferation; cancer; ageing; ribonucleoprotein.
XX
XX Synthetic.
OS Homo sapiens.
XX GB2317891-A.
XX
PD 08-APR-1998.
XX
PF 01-OCT-1997; 97GB-0020890.
XX
PR 14-AUG-1997; 97US-0915503.
PR 01-OCT-1996; 96US-0724643.
PR 18-APR-1997; 97US-0844419.
PR 25-APR-1997; 97US-0846017.
PR 06-MAY-1997; 97US-0851843.
PR 09-MAY-1997; 97US-0854050.
PR 14-AUG-1997; 97US-0911312.
PR 14-AUG-1997; 97US-0912951.
XX (GERO-) GERON CORP.
PA

us-08-854-050-114.rag

Thu Nov 13 12:07:04 2003

```

PR 09-MAY-1997; 97US-0854050.
PR 14-AUG-1997; 97US-0911312.
PR 14-AUG-1997; 97US-0912951.
PA (UYTE-) UNIV TECHNOLOGY CORP.
XX Andrews WH, Cech TR, Chapman KB, Harley C, Lingner J;
XX Morin GB, Nakamura T, Harley CB;
XX WPI; 1998-171633/16.
XX Pure and recombinant human Telomerase Reverse Transcriptase and its
XX variants - are useful in the diagnosis, prognosis and treatment of
XX cell proliferation conditions especially cancer and ageing
XX Example 8; Fig 54; 387pp; English.
XX The present sequence represents an antigenic peptide from human
XX telomerase reverse transcriptase (hTERT), from the present invention. The
XX present invention also describes the following methods: (A) determining
XX whether a test compound is a modulator of hTERT, by detecting the change
XX in hTERT recombinant protein or polynucleotide, on administration of the
XX compound; (B) preparation of recombinant telomerase by contacting a
XX protein preparation of hTERT with a telomerase RNA component; (C)
XX detection of the hTERT RNA or protein in a sample by binding a relevant
XX probe to the sample and detecting the complex formed or in the case of
XX RNA detection, amplifying the product with presence of hTERT in the sample;
XX and (D) increasing the proliferation of a vertebrate cell by increasing
XX cell vertebrate cell proliferation to create a medicament that inhibits
XX ageing. A protein preparation of hTERT and the polynucleotide encoding
XX hTERT can be used in the manufacture of medicaments for inhibiting the
XX effect of ageing or cancer. Inhibitors of telomerase activity can be
XX used to treat conditions that are associated with high telomerase
XX activity. A protein preparation of hTERT can also be used in the new
XX methods.
XX SQ Sequence 27 AA;
XX Query Match 100.0%; Score 130; DB 19; Length 27;
XX Best Local Similarity 100.0%; Pred. No. 1e-12; 0; Indels 0; Gaps 0;
XX Matches 27; Conservative 0; Mismatches 0;
OY 1 ARTFREKRAERLTSRVKALFSLVNYE 27
Db 1 ARTFREKRAERLTSRVKALFSLVNYE 27
RESULT 3
ID ABB99682
XX ABB99682 standard; protein; 108 AA.
XX AC ABB99682;
XX DT 28-MAR-2003 (first entry)
XX DE Splice variant of a human telomerase reverse transcriptase fragment.
XX KW Human; telomerase reverse transcriptase; hTERT; T cell response;
XX OS Homo sapiens.
XX PN WO200294312-A1.
XX PD 28-NOV-2002.
XX PF 16-MAY-2002; 2002WO-NO00176.
XX PR 21-MAY-2001; 2001GB-0012342.

```


XX SQ Sequence 131 AA;

Query Match 100.0%; Score 130; DB 20; Length 131;
Best Local Similarity 100.0%; Pred. No. 5.8e-12;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 1 ARTFREKRAERLTSRVKALFSLVNYE 27
|||||
DB 101 ARTFREKRAERLTSRVKALFSLVNYE 127

RESULT 5
ABB99681
ID ABB99681 standard; protein; 174 AA.
XX AC ABB99681;
XX DT 28-MAR-2003 (first entry)
XX DE Splice variant of a human telomerase reverse transcriptase fragment.
XX KW Human; telomerase reverse transcriptase; hTERT; T cell response;
XX KW vaccine; cancer.
XX OS Homo sapiens.
XX PN WO200294312-A1.
XX PD 28-NOV-2002.
XX PF 16-MAY-2002; 2002WO-NO00176.
XX PR 21-MAY-2001; 2001GB-0012342.
XX (GEMV-) GEMVAX AS.
XX PI Eriksen JA, Gaudernack G, Moller M, Saeboe-Larsen S;
XX DR WPI; 2003-129380/12.
XX PT New polypeptides derived from human telomerase reverse transcriptase,
XX PT useful in preparing a medicament for treating or preventing cancer, or
XX PT in preparing a diagnostic for diagnosing cancer, e.g. breast cancer or
XX PT prostate cancer -
XX PS Disclosure; Fig 2; 56pp; English.
XX CC The present sequence represents a splice variant of a fragment of human
XX CC telomerase reverse transcriptase (hTERT). The specification describes
XX CC peptides derived from hTERT, which are capable of inducing a T cell
XX CC response and are used in medicine. The hTERT peptides and nucleic acids
XX CC encoding them are useful in preparing a medicament, which is a vaccine,
XX CC an antisense molecule, or is capable of generating an antisense molecule
XX CC in vivo, for treating cancer, or in preparing a diagnostic for diagnosing
XX CC cancer. The cancer is, for example, breast cancer, prostate cancer,
XX CC pancreatic cancer, colo-rectal cancer, lung cancer, malignant melanoma,
XX CC leukemia, lymphoma, ovarian cancer, cervical cancer, or a biliary tract
XX CC carcinoma.
XX SQ Sequence 174 AA;

Query Match 100.0%; Score 130; DB 24; Length 174;
Best Local Similarity 100.0%; Pred. No. 7.9e-12;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARTFREKRAERLTSRVKALFSLVNYE 27
|||||
DB 9 ARTFREKRAERLTSRVKALFSLVNYE 35

RESULT 6
AAW46998

PA (GEMV-) GEMVAX AS.
XX Eriksen JA, Gaudernack G, Moller M, Saeboe-Larsen S;
XX WPI; 2003-129380/12.
XX New polypeptides derived from human telomerase reverse transcriptase,
XX useful in preparing a medicament for treating or preventing cancer, or
XX PT in preparing a diagnostic for diagnosing cancer, e.g. breast cancer or
XX PT prostate cancer -
XX PS Disclosure; Fig 2; 56pp; English.
XX CC The present sequence represents a splice variant of a fragment of human
XX CC telomerase reverse transcriptase (hTERT). The specification describes
XX CC peptides derived from hTERT, which are capable of inducing a T cell
XX CC response and are used in medicine. The hTERT peptides and nucleic acids
XX CC encoding them are useful in preparing a medicament, which is a vaccine,
XX CC an antisense molecule, or is capable of generating an antisense molecule
XX CC in vivo, for treating cancer, or in preparing a diagnostic for diagnosing
XX CC cancer. The cancer is, for example, breast cancer, prostate cancer,
XX CC pancreatic cancer, colo-rectal cancer, lung cancer, malignant melanoma,
XX CC leukemia, lymphoma, ovarian cancer, cervical cancer, or a biliary tract
XX CC carcinoma.
XX SQ Sequence 108 AA;

Query Match 100.0%; Score 130; DB 24; Length 108;
Best Local Similarity 100.0%; Pred. No. 4.7e-12;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARTFREKRAERLTSRVKALFSLVNYE 27
|||||
DB 9 ARTFREKRAERLTSRVKALFSLVNYE 35

RESULT 4
AAW97385
ID AAW97385 standard; Protein; 131 AA.
XX AC AAW97385;
XX DT 14-MAY-1999 (first entry)
XX DE Amino acid sequence of the specification.
XX KW Catalytic telomerase; diagnosis; disease; telomerase activity.
XX OS Homo sapiens.
XX PN JP11046768-A.
XX PD 23-FEB-1999.
XX PF 01-AUG-1997; 97JP-0207708.
XX PR 01-AUG-1997; 97JP-0207708.
XX (MITU) MITSUBISHI CHEM CORP.
XX WPI; 1999-208111/18.
XX N-PSDB; AAX15924.
XX New catalytic protein of telomerase of a higher animal and a gene
XX PT coding it, useful for diagnosis of diseases caused by the change in
XX PT activity of a telomerase
XX Example 1; Page 14; 18pp; Japanese.
XX CC The specification describes a human catalytic telomerase protein.
XX CC The products are useful in drug compositions for the diagnosis
XX CC of diseases caused by the change in activity of telomerase. The
XX CC present sequence appears in the specification.

us-08-854-050-114.rag

Thu Nov 13 12:07:04 2003

AAW46998 standard; Protein; 259 AA.
AAW46998;
13-AUG-1998 (first entry)
Human telomerase reverse transcriptase protein from cDNA clone 712562.
Human; telomerase reverse transcriptase; hTERT; TERT; diagnosis;
prognosis; cell proliferation; cancer; ageing; ribonucleoprotein.
Homo sapiens.
GB2317891-A.
08-APR-1998.
01-OCT-1997; 97GB-0020890.
14-AUG-1997; 97US-0915503.
01-OCT-1996; 96US-0724643.
18-APR-1997; 97US-0844419.
25-APR-1997; 97US-0846017.
06-MAY-1997; 97US-0851843.
09-MAY-1997; 97US-0854050.
14-AUG-1997; 97US-0911312.
14-AUG-1997; 97US-0912951.
(GERO-) GERON CORP.
(UYTE-) UNIV TECHNOLOGY CORP.
Andrews WH, Cech TR, Chapman KB, Harley C, Lingner J;
Morin GB, Nakamura T, Harley CB;
WPI; 1998-171633/16.
N-PSDB; AA22379.
Pure and recombinant human Telomerase Reverse Transcriptase and its
variants - are useful in the diagnosis, prognosis and treatment of
cell proliferation conditions especially cancer and ageing
Example 1; Fig 19; 387pp; English.
The present sequence represents a human telomerase reverse transcriptase
(hTERT) protein from a cDNA clone from the present invention. The present
invention also describes the following methods: (A) determining whether
a test compound is a modulator of hTERT, by detecting the change in hTERT
recombinant protein or polynucleotide, on administration of the compound;
(B) preparation of recombinant telomerase by contacting a protein
preparation of hTERT with a telomerase RNA component; (C) detection of
the hTERT RNA or protein in a sample by binding a relevant probe to the
sample and detecting the complex formed or in the case of RNA detection,
amplifying the product with presence of hTERT in the sample; and (D)
increasing the proliferation of a vertebrate cell by increasing hTERT
expression; and (E) the use of an agent that causes an increase in cell
proliferation to create a medicament that inhibits
vertebrate cell proliferation of hTERT and the polynucleotide encoding
ageing. A protein preparation of hTERT and the polynucleotide encoding
hTERT can be used in the manufacture of medicaments for inhibiting the
effect of ageing or cancer. Inhibitors of telomerase activity can be
used to treat conditions that are associated with high telomerase
activity. A protein preparation of hTERT can also be used in the new
methods.
SQ Sequence 259 AA;
Query Match 100.0%; Score 130; DB 19; Length 259;
Best Local Similarity 100.0%; Pred. No. 1.2e-11;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ARTFREKRAERLTSRVKALFSLVNYE 27
DB 94 ARTFREKRAERLTSRVKALFSLVNYE 120
AAW46998 standard; Protein; 259 AA.
AAW46998;
13-AUG-1998 (first entry)
Human telomerase reverse transcriptase protein from cDNA clone 712562.
Human; telomerase reverse transcriptase; hTERT; TERT; diagnosis;
prognosis; cell proliferation; cancer; ageing; ribonucleoprotein.
Homo sapiens.
GB2317891-A.
08-APR-1998.
01-OCT-1997; 97GB-0020890.
14-AUG-1997; 97US-0915503.
01-OCT-1996; 96US-0724643.
18-APR-1997; 97US-0844419.
25-APR-1997; 97US-0846017.
06-MAY-1997; 97US-0851843.
09-MAY-1997; 97US-0854050.
14-AUG-1997; 97US-0911312.
14-AUG-1997; 97US-0912951.
(GERO-) GERON CORP.
(UYTE-) UNIV TECHNOLOGY CORP.
Andrews WH, Cech TR, Chapman KB, Harley C, Lingner J;
Morin GB, Nakamura T, Harley CB;
WPI; 1998-171633/16.
N-PSDB; AA22379.
Pure and recombinant human Telomerase Reverse Transcriptase and its
variants - are useful in the diagnosis, prognosis and treatment of
cell proliferation conditions especially cancer and ageing
Example 1; Fig 19; 387pp; English.
The present sequence represents a human telomerase reverse transcriptase
(hTERT) protein from a cDNA clone from the present invention. The present
invention also describes the following methods: (A) determining whether
a test compound is a modulator of hTERT, by detecting the change in hTERT
recombinant protein or polynucleotide, on administration of the compound;
(B) preparation of recombinant telomerase by contacting a protein
preparation of hTERT with a telomerase RNA component; (C) detection of
the hTERT RNA or protein in a sample by binding a relevant probe to the
sample and detecting the complex formed or in the case of RNA detection,
amplifying the product with presence of hTERT in the sample; and (D)
increasing the proliferation of a vertebrate cell by increasing hTERT
expression; and (E) the use of an agent that causes an increase in cell
proliferation to create a medicament that inhibits
vertebrate cell proliferation of hTERT and the polynucleotide encoding
ageing. A protein preparation of hTERT and the polynucleotide encoding
hTERT can be used in the manufacture of medicaments for inhibiting the
effect of ageing or cancer. Inhibitors of telomerase activity can be
used to treat conditions that are associated with high telomerase
activity. A protein preparation of hTERT can also be used in the new
methods.
SQ Sequence 259 AA;
Query Match 100.0%; Score 130; DB 19; Length 259;
Best Local Similarity 100.0%; Pred. No. 1.2e-11;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ARTFREKRAERLTSRVKALFSLVNYE 27
DB 94 ARTFREKRAERLTSRVKALFSLVNYE 120

RESULT 7
AA43128
ID AAY43128 standard; Protein; 283 AA.
XX
AC AAY43128;
XX
DT 20-DEC-1999 (first entry)
XX
DE Human telomerase reverse transcriptase.
XX
DE Human telomerase reverse transcriptase; hTERT; antibody; diagnosis;
XX
KW Human telomerase-related disease; cancer.
KW
XX Homo sapiens.
OS
XX WO9950407-A1.
PN
XX 07-OCT-1999.
PD
XX 26-MAR-1999; 99WO-JP01557.
PF
XX 26-MAR-1998; 98JP-0098486.
PR
XX (KYOW) KYOWA HAKKO KOGYO KK.
PA
XX Hanai N, Yamasaki M, Shibata K, Furuya A, Mikuni O, Anazawa H;
PI
XX WPI; 1999-591316/50.
DR
XX New monoclonal antibody recognizing human telomerase catalytic subunit
XX (hTERT) useful for treating and diagnosing cancer -
PT
XX Claim 2; Page 72-73; 78pp; Japanese.
PS
XX This sequence represents the human telomerase reverse transcriptase
XX (hTERT). The invention relates to a monoclonal antibody recognising the
CC hTERT. The antibody can be used for the investigation, diagnosis and
CC treatment of telomerase-related diseases, especially diseases in which
CC telomerase expression is up-regulated e.g. cancers.
CC
XX Sequence 283 AA;
SQ
Query Match 100.0%; Score 130; DB 20; Length 283;
Best Local Similarity 100.0%; Pred. No. 1.4e-11;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ARTFREKRAERLTSRVKALFSLVNYE 27
DB 94 ARTFREKRAERLTSRVKALFSLVNYE 120
RESULT 8
ABB99680
ID ABB99680 standard; protein; 436 AA.
XX
AC ABB99680;
XX
DT 28-MAR-2003 (first entry)
XX
DE Splice variant of a human telomerase reverse transcriptase fragment.
XX
KW Human; telomerase reverse transcriptase; hTERT; T cell response;
KW vaccine; cancer.
XX
OS Homo sapiens.
XX
PN WO200294312-A1.
XX
XX 28-NOV-2002.
PD
XX 16-MAY-2002; 2002WO-NO00176.
PF

XX PR 21-MAY-2001; 2001GB-0012342.
 XX PA (GEMV-) GEMVAX AS.
 XX PI Eriksen JA, Gaudernack G, Moller M, Saeboe-Larssen S;
 XX PS WPI; 1999-430393/36.
 XX PT Novel gene, useful in detection of telomerase activity and cancer
 XX PT cells as well as screening telomerase inhibitors for treatment of
 XX PT cancers
 XX PS Claim 2; Page 31-32; 44pp; Japanese.
 XX CC This invention describes novel human CRT-1 genes and their encoded
 XX CC proteins containing a reverse transcriptase motif, which act as
 XX CC telomerase inhibitors. The gene, its encoded protein and derived
 XX CC antibodies can be used to provide base sequence information, detect
 XX CC telomerase activity and cancer cells, and to screen telomerase
 XX CC inhibitors. The detection method is simple and effective.
 XX SQ Sequence 437 AA;
 CC Query Match 100.0%; Score 130; DB 24; Length 436;
 CC Best Local Similarity 100.0%; Pred. No. 2.2e-11;
 CC Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ARTFRREKRAERLTSRVKALFSLVNYE 27
 DB 9 ARTFRREKRAERLTSRVKALFSLVNYE 35
 RESULT 9
 AAY25461
 ID AAY25461 standard; Protein; 437 AA.
 AC AAY25461;
 DT 22-SEP-1999 (first entry)
 DE Human CRT-1 protein #1.
 KW CRT-1; reverse transcriptase; telomerase; inhibitor; detection;
 KW telomerase activity; cancer cell; screening; human.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT Protein 1..437
 FT /label= CRT-1
 FT /note= "Partial sequence, no stop codon given"
 PN WO9935261-A1.
 XX 15-JUL-1999.
 XX 08-JAN-1999; 99WO-JP00039.
 XX 06-MAY-1998; 98JP-0139177.
 XX 08-JAN-1998; 98JP-0013232.
 XX 30-JAN-1998; 98JP-0033584.
 XX (CHUS) CHUGAI SEIYAKU KK.
 XX Tsuchiya M, Yoshida K;
 XX WPI; 1999-430393/36.
 XX N-PSDB; AAX88250.
 XX Novel gene, useful in detection of telomerase activity and cancer
 XX PT cells as well as screening telomerase inhibitors for treatment of
 XX PT cancers
 XX PS Example 1; Page 35-36; 44pp; Japanese.
 XX CC This invention describes novel human CRT-1 genes and their encoded
 XX CC proteins containing a reverse transcriptase motif, which act as
 XX CC telomerase inhibitors. The gene, its encoded protein and derived

DR WPI; 1999-430393/36.
 XX N-PSDB; AAX88243.
 PT Novel gene, useful in detection of telomerase activity and cancer
 PT cells as well as screening telomerase inhibitors for treatment of
 PT cancers
 XX Claim 2; Page 31-32; 44pp; Japanese.
 XX This invention describes novel human CRT-1 genes and their encoded
 XX proteins containing a reverse transcriptase motif, which act as
 XX telomerase inhibitors. The gene, its encoded protein and derived
 XX antibodies can be used to provide base sequence information, detect
 XX telomerase activity and cancer cells, and to screen telomerase
 XX inhibitors. The detection method is simple and effective.
 XX SQ Sequence 437 AA;
 CC Query Match 100.0%; Score 130; DB 20; Length 437;
 CC Best Local Similarity 100.0%; Pred. No. 2.2e-11;
 CC Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ARTFRREKRAERLTSRVKALFSLVNYE 27
 DB 132 ARTFRREKRAERLTSRVKALFSLVNYE 158
 RESULT 10
 AAY25462
 ID AAY25462 standard; Protein; 438 AA.
 AC AAY25462;
 DT 22-SEP-1999 (first entry)
 DE Human CRT-1 protein #2.
 KW CRT-1; reverse transcriptase; telomerase; inhibitor; detection;
 KW telomerase activity; cancer cell; screening; human.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT Protein 1..438
 FT /label= CRT-1
 FT /note= "Partial sequence, no stop codon given"
 PN WO9935261-A1.
 XX 15-JUL-1999.
 XX 08-JAN-1999; 99WO-JP00039.
 XX 06-MAY-1998; 98JP-0139177.
 XX 08-JAN-1998; 98JP-0013232.
 XX 30-JAN-1998; 98JP-0033584.
 XX (CHUS) CHUGAI SEIYAKU KK.
 XX Tsuchiya M, Yoshida K;
 XX WPI; 1999-430393/36.
 XX N-PSDB; AAX88250.
 XX Novel gene, useful in detection of telomerase activity and cancer
 XX PT cells as well as screening telomerase inhibitors for treatment of
 XX PT cancers
 XX PS Example 1; Page 35-36; 44pp; Japanese.
 XX CC This invention describes novel human CRT-1 genes and their encoded
 XX CC proteins containing a reverse transcriptase motif, which act as
 XX CC telomerase inhibitors. The gene, its encoded protein and derived

xx	The present sequence represents a splice variant of a fragment of human
xx	telomerase reverse transcriptase (hTERT). The specification describes
cc	peptides derived from hTERT, which are capable of inducing a T cell
cc	response and are used in medicine. The hTERT peptides and nucleic acids
cc	encoding them are useful in preparing a medicament, which is a vaccine,
cc	an antisense molecule, or is capable of generating an antisense molecule
cc	in vivo, for treating cancer, or in preparing a diagnostic for diagnosing
cc	cancer. The cancer is, for example, breast cancer, prostate cancer,
cc	pancreatic cancer, colo-rectal cancer, lung cancer, malignant melanoma,
cc	leukemia, lymphoma, ovarian cancer, cervical cancer, or a biliary tract
cc	carcinoma.
xx	
SQ	Sequence 463 AA;
	Query Match 100.0%; Score 130; DB 24; Length 463;
	Best Local Similarity 100.0%; Pred.No. 2.3e-11;
	Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0
Qy	1 ARTPREKRAELTISRVALFSVLNYYE 27
Dp	9 ARTPREKRAELTISRVALFSVLNYYE 35

XX	The present sequence represents a fragment of human telomerase reverse
CC	transcriptase (hTERT). The specification describes peptides derived from
CC	hTERT, which are capable of inducing a T cell response and are used in
CC	medicine. The hTERT peptides and nucleic acids encoding them are useful
CC	in preparing a medicament, which is a vaccine, an antisense molecule, or
CC	is capable of generating an antisense molecule in vivo, for treating
CC	cancer, or in preparing a diagnostic for diagnosing cancer. The cancer
CC	is, for example, breast cancer, prostate cancer, pancreatic cancer,
CC	colo-rectal cancer, lung cancer, malignant melanoma, leukemia, lymphoma,
CC	ovarian cancer, cervical cancer, or a biliary tract carcinoma.
XX	
SQ	Sequence 499 AA;
	Query Match 100.0%; Score 130; DB 24; Length 499;
	Best Local Similarity 100.0%; Pred. No. 2.5e-11;
	Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy	1 ARTFRREKRAERLTSRVKALFSLVNYE 27
Db	9 ARTFRREKRAERLTSRVKALFSLVNYE 35
RESULT 13	
AAM47002	ID AAM47002 standard; Protein; 531 AA.
XX AC	AAM47002;
XX DT	13-AUG-1998 (first entry)
XX DE	Glutathione-S-transferase and hTERT fusion protein 2.
XX KW	Human; telomerase reverse transcriptase; hTERT; TBT; diagnosis;
XX OS	prognosis; cell proliferation; cancer; ageing; ribonucleoprotein.
XX	Synthetic.

```

OS Homo sapiens.
XX
FH Key
FT Region 1..221 Location/Qualifiers
FT /note= "glutathione-S-transferase fragment"
FT Region 249..531
FT /note= "hTERT protein fragment"
XX
PN GB2317891-A.
XX
XX
PD 08-APR-1998.
XX
XX
PE 01-OCT-1997; 97GB-0020890.
XX
XX
PR 14-AUG-1997; 97US-0915503.
PR 01-OCT-1996; 96US-0724643.
PR 18-APR-1997; 97US-0844419.
PR 25-APR-1997; 97US-0846017.
PR 06-MAY-1997; 97US-0851843.
PR 09-MAY-1997; 97US-0854050.
PR 14-AUG-1997; 97US-0911312.
PR 14-AUG-1997; 97US-0912951.
XX
XX (GERO-) GERON CORP.
XX (UYTE-) UNIV TECHNOLOGY CORP.
XX
XX Andrews WH, Cech TR, Chapman KB, Harley C, Lingner J;
XX Morin GB, Nakamura T, Harley CB;
XX WPI; 1998-171633/16.
XX
XX Pure and recombinant human Telomerase Reverse Transcriptase and its
XX variants - are useful in the diagnosis, prognosis and treatment of
XX cell proliferation conditions especially cancer and ageing
XX
XX Example 6; Page 225; 387pp; English.
XX
XX The present sequence represents a fusion protein from an example
XX of the present invention which describes human telomerase reverse
XX transcriptase (hTERT). The present invention also describes the
XX following methods: (A) determining whether a test compound is
XX a modulator of hTERT, by detecting the change in hTERT recombinant
XX protein or polynucleotide, on administration of the compound;
XX (B) preparation of recombinant telomerase by contacting a protein
XX preparation of hTERT with a telomerase RNA component; (C) detection
XX of the hTERT RNA or protein in a sample by binding a relevant
XX probe to the sample and detecting the complex formed or in the case of
XX RNA detection, amplifying the product and correlating the presence of
XX complex or amplification product with presence of hTERT in the sample;
XX and (D) increasing the proliferation of a vertebrate cell by increasing
XX hTERT expression; and (E) the use of an agent that causes an increase in
XX cell vertebrate cell proliferation to create a medicament that inhibits
XX ageing. A protein preparation of hTERT and the polynucleotide encoding
XX hTERT can be used in the manufacture of medicaments for inhibiting the
XX effect of ageing or cancer. Inhibitors of telomerase activity can be
XX used to treat conditions that are associated with high telomerase
XX activity. A protein preparation of hTERT can also be used in the new
XX methods.
XX
XX Sequence 531 AA;
SQ
Query Match 100.0%; Score 130; DB 19; Length 531;
Best Local Similarity 100.0%; Pred. No. 2.7e-11;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ARTFREKKAERLTSSVKALFSLVNYE 27
DB 342 ARTFREKKAERLTSSVKALFSLVNYE 368
RESULT 14
AAW97384
ID AAW97384 standard; Protein; 591 AA.

```

```

XX AAW97384;
XX
XX 14-MAY-1999 (first entry)
XX
XX A catalytic telomerase protein.
XX
XX Catalytic telomerase; diagnosis; disease; telomerase activity.
XX
XX Homo sapiens.
XX
XX JP11046768-A.
XX
XX 23-FEB-1999.
XX
XX 01-AUG-1997; 97JP-0207708.
XX
XX 01-AUG-1997; 97JP-0207708.
XX (MITU ) MITSUBISHI CHEM CORP.
XX
XX WPI; 1999-208111/18.
XX N-PSDB; AAX15923.
XX
XX New catalytic protein of telomerase of a higher animal and a gene
XX coding it - useful for diagnosis of diseases caused by the change in
XX activity of a telomerase
XX
XX Claim 1; Page 11-14; 18pp; Japanese.
XX
XX The present sequence represents a catalytic telomerase protein.
XX The products are useful in drug compositions for the diagnosis
XX of diseases caused by the change in activity of telomerase.
XX
XX Sequence 591 AA;
SQ
Query Match 100.0%; Score 130; DB 20; Length 591;
Best Local Similarity 100.0%; Pred. No. 3.1e-11;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ARTFREKKAERLTSSVKALFSLVNYE 27
DB 101 ARTFREKKAERLTSSVKALFSLVNYE 127
RESULT 15
AAW97384
ID AAY25463 standard; Protein; 622 AA.
XX
XX AAY25463;
XX
XX 22-SEP-1999 (first entry)
XX
XX Human CRT-1 protein #3.
XX
XX CRT-1; reverse transcriptase; telomerase; inhibitor; detection;
XX telomerase activity; cancer cell; screening; human.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX Protein 1..622
XX /label= CRT-1
XX /note= "Partial sequence, no stop codon given"
XX
XX WO9935261-A1.
XX
XX 15-JUL-1999.
XX
XX 08-JAN-1999; 99WO-JP000039.
XX
XX 06-MAY-1998; 98JP-0139177.
XX 08-JAN-1998; 98JP-0013232.

```


GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 12, 2003, 19:43:50 ; Search time 12.566 Seconds
(without alignments)
90.911 Million cell updates/sec

Title: US-08-854-050-114

Perfect score: 130

Sequence: 1 ATFRKRAELTSRKALFSLVLYE 27

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

1: /cgn2_6/prodata/1/iaa/5A COMB.pep.*

2: /cgn2_6/prodata/1/iaa/5B COMB.pep.*

3: /cgn2_6/prodata/1/iaa/6A COMB.pep.*

4: /cgn2_6/prodata/1/iaa/6B COMB.pep.*

5: /cgn2_6/prodata/1/iaa/PCBUS COMB.pep.*

6: /cgn2_6/prodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	130	100.0	27	3	US-08-851-843A-114
2	130	100.0	27	3	US-08-851-843A-114
3	130	100.0	27	3	US-08-851-843A-114
4	130	100.0	27	3	US-08-851-843A-114
5	130	100.0	27	3	US-08-851-843A-114
6	130	100.0	27	3	US-08-851-843A-114
7	130	100.0	27	3	US-08-851-843A-114
8	130	100.0	27	3	US-08-851-843A-114
9	130	100.0	27	3	US-08-851-843A-114
10	130	100.0	27	3	US-08-851-843A-114
11	130	100.0	27	3	US-08-851-843A-114
12	130	100.0	27	3	US-08-851-843A-114
13	130	100.0	27	3	US-08-851-843A-114
14	130	100.0	27	3	US-08-851-843A-114
15	130	100.0	27	3	US-08-851-843A-114
16	130	100.0	27	3	US-08-851-843A-114
17	130	100.0	27	3	US-08-851-843A-114
18	130	100.0	27	3	US-08-851-843A-114
19	130	100.0	27	3	US-08-851-843A-114
20	130	100.0	27	3	US-08-851-843A-114
21	130	100.0	27	3	US-08-851-843A-114
22	130	100.0	27	3	US-08-851-843A-114
23	130	100.0	27	3	US-08-851-843A-114
24	130	100.0	27	3	US-08-851-843A-114
25	130	100.0	27	3	US-08-851-843A-114
26	130	100.0	27	3	US-08-851-843A-114
27	130	100.0	27	3	US-08-851-843A-114

28 130 100.0 1132 4 US-09-052-919-2 Sequence 2, Appli
29 130 100.0 1132 4 US-08-912-951-2 Sequence 2, Appli
30 130 100.0 1154 3 US-08-974-549A-611 Sequence 611, App
31 130 100.0 1154 4 US-08-912-951-323 Sequence 323, App
32 130 100.0 1189 3 US-08-974-549A-613 Sequence 613, App
33 130 100.0 1189 4 US-08-912-951-325 Sequence 325, App
34 130 100.0 1200 3 US-08-974-549A-612 Sequence 612, App
35 130 100.0 1200 4 US-08-912-951-324 Sequence 324, App
36 130 100.0 1285 3 US-08-974-549A-600 Sequence 600, App
37 130 100.0 1285 4 US-08-912-951-314 Sequence 314, App
38 130 100.0 1407 3 US-08-974-549A-628 Sequence 628, App
39 130 100.0 1407 4 US-08-912-951-334 Sequence 334, App
40 124 95.4 564 3 US-08-851-843A-101 Sequence 101, App
41 124 95.4 564 3 US-08-974-549A-267 Sequence 267, App
42 124 95.4 564 3 US-08-854-050-101 Sequence 101, App
43 124 95.4 564 4 US-09-430-323-101 Sequence 101, App
44 115.5 88.8 515 3 US-08-974-549A-604 Sequence 604, App
45 115.5 88.8 515 4 US-08-912-951-318 Sequence 318, App

ALIGNMENTS

RESULT 1
US-08-851-843A-114
; Sequence 114, Application US/08851843A
; Patent No. 6093809
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: No. 6093809el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/851,843A
; FILING DATE: 06-MAY-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002930US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 114:

```
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-851-843A-114

Query Match          100.0%; Score 130; DB 3; Length 27;
Best Local Similarity 100.0%; Pred. No. 4.5e-13;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARTFRREKRAERLTSRVKALFSLVNYE 27
      |||||
Db 1 ARTFRREKRAERLTSRVKALFSLVNYE 27
      |||||

RESULT 2
US-08-974-549A-234
; Sequence 234, Application US/08974549A
; Patent No. 6166178
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin B.
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 727
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,549A
; FILING DATE: 19-NOV-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/911,312
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/912,951
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/915,503
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/17618

; FILING DATE: 01-OCT-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/17885
; FILING DATE: 01-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph Ted
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002610US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 234:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-974-549A-234

Query Match          100.0%; Score 130; DB 3; Length 27;
Best Local Similarity 100.0%; Pred. No. 4.5e-13;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARTFRREKRAERLTSRVKALFSLVNYE 27
      |||||
Db 1 ARTFRREKRAERLTSRVKALFSLVNYE 27
      |||||

RESULT 3
US-08-854-050-114
; Sequence 114, Application US/08854050
; Patent No. 6261836
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: No. 6261836el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/854,050
; FILING DATE: 09-MAY-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
```



```
; FILING DATE: 01-OCT-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002930US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 114:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 amino acids
; TYPE: amino acid
; STRANDEDNESS: linear
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-854-050-114

Query Match 100.0%; Score 130; DB 3; Length 27;
Best Local Similarity 100.0%; Pred. No. 4.5e-13;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARTFREKRAERLTSRVKALFSLVNYE 27
Db 1 ARTFREKRAERLTSRVKALFSLVNYE 27

RESULT 4
US-09-430-323-114
; Sequence 114, Application US/09430323
; Patent No. 6309867
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; LINGNER, JOACHIM
; NAKAMURA, TORU
; CHAPMAN, KAREN B.
; MORIN, GREGG B.
; HARLEY, CALVIN
; ANDREWS, WILLIAM H.
; TITLE OF INVENTION: HUMAN TETRAHYDROXYMETHYL TELOMERASE
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/430,323
; FILING DATE: 29-Oct-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002930US
; TELECOMMUNICATION INFORMATION:
```

```
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 114:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 114:
US-09-430-323-114

Query Match 100.0%; Score 130; DB 4; Length 27;
Best Local Similarity 100.0%; Pred. No. 4.5e-13;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARTFREKRAERLTSRVKALFSLVNYE 27
Db 1 ARTFREKRAERLTSRVKALFSLVNYE 27

RESULT 5
US-08-912-951-115
; Sequence 115, Application US/08912951
; Patent No. 6475789
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; LINGNER, JOACHIM
; NAKAMURA, TORU
; CHAPMAN, KAREN B.
; MORIN, GREGG B.
; HARLEY, CALVIN
; ANDREWS, WILLIAM H.
; TITLE OF INVENTION: HUMAN TETRAHYDROXYMETHYL TELOMERASE
; NUMBER OF SEQUENCES: 335
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/912,951
; FILING DATE: 14-AUG-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
```

```
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002600US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 115:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; NAME/KEY: Peptide
; LOCATION: 1..129
; OTHER INFORMATION: /note= "TRT motifs from human"
; US-08-912-951-115

Query Match 100.0%; Score 130; DB 4; Length 27;
Best Local Similarity 100.0%; Pred. No. 4.5e-13;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARTFREKRAERLTSRVKALFSLVNYE 27
Db 1 ARTFREKRAERLTSRVKALFSLVNYE 27

RESULT 6
US-08-951-843A-67
; Sequence 67, Application US/08851843A
; Patent No. 6093809
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin B.
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: No. 6093809a1 Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/951,843A
; FILING DATE: 06-MAY-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002930US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0300
; TELEFAX: (415) 576-0300

; INFORMATION FOR SEQ ID NO: 67:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 129 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; NAME/KEY: Peptide
; LOCATION: 1..129
; OTHER INFORMATION: /note= "TRT motifs from human"
; US-08-851-843A-67

Query Match 100.0%; Score 130; DB 3; Length 129;
Best Local Similarity 100.0%; Pred. No. 2.6e-12;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARTFREKRAERLTSRVKALFSLVNYE 27
Db 101 ARTFREKRAERLTSRVKALFSLVNYE 127

RESULT 7
US-08-974-549A-13
; Sequence 13, Application US/08974549A
; Patent No. 6166178
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin B.
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 727
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,549A
; FILING DATE: 19-NOV-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/911,312
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/912,951
; FILING DATE: 14-AUG-1997
```

```
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/915,503
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/17618
; FILING DATE: 01-OCT-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/17885
; FILING DATE: 01-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph Ted
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002610US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 129 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..129
; OTHER INFORMATION: /note= "TRT motifs from human"
;
US-08-974-549A-13

Query Match 100.0%; Score 130; DB 3; Length 129;
Best Local Similarity 100.0%; Pred. No. 2.6e-12;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARTFREKRAERLTSRVKALFSLVNYE 27
|||
Db 101 ARTFREKRAERLTSRVKALFSLVNYE 127

RESULT 8
US-08-854-050-67
; Sequence 67, Application US/08854050
; Patent No. 6261836
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: No. 6261836el Telomerase
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/854,050
; FILING DATE: 09-MAY-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
```

```
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002930US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 67:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 129 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..129
; OTHER INFORMATION: /note= "TRT motifs from human"
;
US-08-854-050-67

Query Match 100.0%; Score 130; DB 3; Length 129;
Best Local Similarity 100.0%; Pred. No. 2.6e-12;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARTFREKRAERLTSRVKALFSLVNYE 27
|||
Db 101 ARTFREKRAERLTSRVKALFSLVNYE 127

RESULT 9
US-09-430-323-67
; Sequence 67, Application US/09430323
; Patent No. 6309867
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: No. 6309867el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/430,323
; FILING DATE: 29-Oct-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
```

APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 67:
SEQUENCE CHARACTERISTICS:
LENGTH: 129 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
MOLECULE TYPE: linear
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..129
OTHER INFORMATION: /note= "TRT motifs from human"
SEQUENCE DESCRIPTION: SEQ ID NO: 67:
US-09-430-323-67

Query Match 100.0%; Score 130; DB 4; Length 129;
Best Local Similarity 100.0%; Pred. No. 2.6e-12;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARTFREKRAERLTSRVKALFSLVNYE 27
Db 101 ARTFREKRAERLTSRVKALFSLVNYE 127

RESULT 10

US-08-912-951-13
Sequence 13, Application US/08912951
Patent No. 6475789

GENERAL INFORMATION:

APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin
APPLICANT: Andrews, William H.
TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND
THERAPEUTIC METHODS
NUMBER OF SEQUENCES: 335
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/912,951
FILING DATE: 14-AUG-1997
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002600US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 129 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..129
OTHER INFORMATION: /note= "TRT motifs from human"
US-08-912-951-13

Query Match 100.0%; Score 130; DB 4; Length 129;
Best Local Similarity 100.0%; Pred. No. 2.6e-12;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARTFREKRAERLTSRVKALFSLVNYE 27
Db 101 ARTFREKRAERLTSRVKALFSLVNYE 127

RESULT 11

US-08-974-549A-10
Sequence 10, Application US/08974549A
Patent No. 6166178

GENERAL INFORMATION:

APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin B.
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,549A

```

; FILING DATE: 19-NOV-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/911,312
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/912,951
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/915,503
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/17618
; FILING DATE: 01-OCT-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/17885
; FILING DATE: 01-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph Ted
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002610US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 259 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..259
; OTHER INFORMATION: /note= "protein encoded by clone 712562"
;
US-08-974-549A-10

Query Match 100.0%; Score 130; DB 3; Length 259;
Best Local Similarity 100.0%; Pred. No. 5.8e-12;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARTFRKKAERLTSRVKALFSLVNYE 27
Db 94 ARTFRKKAERLTSRVKALFSLVNYE 120

RESULT 12
US-08-912-951-10
; Sequence 10, Application US/08912951
; Patent No. 6475789
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin
; APPLICANT: Andrews, William H.

```

```

; TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND
; TITLE OF INVENTION: THERAPEUTIC METHODS
; NUMBER OF SEQUENCES: 335
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/912,951
; FILING DATE: 14-AUG-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002600US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 259 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..259
; OTHER INFORMATION: /note= "protein encoded by clone 712562"
;
US-08-912-951-10

Query Match 100.0%; Score 130; DB 4; Length 259;
Best Local Similarity 100.0%; Pred. No. 5.8e-12;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARTFRKKAERLTSRVKALFSLVNYE 27
Db 94 ARTFRKKAERLTSRVKALFSLVNYE 120

RESULT 13
US-08-974-549A-603
; Sequence 603, Application US/08974549A
; Patent No. 6166178
; GENERAL INFORMATION:

```



```
;
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 317:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 530 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-912-951-317

Query Match 100.0%; Score 130; DB 4; Length 530;
Best Local Similarity 100.0%; Pred. No. 1.3e-11;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARTFREKRAERLTSRVKALFSLVNYE 27
|||||
Db 341 ARTFREKRAERLTSRVKALFSLVNYE 367

RESULT 15
US-08-974-549A-5
; Sequence 5, Application US/08974549A
; Patent No. 6166178
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin B.
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 727
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,549A
; FILING DATE: 19-NOV-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/911,312
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/912,951
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/915,503
; FILING DATE: 14-AUG-1997

; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/17618
; FILING DATE: 01-OCT-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/17885
; FILING DATE: 01-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph Ted
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002610US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 807 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-974-549A-5

Query Match 100.0%; Score 130; DB 3; Length 807;
Best Local Similarity 100.0%; Pred. No. 2.1e-11;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARTFREKRAERLTSRVKALFSLVNYE 27
|||||
Db 642 ARTFREKRAERLTSRVKALFSLVNYE 668

Search completed: November 12, 2003, 19:53:27
Job time : 12.566 secs
```

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993-2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 12, 2003, 19:41:59 ; Search time 4.98113 Seconds
(without alignments)
226.583 Million cell updates/sec

Title: US-08-854-050-112.
Perfect score: 131
Sequence: 1 FFYVTTTQKRLFFYRKVWSK 24

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	131	100.0	1132	1	TERT_HUMAN
2	126	96.2	1122	1	TERT_MOUSE
3	70	53.4	988	1	TERT_SCHPO
4	69	52.7	1132	1	TERT_OXYTR
5	66	50.4	1031	1	TERT_EUPAE
6	63	48.1	1117	1	TERT_TETH
7	47	35.9	791	1	CO13_TETH
8	46	35.1	383	1	YGEW_ECOLI
9	46	35.1	659	1	CYOB_BUCAP
10	46	35.1	662	1	CYOB_BUCAI
11	45.5	34.7	146	1	ADP6_ARATH
12	45	34.4	420	1	BACA_RHIME
13	45	34.4	663	1	CYOB_ECOLI
14	45	34.4	4196	1	DYHC_SCHPO
15	44.5	34.0	385	1	YCT2_BACFI
16	44	33.6	239	1	UL24_HSV7J
17	44	33.6	535	1	YHIL_ECOLI
18	43.5	33.2	143	1	ADF2_PETHY
19	42.5	32.4	139	1	ADF_LILLO
20	42	32.1	154	1	OM23_NEUCR
21	42	32.1	190	1	CAKB_CANFA
22	42	32.1	190	1	CAKB_RAT
23	42	32.1	313	1	CCSA_TOBAC
24	42	32.1	331	1	COAA_RHIME
25	42	32.1	349	1	VP7_BT10
26	42	32.1	349	1	VP7_BT17
27	42	32.1	349	1	VP7_BT15
28	42	32.1	349	1	VP7_BT2A
29	42	32.1	382	1	OPS5_DROME
30	42	32.1	821	1	SVI_TETH
31	41.5	31.7	139	1	ADP3_MAIZE
32	41.5	31.7	469	1	NRAM_IATIT
33	41.5	31.7	469	1	NRAM_IAUDO

34	41.5	31.7	469	1	NRAM_IATV17
35	41.5	31.7	469	1	NRAM_IAZHS
36	41	31.3	139	1	ADFI_PETHY
37	41	31.3	190	1	CAKB_BOVIN
38	41	31.3	190	1	CAKB_HUMAN
39	41	31.3	244	1	YMI6_MARPO
40	41	31.3	352	1	MATK_SAXOP
41	41	31.3	362	1	TRMA_NEIMA
42	41	31.3	362	1	TRMA_NEIMB
43	41	31.3	426	1	YCXK_ASTLO
44	41	31.3	483	1	APM3_YEAST
45	41	31.3	492	1	NHR4_CAEEL

ALIGNMENTS

RESULT 1
TERT_HUMAN STANDARD; PRT; 1132 AA.
AC O14746; O14783;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Telomerase reverse transcriptase (EC 2.7.7.-) (Telomerase catalytic subunit) (HEST2).
GN TERT OR TRT OR EST2 OR TCS1.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97400623; PubMed=9252327;
RA Nakamura T.M., Morin G.B., Chapman K.B., Weinrich S.L., Andrews W.H., Lingner J., Harley C.B., Cech T.R.;
RT "Telomerase catalytic subunit homologs from fission yeast and human.";
RL Science 277:955-959(1997).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=97433088; PubMed=9288757;
RA Meyerson M., Counter C.M., Eaton E.N., Ellisen L.W., Steiner P., Caddle S.D., Ziaugra L., Beijersbergen R.L., Davidoff M.J., Liu Q., Bacchetti S., Haber D.A., Weinberg R.A.;
RT "hEST2, the putative human telomerase catalytic subunit gene, is up-regulated in tumor cells and during immortalization.";
RL Cell 90:785-795(1997).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=99267414; PubMed=10333526;
RA Wick M., Zubov D., Hagen G.;
RT "Genomic organization and promoter characterization of the gene encoding the human telomerase reverse transcriptase (hTERT).";
RL Gene 238:97-106(1999).
RN [4]
RP SEQUENCE FROM N.A.
RA Londono-Vallejo J.A.;
RT "Sequence of a BAC carrying the entire hTERT gene.";
RL Submitted (Oct-2001) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: TELOMERASE IS A RIBONUCLEOPROTEIN ENZYME ESSENTIAL FOR THE REPLICATION OF CHROMOSOME TERMINI IN MOST EUKARYOTES. IT ELONGATES TELOMERES. IT IS A REVERSE TRANSCRIPTASE THAT ADDS SIMPLE SEQUENCE REPEATS TO CHROMOSOME ENDS BY COPYING A TEMPLATE SEQUENCE WITHIN THE RNA COMPONENT OF THE ENZYME.
CC -!- SUBUNIT: Interacts with PINK1.
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- DISEASE: ACTIVATION OF TELOMERASE HAS BEEN IMPLICATED IN CELL IMMORTALIZATION AND CANCER CELL PATHOGENESIS.
CC -!- SIMILARITY: BELONGS TO THE REVERSE TRANSCRIPTASE FAMILY. TELOMERASE SUBFAMILY.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration

CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).

CC EMBL; AF015950; AAC51672.1; -
 CC EMBL; AF018167; AAC51724.1; -
 CC EMBL; AF128894; AAD30037.1; -
 CC EMBL; AF128893; AAD30037.1; JOINED.
 CC EMBL; AY007685; AAG32389.1; -
 CC PIR; T03844; T03844.
 CC Genew; HGNC:11730; TERT.
 CC MIM; 187270; -
 CC GO; GO:0005696; C:telomere; TAS.
 CC GO; GO:0003721; P:telomeric template RNA reverse transcriptase...; TAS.
 CC GO; GO:0007003; P:telomeric binding; TAS.
 CC InterPro; IPR000477; RVTse.
 CC InterPro; IPR003545; Telomerase_RT.
 CC Pfam; PF00078; rvt; 1.
 CC PRINTS; PRO1365; TELOMERASERT.
 CC Transferase; RNA-directed DNA polymerase; Telomere; Nuclear protein;
 CC DNA-binding.
 CC CONFLICT 516 516 D -> G (IN REF. 2).
 CC SEQUENCE 1132 AA; 126996 MW; 94E35469CA33A0 CRC64;

Query Match 100.0%; Score 131; DB 1; Length 1132;
 Best Local Similarity 100.0%; Pred. No. 1.2e-12;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FFYVTTTFQKNRLFFYRKSWSK 24
 Db 560 FFYVTTTFQKNRLFFYRKSWSK 583

RESULT 2

TERT_MOUSE
 ID TERT_MOUSE STANDARD; PRT; 1122 AA.
 AC 070372; Q35432;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Telomerase reverse transcriptase (EC 2.7.7.-) (Telomerase catalytic
 DE subunit).
 GN TERT.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 [1]
 RN SEQUENCE FROM N.A.
 RP MEDLINE=98241176; PubMed=9582020;
 RA Greenberg R.A., Allsopp R.C., Chin L., Morin G.B., Depinho R.A.;
 RT "Expression of mouse telomerase reverse transcriptase during
 RT development, differentiation and proliferation."
 RL Oncogene 16:1723-1730(1998).
 [2]
 RN SEQUENCE FROM N.A.
 RP MEDLINE=98393668; PubMed=9724727;
 RA Martin-Rivera L., Herrera E., Albar J.P., Blasco M.A.;
 RT "Expression of mouse telomerase catalytic subunit in embryos and
 RT adult tissues."
 RL Proc. Natl. Acad. Sci. U.S.A. 95:10471-10476(1998).
 [3]
 RN SEQUENCE OF "550-616 FROM N.A."
 RP Drissi R., Cleveland J.L.;
 RT "Partial sequence of Mus musculus telomerase catalytic subunit
 RT homologous."
 RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: TELOMERASE IS A RIBONUCLEOPROTEIN ENZYME ESSENTIAL FOR
 CC THE REPLICATION OF CHROMOSOME TERMINI IN MOST EUKARYOTES. IT
 CC ELONGATES TELOMERES. IT IS A REVERSE TRANSCRIPTASE THAT ADDS

CC SIMPLE SEQUENCE REPEATS TO CHROMOSOME ENDS BY COPYING A TEMPLATE
 CC SEQUENCE WITHIN THE RNA COMPONENT OF THE ENZYME.
 CC -!- SUBUNIT: Interacts with PINK1 (By similarity).
 CC -!- SUBCELLULAR LOCATION: Nuclear.
 CC -!- SIMILARITY: BELONGS TO THE REVERSE TRANSCRIPTASE FAMILY.
 CC TELOMERASE SUBFAMILY.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).

CC EMBL; AF051911; AAC09323.1; -
 CC EMBL; AF073311; AAC34821.1; -
 CC EMBL; AF029235; AAB84200.1; -
 CC MGD; MGI:1202709; TERT.
 CC InterPro; IPR000477; RVTse.
 CC InterPro; IPR003545; Telomerase_RT.
 CC Pfam; PF00078; rvt; 1.
 CC PRINTS; PRO1365; TELOMERASERT.
 CC Transferase; RNA-directed DNA polymerase; Telomere; Nuclear protein;
 CC DNA-binding.
 CC CONFLICT 553 553 I -> V (IN REF. 3).
 CC SEQUENCE 1122 AA; 127977 MW; F85266905DD6558C CRC64;

Query Match 96.2%; Score 126; DB 1; Length 1122;
 Best Local Similarity 91.7%; Pred. No. 7.2e-12;
 Matches 22; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FFYVTTTFQKNRLFFYRKSWSK 24
 Db 550 FFYVTTTFQKNRLFFYRKSWSK 573

RESULT 3

TERT_SCHPO
 ID TERT_SCHPO STANDARD; PRT; 988 AA.
 AC O13339; O13338;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Telomerase reverse transcriptase (EC 2.7.7.-) (Telomerase catalytic
 DE subunit).
 GN TRT1 OR SPBC29A3.14C.
 OS Schizosaccharomyces pombe (Fission yeast).
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 OC Schizosaccharomycetales; Schizosaccharomycetaceae.
 OX NCBI_TaxID=4896;
 [1]
 RN SEQUENCE FROM N.A.
 RP STRAIN=972;
 RX MEDLINE=97400623; PubMed=9252327;
 RA Nakamura T.M., Morin G.B., Chapman K.B., Weinrich S.L., Andrews W.H.,
 RA Lingner J., Harley C.B., Cech T.R.;
 RT "Telomerase catalytic subunit homologs from fission yeast and human."
 RL Science 277:955-959(1997).
 [2]
 RN SEQUENCE FROM N.A.
 RP STRAIN=972;
 RX MEDLINE=21848401; PubMed=11859360;
 RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
 RA Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
 RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
 RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
 RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
 RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
 RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
 RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
 RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,

```

RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
RA Woltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H.,
RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Carrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Sipakovski G.V., Ussery D., Barrell B.G., Nurse P.,
RA "The genome sequence of Schizosaccharomyces pombe.";
RT Nature 415:871-880(2002).
CC
CC -!- FUNCTION: TELOMERASE IS A RIBONUCLEOPROTEIN ENZYME ESSENTIAL FOR
CC THE REPLICATION OF CHROMOSOME TERMINI IN MOST EUKARYOTES. IT
CC ELONGATES TELOMERES. IT IS A REVERSE TRANSCRIPTASE THAT ADDS
CC SIMPLE SEQUENCE REPEATS TO CHROMOSOME ENDS BY COPYING A TEMPLATE
CC SEQUENCE WITHIN THE RNA COMPONENT OF THE ENZYME.
CC
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC Name=2;
CC IsoId=O13339-1; Sequence=Displayed;
CC IsoId=O13339-2; Sequence=VSP_006395;
CC -!- MISCELLANEOUS: DELETION CAUSES TELOMERASE SHORTENING AND SENESCENCE.
CC -!- SIMILARITY: BELONGS TO THE REVERSE TRANSCRIPTASE FAMILY.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AF015783; AAC49802.1; -
CC EMBL; AF015783; AAC49803.1; -
CC EMBL; AL022299; CAA18391.1; -
CC PIR; T03838; T03838.
CC GeneDB SPombe; SPBC29A3.14c; -
CC InterPro; IPR000477; RVTse
CC Pfam; PF00078; rvt; 2.
CC PRINTS; PR01365; TELOMERASERT.
CC Transfaser; RNA-directed DNA polymerase; Telomere; Nuclear protein;
CC DNA-binding; Alternative splicing.
CC VARGPLIC 524 524 K -> KQ (in isoform 2).
CC FT /FTId=VSP_006395.
CC SQ SEQUENCE 988 AA; 116328 MW; AB2DC7030228F443 CRC64;

Query Match 53.4%; Score 70; DB 1; Length 988;
Best Local Similarity 45.5%; Pred. No. 0.0038;
Matches 10; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

OY 1 PFYVTTTFQKNRLFYRKSVW 22
DB 443 FFYITESSDLRNRITVYFRKDIW 464

RESULT 4
TERT_OXYTR
ID TERT_OXYTR STANDARD; PRT; 1132 AA.
AC O76332;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Telomerase reverse transcriptase (EC 2.7.7.-) (Telomerase catalytic

```

```

DE subunit) (Telomerase subunit P133).
GN TERT.
OS Oxytricha trifallax.
OC Eukaryota; Alveolata; Ciliophora; Spirotrichea; Stichotrichia;
OC Stichotrichida; Oxytrichidae; Oxytricha.
OX NCBI_TaxID=5946;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98337940; PubMed=9671703;
RA Bryan T.M., Sperger J.M., Chapman K.B., Cech T.R.;
RT "Telomerase reverse transcriptase genes identified in Tetrahymena
RT thermophila and Oxytricha trifallax.";
RL Proc. Natl. Acad. Sci. U.S.A. 95:8479-8484(1998)
CC -!- FUNCTION: TELOMERASE IS A RIBONUCLEOPROTEIN ENZYME ESSENTIAL FOR
CC THE REPLICATION OF CHROMOSOME TERMINI IN MOST EUKARYOTES. IT
CC ELONGATES TELOMERES. IT IS A REVERSE TRANSCRIPTASE THAT ADDS
CC SIMPLE SEQUENCE REPEATS TO CHROMOSOME ENDS BY COPYING A TEMPLATE
CC SEQUENCE WITHIN THE RNA COMPONENT OF THE ENZYME.
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- SIMILARITY: BELONGS TO THE REVERSE TRANSCRIPTASE FAMILY.
CC TELOMERASE SUBFAMILY.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AF060230; AAC39163.1; -
CC PIR; T31107; T31107.
CC InterPro; IPR003545; Telomerase_RT.
CC PRINTS; PR01365; TELOMERASERT.
CC Transfaser; RNA-directed DNA polymerase; Telomere; Nuclear protein;
CC DNA-binding.
CC SQ SEQUENCE 1132 AA; 134124 MW; 81E145F5F24392DC CRC64;

Query Match 52.7%; Score 69; DB 1; Length 1132;
Best Local Similarity 43.5%; Pred. No. 0.0063;
Matches 10; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

OY 1 PFYVTTTFQKNRLFYRKSVWS 23
DB 559 VFYSTEKAKEVQRFYFRKNINW 581

RESULT 5
TERT_EUPAE
ID TERT_EUPAE STANDARD; PRT; 1031 AA.
AC O00939;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Telomerase reverse transcriptase (EC 2.7.7.-) (Telomerase catalytic
DE subunit) (Telomerase subunit P123).
OS Euplotes aediculatus.
OC Eukaryota; Alveolata; Ciliophora; Spirotrichea; Hypotrichia;
OC Euplotida; Euplotidae; Euplotes.
OX NCBI_TaxID=5940;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97274210; PubMed=9110970;
RA Lingner J., Hughes T.R., Shevchenko A., Mann M., Lundblad V.,
RA Cech T.R.;
RT "Reverse transcriptase motifs in the catalytic subunit of
RT telomerase.";
RL Science 276:561-567(1997).
CC -!- FUNCTION: TELOMERASE IS A RIBONUCLEOPROTEIN ENZYME ESSENTIAL FOR
CC THE REPLICATION OF CHROMOSOME TERMINI IN MOST EUKARYOTES. IT
CC ELONGATES TELOMERES. IT IS A REVERSE TRANSCRIPTASE THAT ADDS
CC SIMPLE SEQUENCE REPEATS TO CHROMOSOME ENDS BY COPYING A TEMPLATE
CC SEQUENCE WITHIN THE RNA COMPONENT OF THE ENZYME.

```

Thu Nov 13 12:06:56 2003

CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>)
 CC or send an email to license@isb-sib.ch.
 CC -----

CC -1- SUBCELLULAR LOCATION: Nuclear.
 CC -1- SIMILARITY: BELONGS TO THE REVERSE TRANSCRIPTASE FAMILY.
 CC TELOMERASE SUBFAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>)
 CC or send an email to license@isb-sib.ch.
 CC -----

CC EMBL: U95964; AAC47515.1; -
 CC InterPro: IPR000477; RVTse.
 CC InterPro: IPR003545; Telomerase_RT.
 CC Pfam: PF00078; rvt; 1.
 CC PRINTS: PR01365; TELOMERASERT.
 CC Transferase; RNA-directed DNA polymerase; Telomere; Nuclear protein;
 CC DNA-binding.
 CC KW SEQUENCE 1031 AA; 122562 MW; 57B87A63A1FED60F CRC64;
 CC

Query Match 50.4%; Score 66; DB 1; Length 1031;
 Best Local Similarity 45.5%; Pred. No. 0.017; 6; Indels 0; Gaps 0;
 Matches 10; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 1 FFVTTTQKRLFFYRKSVW 22
 ||||| : : : : :
 DB 455 FFVTEQOKSKYKYYRKNIW 476

RESULT 6

CC ID TERT TETH STANDARD; PRT; 1117 AA.
 CC AC Q77448;
 CC 30-MAY-2000 (Rel. 39, Created)
 CC 30-MAY-2000 (Rel. 39, Last sequence update)
 CC 30-MAY-2000 (Rel. 39, Last annotation update)
 CC Telomerase reverse transcriptase (EC 2.7.7.-) (Telomerase catalytic
 CC subunit) (Telomerase subunit P133).
 CC GN TERT.
 CC OS Tetrahymena thermophila.
 CC OC Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Hymenostomatida;
 CC OC Tetrahymenina; Tetrahymena.
 CC OC NCBI_TaxID=5911;
 CC [1]
 CC SEQUENCE FROM N.A.
 CC STRAIN=B7;
 CC MEDLINE=98337940; PubMed=9671703;
 CC Bryan T.M., Sperger J.M., Chapman K.B., Cech T.R.;
 CC "Telomerase reverse transcriptase genes identified in Tetrahymena
 CC thermophila and Oxytricha trifallax."
 CC Proc. Natl. Acad. Sci. U.S.A. 95:8479-8484 (1998).
 CC [2]
 CC SEQUENCE FROM N.A.
 CC MEDLINE=98337941; PubMed=9671704;
 CC Collins K., Gandhi L.;
 CC "The reverse transcriptase component of the Tetrahymena telomerase
 CC ribonucleoprotein complex."
 CC Proc. Natl. Acad. Sci. U.S.A. 95:8485-8490 (1998).
 CC -1- FUNCTION: TELOMERASE IS A RIBONUCLEOPROTEIN ENZYME ESSENTIAL FOR
 CC THE REPLICATION OF CHROMOSOME TERMINI IN MOST EUKARYOTES. IT
 CC ELONGATES TELOMERES. IT IS A REVERSE TRANSCRIPTASE THAT ADDS
 CC SIMPLE SEQUENCE REPEATS TO CHROMOSOME ENDS BY COPYING A TEMPLATE
 CC SEQUENCE WITHIN THE RNA COMPONENT OF THE ENZYME.
 CC -1- SUBCELLULAR LOCATION: Nuclear.
 CC -1- SIMILARITY: BELONGS TO THE REVERSE TRANSCRIPTASE FAMILY.
 CC TELOMERASE SUBFAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial

CC EMBL: AF062652; AAC39135.1; -
 CC EMBL: AF061284; AAC39140.1; -
 CC PIR: T14891; T14891.
 CC InterPro: IPR000477; RVTse.
 CC InterPro: IPR003545; Telomerase_RT.
 CC Pfam: PF00078; rvt; 2.
 CC PRINTS: PR01365; TELOMERASERT.
 CC Transferase; RNA-directed DNA polymerase; Telomere; Nuclear protein;
 CC DNA-binding.
 CC KW SEQUENCE 1117 AA; 133317 MW; ESAP15E86B0F0CD8 CRC64;
 CC

Query Match 48.1%; Score 63; DB 1; Length 1117;
 Best Local Similarity 42.9%; Pred. No. 0.054;
 Matches 9; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY 2 FVVTETTFQKRLFFYRKSVW 22
 ||||| : : : : :
 DB 476 FYITEKHKGSGIFYYRKPIW 496

RESULT 7

CC ID COL3 TETH STANDARD; PRT; 791 AA.
 CC AC P98005;
 CC 01-FEB-1996 (Rel. 33, Created)
 CC 01-FEB-1996 (Rel. 33, Last sequence update)
 CC 15-SEP-2003 (Rel. 42, Last annotation update)
 CC Cytochrome c oxidase polypeptide I+III (EC 1.9.3.1) (Cytochrome c
 CC aa(3) subunit 1) (Cytochrome caa3) (A-protein).
 CC GN CAAA OR CTAD.
 CC OS Thermus thermophilus.
 CC OC Bacteria; Deinococcus-Thermus; Deinococci; Thermaceae;
 CC OC Thermus.
 CC OC NCBI_TaxID=274;
 CC [1]
 CC SEQUENCE FROM N.A.
 CC STRAIN=HB8 / ATCC 27634;
 CC MEDLINE=93194828; PubMed=8383670;
 CC Mather M.W., Springer P., Hensel S., Buse G., Fee J.A.;
 CC "Cytochrome oxidase genes from Thermus thermophilus. Nucleotide
 CC sequence of the fused gene and analysis of the deduced primary
 CC structures for subunits I and III of cytochrome caa3."
 CC J. Biol. Chem. 268:5395-5408 (1993).
 CC -1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY
 CC CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNIT 1 -
 CC 3 FORM THE FUNCTIONAL CORE OF THE ENZYME. ELECTRONS ORIGINATING IN
 CC CATALYTIC SUBUNIT OF THE ENZYME. ELECTRONS ORIGINATING IN
 CC CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2
 CC AND HEME A OF SUBUNIT 1 TO THE BINETALLIC CENTER FORMED BY HEME A3
 CC AND COPPER B. THIS CYTOCHROME C OXIDASE SHOWS PROTON PUMP ACTIVITY
 CC ACROSS THE MEMBRANE IN ADDITION TO THE ELECTRON TRANSFER.
 CC -1- CATALYTIC ACTIVITY: 4 ferrocycytochrome c + O(2) = 4 ferrocycytochrome
 CC c + 2 H(2)O.
 CC -1- COFACTOR: TWO HEME GROUPS AND COPPER B.
 CC -1- PATHWAY: Respiratory chain; terminal step.
 CC -1- SUBUNIT: POSSIBLY A HETERODIMER OF A-PROTEIN (CONTAINS: CYTOCHROME
 CC C OXIDASE SUBUNIT I AND III) AND SUBUNIT II. THE A-PROTEIN COULD
 CC ALSO PRESENT A PRECURSOR FORM OF SUBUNIT I AND III.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE HEME-COPPER
 CC RESPIRATORY OXIDASE FAMILY.
 CC -1- SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS TO THE CYTOCHROME C
 CC OXIDASE SUBUNIT 3 FAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>)
 CC or send an email to license@isb-sib.ch.
 CC -----

```

CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; M84341; AAA27485.1; -.
CC DR PIR; A46616; A46616.
CC DR HSSP; P18401; 1PFT.
CC DR -----
CC DR InterPro; IPR000883; COX1.
CC DR Pfam; PF00115; COX1; 1.
CC DR Pfam; PF00510; COX3; 1.
CC DR PRINTS; PR01165; CYCOXIDASE1.
CC DR PRODOM; PD000382; CytC_oxdse_III; 1.
CC DR PROSITE; PS00077; COX1; 1.
CC DR PROSITE; PS02533; COX3; 1.
CC KW Oxidoreductase; Heme; Copper; Transmembrane; Respiratory chain;
KW Hydrogen ion transport.
CC FT DOMAIN 1 473
CC FT COX1.
CC FT DOMAIN 545 791
CC FT TRANSMEM 29 49
CC FT TRANSMEM 78 98
CC FT TRANSMEM 111 131
CC FT TRANSMEM 155 175
CC FT TRANSMEM 201 221
CC FT TRANSMEM 244 264
CC FT TRANSMEM 282 302
CC FT TRANSMEM 312 332
CC FT TRANSMEM 347 367
CC FT TRANSMEM 381 401
CC FT TRANSMEM 423 443
CC FT TRANSMEM 464 484
CC FT TRANSMEM 556 586
CC FT TRANSMEM 617 637
CC FT TRANSMEM 657 677
CC FT TRANSMEM 691 711
CC FT TRANSMEM 729 749
CC FT TRANSMEM 771 791
CC FT METAL 73 73
CC FT METAL 250 250
CC FT METAL 254 254
CC FT METAL 299 299
CC FT METAL 300 300
CC FT METAL 385 385
CC FT METAL 387 387
CC FT METAL 250 254
CC FT CROSSLNK 250 254
CC FT SEQUENCE 791 AA; 89213 MW; F4DCF3E8AFF07606 CRC64;

Query Match 35.9%; Score 47; DB 1; Length 791;
Best Local Similarity 44.4%; Pred. No. 12;
Matches 8; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 7 TTFQKRLFFYRKSWSK 24
DB 269 STFARKPLFGYRQMWQAQ 286

RESULT 8
YGEW ECOLI ID YGEW ECOLI STANDARD; PRT; 363 AA.
AC Q46803;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein ygeW.
GN YGEW OR B2870.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R.; Plunkett G. III; Bloch C.A.; Perna N.T.; Burland V.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,

or send an email to license@isb-sib.ch).
RA -----
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RA "The complete genome sequence of Escherichia coli K-12.";
RA Science 277:1453-1474(1997).
RA RL -----
RA -!- SIMILARITY: SOME, TO ORNITHINE CARBAMOYLTRANSFERASE.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U28375; AAA83051.1; -.
CC DR EMBL; AE000370; AAC75908.1; -.
CC DR PIR; F65070; F65070.
CC DR EcoGene; EG13053; ygeW.
CC DR InterPro; IPR006130; Asp/Orn Cotranf.
CC DR InterPro; IPR006131; OTCace_O.
CC DR InterPro; IPR006132; OTCace_P.
CC DR Pfam; PF00185; OTCace; 1.
CC DR Pfam; PF02729; OTCace_N; 1.
CC DR PRINTS; PR0100; AOTCACE.
CC KW Hypothetical protein; Complete proteome.
KW SEQUENCE 363 AA; 40212 MW; F8436BC00BF2DC83 CRC64;

Query Match 35.1%; Score 46; DB 1; Length 363;
Best Local Similarity 42.1%; Pred. No. 7.6;
Matches 8; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 4 VTETTFQKRLFFYRKSWW 22
DB 321 VTEGVFEKYRIATYKEASW 339

RESULT 9
CYOB_BUCAP ID CYOB_BUCAP STANDARD; PRT; 659 AA.
AC Q8K994;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ubiquinol oxidase polypeptide I (EC 1.10.3.-) (Cytochrome O subunit 1)
DE (Oxidase BO(3) subunit 1) (Cytochrome O ubiquinol oxidase subunit 1).
DE CYOB OR BUSG455.
GN Buchnera aphidicola (subsp. Schizaphis graminum).
OS Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Buchnera.
OX NCBI_TaxID=98794;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22084549; PubMed=12089438;
RA Tamas I., Klason L., Canbaeck B., Naeslund A.K., Eriksson A.-S.,
RA Wernegreen J.J., Sandstroem J.P., Moran N.A., Andersson S.G.E.;
RA "50 million years of genomic stasis in endosymbiotic bacteria.";
RA Science 296:2376-2379(2002).
RL -----
RL -!- FUNCTION: Cytochrome O terminal oxidase complex is the component
RL of the aerobic respiratory chain that predominates when cells are
RL grown at high aeration. This ubiquinol oxidase shows proton pump
RL activity across the membrane in addition to the electron transfer
RL (By similarity).
CC -----
CC -!- CATALYTIC ACTIVITY: Ubiquinol-8 + O(2) = Ubiquinone-8 + H(2)O.
CC -!- COFACTOR: Contains two protoheme IX (heme B55 and B562) and
CC copper B (By similarity).
CC -!- PATHWAY: Ubiquinol oxidase catalyzes the terminal step in the
CC electron transport chain.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -!- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its

```

use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

[illegible]

Query Match	35.1%;	Score 48;	DB 1;	2893
Best Local Similarity	56.2%;	Pred. No. 14;		
Matches	9;	Conservative	1;	Mismatches
			6;	Indels
			0;	Gaps
			0;	

8 TFQKNRLFFYRKSVWS 23
||| ||| ||| |||:
304 TFSKKRLFGYVSLVWA 319

RESULT 10
YOBO_BUCAI
STANDARD.
PRT: 662 AA.

C P57543; 16-OCT-2001 (Rel. 40, Created)
 T 16-OCT-2001 (Rel. 40, Last sequence update)
 T 16-OCT-2001 (Rel. 40, Last annotation update)
 T 15-SEP-2003 (Rel. 42, Last sequence update)
 T 15-SEP-2003 (Rel. 42, Last annotation update)
 E ubiquinol oxidase polypeptide 1 (EC 1.10.3.-) (Cytochrome O subunit 1)
 E (Oxidase BO(3) subunit 1) (Cytochrome O ubiquinol oxidase subunit 1)
 N CYOB OR BU471.
 N CYOB OR BU471.
 N Cybnera apidicola (subsp. Acyrthosiphon pisum) (Acyrthosiphon pisum)

synbiotic bacterium).
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Buchnera.
NCBI_TaxID=118099;
[1]
SEQUENCE FROM N.A.
STRAIN=Tokyo 1998;
MEDLINE=20445173; PubMed=10993077;
Shigenobu S., Watanabe H., Hattori M., Sakaki Y., Ishikawa H.;
"Genome sequence of the endocellular bacterial symbiont of aphids
Buchnera sp. APS.";
Buchnera sp. APS.;
Nature 407:81-86(2000).
-!- FUNCTION: CYTOCHROME O TERMINAL OXIDASE COMPLEX IS THE COMPONENT
OF THE AEROBIC RESPIRATORY CHAIN THAT PREDOMINATES WHEN CELLS ARE
GROWN AT HIGH AERATION. THIS UBIQUINOL OXIDASE SHOWS PROTON PUMP
ACTIVITY ACROSS THE MEMBRANE IN ADDITION TO THE ELECTRON TRANSFER
(BY SIMILARITY).
-!- CATALYTIC ACTIVITY: Ubiquinol-8 + O(2) = Ubiquinone-8 + H(2)O.
-!- COFACTOR: CONTAINS TWO PROTOHEME IX (HEME B55 AND B562) AND
COPPER B (BY SIMILARITY).
-!- PATHWAY: UBIQUINOL OXIDASE CATALYZES THE TERMINAL STEP IN THE
ELECTRON TRANSPORT CHAIN.
-!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
-!- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.

THIS SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See [http://www.isb-sib.ch/announce/](http://www.isb-sib.ch/announce/licenses/eib-sib.ch)
<http://www.ebi.ac.uk/licenses/eib-sib.ch>).

```
CC -----  
DR EMBL; AP001119; BAEI3168.1; --  
DR HSP; P18401; 1FFT.  
DR InterPro; IPR000883; COX1.  
DR Pfam; PF00115; COX1; 1.  
DR Pfam; PF00115; COX1; 1.  
DR Pfam; PF00115; COX1; 1.
```

DR	PRINSE; PS00077; COX1; 1
DR	Oxidoreductase; Respiratory chain; Transmembrane; Heme; Copper;
KW	Oxidoreductase; Respiratory Complete proteome
KW	Hydrogen ion transport; Complete proteome
FT	DOMAIN 1 14
FT	TRANSMEM 15 35
FT	DOMAIN 36 58
FT	TRANSMEM 59 79
FT	DOMAIN 80 106
FT	TRANSMEM 107 127
FT	DOMAIN 128 145
FT	TRANSMEM 146 166
FT	DOMAIN 167 189
FT	TRANSMEM 190 210
FT	DOMAIN 211 232
FT	TRANSMEM 233 253
FT	DOMAIN 254 277
FT	TRANSMEM 278 298
FT	DOMAIN 299 309
FT	TRANSMEM 310 330
FT	DOMAIN 331 346
FT	TRANSMEM 347 367
FT	DOMAIN 368 380
FT	TRANSMEM 381 401
FT	DOMAIN 402 413
FT	TRANSMEM 414 434
FT	DOMAIN 435 456
FT	TRANSMEM 457 477
FT	DOMAIN 478 493
FT	TRANSMEM 494 514
FT	DOMAIN 515 586
FT	TRANSMEM 587 607
FT	DOMAIN 608 608
FT	TRANSMEM 609 629
FT	DOMAIN 630 662
FT	DOMAIN 106 106
FT	METAL
PROB	IRON (HEME B AXIAL LIGAND) (PROB)

```
FT METAL 284 284 COPPER B (PROBABLE)
FT METAL 288 288 COPPER B (PROBABLE)
FT METAL 333 333 COPPER B (PROBABLE)
FT METAL 334 334 COPPER B (PROBABLE)
FT METAL 419 419 IRON (HEME O AXIAL LIGAND) (PROBABLE)
FT METAL 421 421 IRON (HEME B AXIAL LIGAND) (PROBABLE)
FT METAL 284 288 1'-histidyl-3'-tyrosine (By similarity)
SQ SEQUENCE 662 AA; 75455 MW; 3F502A628133EA65 CRC64;

Query Match 35.1%; Score 46; DB 1; Length 662;
Best Local Similarity 56.2%; Pred. No. 14;
Matches 9; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 8 TFOKNRLFFYRKSVMS 23
   |||||
Db 304 TFSKRLFGVSLVWA 319

RESULT 11
ADP6_ARATH STANDARD; PRT; 146 AA.
AC Q9SK2; Q93VZ4; Q9SJX6;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE Actin-depolymerizing factor 6 (ADF-6) (AtADF6).
GN ADF6 OR AT2G31200 OR F16D14.4.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OC NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
RC STRAIN=cv. Columbia;
RX MEDLINE=21307188; PubMed=11414611;
RA Dong C.-H., Kost B., Xia G., Chua N.-H.;
RT "Molecular identification and characterization of the Arabidopsis
RT AtADF1, AtADF5 and AtADF6 genes.";
RL Plant Mol. Biol. 45:517-527(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=20083487; PubMed=10617197;
RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblum T.V.,
RA Buell C.R., Ketchum K.A., Lee J.J., Renning C.M., Koo H.L.,
RA Moffat K.S., Cronin L.A., Shen M., Pai G., Van Aken S., Umayam L.,
RA Tallon L.J., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H.,
RA Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss D.,
RA Nietman W.C., White O., Eisen J.A., Salzberg S.L., Fraser C.M.,
RA Venter J.C.;
RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis
RT thaliana.";
RN [3]
RP Nature 402:761-768(1999).
SQ SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RA Shinozaki K., Davis R.W., Ecker J.R., Theologis A.;
RT "RIKEN Arabidopsis full length cDNA clones (RAPFs) sequenced by the
RT SSP consortium (Salk/Stanford/PECC).";
RL Submitted (Oct-2001) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: ACTIN-DEPOLYMERIZING PROTEIN. SEVERAL ACTIN FILAMENTS
CC (F-ACTIN) AND BINDS TO ACTIN MONOMERS.
CC -!- PTM: Phosphorylated.
CC -!- SIMILARITY: BELONGS TO THE ACTIN-BINDING PROTEINS ADF FAMILY.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/)
```

```
CC or send an email to license@isb-sib.ch.
CC
DR EMBL; AF102824; AAD09112.1;
DR EMBL; AF183576; AAF01035.1;
DR EMBL; AC006593; AAD20665.2;
DR EMBL; AY057719; AAL15349.1;
DR EMBL; AF372880; AAK49596.1; ALT_INIT.
DR HSSP; Q39250; 1F7S.
DR InterPro; IPR002108; Actbind cofln.
DR Pfam; PF00241; Cofilin ADF; I.
DR PRINTS; PR00006; COFILIN.
DR ProDom; PD002129; Actbind_cofln; 1.
DR SMART; SM0102; ADF; 1.
DR PROSITE; PS00325; ACTIN DEPOLYMERIZING; FALSE NEG.
KW Actin-binding; Multigene family; Phosphorylation.
FT DOMAIN 99 118 ACTIN-BINDING (POTENTIAL).
FT CONFLICT 1 1 M -> L (IN REF. 3; AAK49596).
SQ SEQUENCE 146 AA; 16708 MW; A97CEFD2CC17A85 CRC64;

Query Match 34.7%; Score 45.5; DB 1; Length 146;
Best Local Similarity 39.1%; Pred. No. 3.5;
Matches 9; Conservative 5; Mismatches 6; Indels 3; Gaps 1;

QY 1 FFYVTTTFQKRLFFYRKSVMS 23
   |||||
Db 79 FDFVTSENCQSKIPFF---AWS 98

RESULT 12
BACA_RHIME STANDARD; PRT; 420 AA.
AC Q08120;
DT 01-OCT-1994 (Rel. 30, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Bacteroid development protein bacA.
GN BACA OR RB1125 OR SMB20999.
OS Rhizobium meliloti (Sinorhizobium meliloti).
OC Plasmid pSymB (megaplasmid 2).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.
OC NCBI_TaxID=382;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1021;
RX MEDLINE=93339575; PubMed=8393417;
RA Glazebrook J., Ichige A., Walker G.C.;
RT "A Rhizobium meliloti homolog of the Escherichia coli peptide-
RT antibiotic transport protein SbmA is essential for bacteroid
RT development.";
RL Genes Dev. 7:1485-1497(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=1021;
RX MEDLINE=21396508; PubMed=11481431;
RA Finan T.M., Weidner S., Wong K., Buhrmester J., Chain P.,
RA Vorhoefer F.J., Hernandez-Lucas I., Becker A., Cowie A., Gouzy J.,
RA Golding B., Puchler A.;
RT "The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-
RT fixing endosymbiont Sinorhizobium meliloti.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:9889-9894(2001).
CC -!- FUNCTION: ACROSS THE INNER MEMBRANE. IS ESSENTIAL FOR BACTEROID
CC PEPTIDES. ACROSS THE INNER MEMBRANE. IS ESSENTIAL FOR BACTEROID
CC DEVELOPMENT.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane.
CC -!- TISSUE SPECIFICITY: NODULES.
CC -!- SIMILARITY: STRONG, TO E.COLI SBMA.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/)
```


entities requires a license agreement (See <http://www.isb-sib.ch/announce/>).

ENBL; X73522; CAA51918.1; -.	
ENBL; AL601646; CAC49525.1; -.	
PIR; A47649; A47649.	
PIR; E95982; E95982.	
Transport; Transmembrane; Inner membrane; Plasmid; Complete proteome.	
TRANSMEM	11
TRANSMEM	31
TRANSMEM	61
TRANSMEM	81
TRANSMEM	92
TRANSMEM	112
TRANSMEM	143
TRANSMEM	210
TRANSMEM	230
TRANSMEM	247
TRANSMEM	267
TRANSMEM	336
TRANSMEM	356
TRANSMEM	128
CONFLICT	128
SEQUENCE	420 AA; A -> P (IN REF. 1).
	548496A86AD1D0FE CRC64;

```

Query Match      34.4%; Score 45; DB 1; Length 420;
Best Local Similarity 44.4%; Pred. No. 13;
Matches 8; Conservative 4; Mismatches 6; Indels 0; Gaps 0;
QY      6  ETTFQKNRLFFYKRSVMS 23
          ::|::|::|::|::|
          3  OSFFPKLFFISSAVMS 20

```

RESULT 13

ID	CYOB_ECOLI	STANDARD;	PRT;	663 MA.
AC	P18401;			
DC	01-NOV-1990 (Rel. 16, Created)			
DT	01-NOV-1990 (Rel. 16, Last sequence update)			
DT	13-SEP-2003 (Rel. 42, Last annotation update)			
DE	Ubiquinol oxidase polypeptide I (BC 1.10.3.-) (Cytochrome O subunit 1)			
DE	(Oxidase BO(3) subunit 1) (Cytochrome O ubiquinol oxidase subunit 1)			
DE	(Ubiquinol oxidase chain A).			
GN	CYOB OR B0431 OR C0542 OR Z0534 OR ECS0485.			
GN	Escherichia coli,			
OS	Escherichia coli O6, and			
OS	Escherichia coli O157:H7.			
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;			
OC	Enterobacteriaceae; Escherichia.			
OX	NCBI_TaxID=562, 217992, 83334;			
RN	[1]			
RN	SEQUENCE FROM N.A.			
RP	MEDLINE=90293062; PubMed=2162835;			
RP	Chepur I.V., Lemaux L., Au D.C.T., Gennis R.B.;			
RA	"The sequence of the cyo operon indicates substantial structural			
RT	similarities between the cytochrome o ubiquinol oxidase of			
RT	Escherichia coli and the aa3-type family of cytochrome c oxidases."			
RT	J. Biol. Chem. 265:11185-11192(1990).			
RL	[2]			
RN	SEQUENCE FROM N.A.			
RP	STRAIN=K12 / MG1655;			
RC	MEDLINE=97426617; PubMed=9278503;			
RX	Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,			
RA	Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,			
RA	Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,			
RA	Mau B., Shao Y.;			
RA	"The complete genome sequence of Escherichia coli K-12.;"			
RT	Science 277:1453-1474(1997).			
RL	[3]			
RN	SEQUENCE FROM N.A.			
RP	Roberts D., Allen E., Araujo R., Apazicio A., Chung E., Davis K.,			
RA	Duncan M., Federspiel N., Hyman R., Kalman S., Komp C., Kurdi O.,			
RA	Lew H., Lin D., Namath A., Oefner P., Schramm S., Davis R.W.;			
RL	Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.			
RL	[4]			
RN	SEQUENCE FROM N.A.			
RP	STRAIN=O6:HI / CFT073 / ATCC 700928;			
RC	MEDLINE=22398234; PubMed=12711157;			
RX	Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,			
RA				

Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J.,
Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
Mobley H.L.T., Sonnenberg M.S., Blattner F.R.;
"Extensive mosaic structure revealed by the complete genome sequence
of uropathogenic *Escherichia coli*."
Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024 (2002).
[5]
SEQUENCE FROM N.A.
RN STRAIN=O157:H7 / EDL933 / ATCC 700927;
RP MEDLINE=21074935; PubMed=11206551;
RC Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
RX Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
RA Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
RA Grobeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
RA Welch R.A., Blattner F.R.;
RN "Genome sequence of enterohaemorrhagic *Escherichia coli* O157:H7";
RT Nature 409:529-533 (2001).
[6]
SEQUENCE FROM N.A.
RN STRAIN=O157:H7 / RIMD 0509952;
RP MEDLINE=21156231; PubMed=11258796;
RC Hayaishi T., Makino K., Onishi M., Kurokawa K., Ishii K., Yokoyama K.,
RX Hayaishi T., Makino K., Onishi M., Kurokawa K., Ishii K., Yokoyama K.,
RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tohe T.,
RA Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
RA Kihara S., Shiba T., Hattori M., Shinagawa H.;
RN "Complete genome sequence of enterohaemorrhagic *Escherichia coli*
O157:H7 and genomic comparison with a laboratory strain K-12.";
RT DNA Res. 8:11-22 (2001).
[7]
TOPOLOGY.
RN MEDLINE=90330636; PubMed=2165491;
RP Thepuri V., Gennis R.B.;
RX "The use of gene fusions to determine the topology of all of the
RA subunits of the cytochrome o terminal oxidase complex of *Escherichia coli*."
RT J. Biol. Chem. 265:12978-12986 (1990).
[8]
TOPOLOGY.
RN MEDLINE=90366572; PubMed=2168206;
RX Cheturi V., Lemieux L., Hill J., Alben J.O., Gennis R.B.;
RA "Recent studies of the cytochrome o terminal oxidase complex of
RT *Escherichia coli*."
RL Biochim. Biophys. Acta 1018:124-127 (1990).
[9]
X-RAY CRYSTALLOGRAPHY (3.5 ANGSTROMS), AND MUTAGENESIS OF ARG-71;
RN ASP-75; HIS-98 AND GLN-101.
RP MEDLINE=20473233; PubMed=11017202;
RX Abramson J., Riisama S., Larsson G., Jasaitis A., Svensson-Bk M.,
RA Puustinen A., Iwata S., Wikstrom M.;
RN "The structure of the ubiquinol oxidase from *Escherichia coli* and its
RT ubiquinone binding site."
RL Nat. Struct. Biol. 7:910-917 (2000).
CC -!- FUNCTION: CYTOCHROME O TERMINAL OXIDASE COMPLEX IS THE COMPONENT
CC OF THE AEROBIC RESPIRATORY CHAIN OF E. COLI THAT PREDOMINATES WHEN
CC CELLS ARE GROWN AT HIGH AERATION. THIS UBIQUINOL OXIDASE SHOWS
CC PROTON PUMP ACTIVITY ACROSS THE MEMBRANE IN ADDITION TO THE
CC ELECTRON TRANSFER.
CC -!- CATALYTIC ACTIVITY: Ubiquinol-8 + O(2) = Ubiquinone-8 + H(2)O.
CC -!- COFACTOR: CONTAINS TWO PROTOHEME IX (HEME B55 AND B562) AND
CC COPPER B.
CC -!- PATHWAY: UBIQUINOL OXIDASE CATALYZES THE TERMINAL STEP IN THE
CC ELECTRON TRANSPORT CHAIN.
CC -!- SUBUNIT: HETEROOCTAMER OF TWO A CHAINS, TWO B CHAINS, TWO C CHAINS
CC AND TWO D CHAINS.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane.
CC -!- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC

us-08-854-050-112.rsp

Thu Nov 13 12:06:56 2003

```

CC      during meiotic prophase.
CC      -!- SUBUNIT: Consists of at least two heavy chains and a number of
CC      intermediate and light chains.
CC      -!- SUBCELLULAR LOCATION: Cytoplasmic. Probably binds indirectly to
CC      the inner plasma membrane.
CC      -!- DOMAIN: Dynein heavy chains probably consist of an N-terminal stem
CC      (which binds cargo and interacts with other dynein components),
CC      and the head or motor domain. The motor contains six tandemly-
CC      linked AAA domains in the head, which form a ring. A stalk-like
CC      structure (formed by two of the coiled coil domains) protrudes
CC      between AAA 4 and AAA 5 and terminates in a microtubule-binding
CC      site. A seventh domain may also contribute to this ring; it is not
CC      clear whether the N-terminus or the C-terminus forms this extra
CC      domain. There are four well-conserved and two non-conserved ATPase
CC      sites, one per AAA domain. Probably only one of these (within AAA
CC      1) actually hydrolyzes ATP, the others may serve a regulatory
CC      function.
CC      -!- SIMILARITY: Belongs to the dynein heavy chain family.
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use by non-profit institutions as long as its content is in no way
CC      modified and this statement is not removed. Usage by and for commercial
CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC      or send an email to license@isb-sib.ch).
CC      EMBL; AB006784; BAA22056.1; -
CC      EMBL; AL355652; CAB90788.1; -
CC      EMBL; AL132839; CAB60251.1; -
CC      PIR; T43274; T43274
CC      GeneDB Spombe; SPAC1093.06c; -
CC      InterPro; IPR003593; AAA_ATPase.
CC      SMART; SM00382; AAA; 3.
CC      Motor protein; Dynein; Microtubules; ATP-binding; Repeat; Coiled coil.
CC      KW      STEM (BY SIMILARITY).
CC      FT      AAA 1 (BY SIMILARITY).
CC      FT      AAA 2 (BY SIMILARITY).
CC      FT      AAA 3 (BY SIMILARITY).
CC      FT      AAA 4 (BY SIMILARITY).
CC      FT      STALK (BY SIMILARITY).
CC      FT      AAA 5 (BY SIMILARITY).
CC      FT      AAA 6 (BY SIMILARITY).
CC      FT      COILED COIL (POTENTIAL).
CC      FT      COILED COIL (POTENTIAL).
CC      FT      COILED COIL (POTENTIAL).
CC      FT      ATP (POTENTIAL).
CC      FT      NP_BIND 2169 2176
CC      FT      NP_BIND 2174 2181
CC      FT      NP_BIND 2520 2527
CC      FT      NP_BIND 4196 AA; 484308 MW; 8F10AE370184FC0C CRC64;
CC      SQ      SEQUENCE 4196 AA; 484308 MW; 8F10AE370184FC0C CRC64;
CC
CC      Query Match      34.4%; Score 45; DB 1; Length 4196;
CC      Best Local Similarity 47.4%; Pred. NO. 1.5e+02; Indels 0; Gaps 0;
CC      Matches 9; Conservative 4; Mismatches 6;
CC
CC      QY      2 FYVTETTFQKNRLFFYRKS 20
CC      DB      1712 FOLFSTSFQIRDFYNNKS 1730
CC
CC      RESULT 15
CC      YCT2_BACFI      STANDARD; PRT; 385 AA.
CC      ID      YCT2_BACFI
CC      AC      Q0454;
CC      DT      01-FEB-1994 (Rel. 28, Created)
CC      DT      01-FEB-1994 (Rel. 28, Last sequence update)
CC      DT      16-OCT-2001 (Rel. 40, Last annotation update)
CC      DE      Hypothetical 43.4 kDa protein in CTAF 3' region (ORF2).
CC      CS      Bacillus firmus.
CC      OC      Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
CC      OX      NCBI_TaxID=1399;
CC      RN      [1]

```

```

RP      SEQUENCE FROM N.A.
RC      STRAIN=OF4;
RC      MEDLINE=93107080; PubMed=7678007;
RX      Quirk P.G., Hicks D.B., Krulwich T.A.;
RA      "Cloning of the cta operon from alkaliphilic Bacillus firmus OF4 and
RT      characterization of the pH-regulated cytochrome caa3 oxidase it
RT      characterizes."
RT      J. Biol. Chem. 268:678-685(1993).
RL      -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC      -!- SIMILARITY: BELONGS TO THE UPF0118 (PERM) FAMILY.
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use by non-profit institutions as long as its content is in no way
CC      modified and this statement is not removed. Usage by and for commercial
CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC      or send an email to license@isb-sib.ch).
CC      EMBL; M94110; AAA22369.1; -
CC      InterPro; IPR002549; UPF0118.
CC      Pfam; PF01594; UPF0118; 1.
CC      KW      Hypothetical protein; Transmembrane.
CC      FT      TRANSMEM 42 62 POTENTIAL.
CC      FT      TRANSMEM 63 83 POTENTIAL.
CC      FT      TRANSMEM 93 113 POTENTIAL.
CC      FT      TRANSMEM 191 211 POTENTIAL.
CC      FT      TRANSMEM 255 275 POTENTIAL.
CC      FT      TRANSMEM 276 296 POTENTIAL.
CC      FT      TRANSMEM 304 324 POTENTIAL.
CC      FT      TRANSMEM 350 370 POTENTIAL.
CC      SQ      SEQUENCE 385 AA; 43410 MW; 9956714C3B4E682A CRC64;
CC
CC      Query Match      34.0%; Score 44.5; DB 1; Length 385;
CC      Best Local Similarity 42.9%; Pred. No. 14;
CC      Matches 9; Conservative 4; Mismatches 7; Indels 1; Gaps 1;
CC
CC      QY      2 FYVTETTFQKNRLFFYRKS 22
CC      DB      25 FYVVERGFEL-AAPFTRTIW 44
CC
CC      Search completed: November 12, 2003, 19:48:00
CC      Job time : 5.98113 secs

```

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 12, 2003, 19:42:29 ; Search time 22.9434 Seconds
(without alignments)
269.937 Million cell updates/sec

Title: US-08-854-050-112

Perfect score: 131

Sequence: 1 FFVYTTTFQKNRFFYRKSVWSK 24

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phage.*
- 10: sp_plant.*
- 11: sp_todent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_ivirus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	131	100.0	795	4 Q8NG38	Q8ng38 homo sapien
2	131	100.0	807	4 Q8N6C3	Q8n6c3 homo sapien
3	131	100.0	1069	4 Q8NG46	Q8ng46 homo sapien
4	126	96.2	575	11 Q9JK99	Q9jk99 rattus norv
5	120	91.6	1128	11 Q9QX24	Q9qx24 mesocricetu
6	110	84.0	1191	13 Q9DE32	Q9de32 xenopus lae
7	93	71.0	52	11 Q9R0B3	Q9r0b3 mus musculu
8	69	52.7	1108	5 Q8I826	Q8i826 sterkiella
9	69	52.7	1135	5 Q8I827	Q8i827 sterkiella
10	65	49.6	823	5 Q8SQ00	Q8sq00 encephalito
11	64	48.9	1032	5 Q8MUB3	Q8mub3 euplotes cr
12	64	48.9	1259	10 Q9AU13	Q9au13 cryza sativ
13	64	48.9	1261	10 Q8LKW0	Q8lkw0 cryza sativ
14	63	48.1	896	5 Q8MU08	Q8mu08 paramecium
15	62	47.3	895	5 Q9GRC5	Q9grc5 paramecium
16	55	42.0	389	10 Q9SJ75	Q9sj75 arabidopsis

17	52	39.7	1123	10 Q8SE99	Q8se99 arabidopsis
18	52	39.7	1123	10 Q8SPU7	Q8spu7 arabidopsis
19	50.5	38.5	267	2 Q9AIZ9	Q9aiz9 carsonella
20	49	37.4	136	5 P9I812	P9i812 toxocara ca
21	49	37.4	205	4 Q9NPT3	Q9npt3 homo sapien
22	48.5	37.0	2049	5 Q8IBD4	Q8ibd4 plasmodium
23	48	36.6	306	10 Q9AVY9	Q9avy9 guillardia
24	48	36.6	503	8 Q8WKK0	Q8wkk0 weddellina
25	48	36.6	602	16 Q8RBX6	Q8rbx6 thermoanaer
26	47.5	36.3	345	16 Q8YK38	Q8yk38 anabaena sp
27	47	35.9	564	11 Q8CIK0	Q8cik0 mus musculu
28	47	35.9	584	11 Q921I2	Q921i2 mus musculu
29	46.5	35.5	60	16 Q8F7I5	Q8f7i5 leptospira
30	46.5	35.5	1083	2 Q8RL19	Q8rl19 providencia
31	46	35.1	270	16 Q8YTL4	Q8ytl4 anabaena sp
32	46	35.1	277	16 Q9CFI2	Q9cfi2 lactococcus
33	46	35.1	321	10 Q9LVR5	Q9lvr5 arabidopsis
34	46	35.1	321	10 Q94B21	Q94b21 arabidopsis
35	46	35.1	396	16 Q8X6C0	Q8x6c0 escherichia
36	46	35.1	396	16 Q8FE91	Q8fe91 escherichia
37	46	35.1	463	4 Q9BVN3	Q9bvn3 homo sapien
38	46	35.1	661	2 Q9LBY2	Q9lby2 shewanella
39	46	35.1	663	16 Q8ZC57	Q8zc57 versinia pe
40	46	35.1	762	3 Q9UTE0	Q9uce0 schizosacch
41	45.5	34.7	140	10 Q9M594	Q9ms94 elaeis guin
42	45.5	34.7	294	16 Q83801	Q83801 treponema p
43	45	34.4	466	2 Q9AQI7	Q9aqi7 streptococc
44	44	34.4	545	10 Q9SW37	Q9sw37 arabidopsis
45	45	34.4	602	10 Q9LNK8	Q9lnk8 arabidopsis

ALIGNMENTS

RESULT 1
Q8NG38
ID Q8NG38 PRELIMINARY; PRT; 795 AA.
AC Q8NG38;
DT 01-OCT-2002 (TRENBLrel. 22, Created)
DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
DE ABG-deleted variant of telomerase reverse transcriptase.
GN TERT.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Stomach;
RT Hisatomi H., Nagao K., Kanamaru T., Hirata H., Miyachi K., Hikiji H.;
RA "Exon 11 deleted variant of human reverse transcriptase.";
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB086950; BAC11015.1; -
DR InterPro; IPR003545; Telomerase_RT.
DR PRINTS; PR01365; TELOMERASERT.
KW RNA-directed DNA polymerase.
SQ SEQUENCE 795 AA; 88965 MW; 6BEAC8A6D1A2E8CB CRC64;

Query Match 100.0%; Score 131; DB 4; Length 795;
Best Local Similarity 100.0%; Pred. NO. 4.3e-12;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FFVYTTTFQKNRFFYRKSVWSK 24
|
Db 560 FFVYTTTFQKNRFFYRKSVWSK 583
|

RESULT 2
Q8N6C3
ID Q8N6C3 PRELIMINARY; PRT; 807 AA.
AC Q8N6C3;
DT 01-OCT-2002 (TRENBLrel. 22, Created)

Thu Nov 13 12:06:57 2003

```

OS Homo sapiens (Human);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Stomach cancer;
RA Hisatomi H., Nagao K., Kanamaru T., Sumida H., Hirata H., Yanamoto M.,
RA Kazumasa H.;
RT "Both beta and gamma deletion isoform of human telomerase reverse
transcriptase.";
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB086379; BAC11014.1; -.
DR InterPro; IPR003545; Telomerase_RT.
DR PRINTS; PR01365; TELOMERASERT.
SQ SEQUENCE 807 AA; 90225 MW; 199664460C56D763 CRC64;

Query Match 100.0%; Score 131; DB 4; Length 807;
Best Local Similarity 100.0%; Pred.No. 4.4e-12;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FFYVTTTQKNRLFFYRKSVWSK 24
DB 560 FFYVTTTQKNRLFFYRKSVWSK 583

RESULT 3
Q8NG46 PRELIMINARY; PRT; 1069 AA.
ID Q8NG46
AC Q8NG46;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 23, Last annotation update)
DE Telomerase reverse transcriptase.
GN HTERT.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Hisatomi H., Nagao K., Hirata H., Hikiji K., Kanamaru T.;
RA "Exon 11 deleted variant of the human telomerase reverse
transcriptase.";
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB085628; BAC11010.1; -.
DR InterPro; IPR003545; Telomerase_RT.
DR PRINTS; PR01365; TELOMERASERT.
DR RNA-directed DNA polymerase.
KW SEQUENCE 1069 AA; 120047 MW; BE1E77A653B1C666 CRC64;
SQ SEQUENCE 1069 AA; 120047 MW; BE1E77A653B1C666 CRC64;

Query Match 100.0%; Score 131; DB 4; Length 1069;
Best Local Similarity 100.0%; Pred.No. 5.7e-12;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FFYVTTTQKNRLFFYRKSVWSK 24
DB 560 FFYVTTTQKNRLFFYRKSVWSK 583

RESULT 4
Q9JK99 PRELIMINARY; PRT; 575 AA.
ID Q9JK99
AC Q9JK99;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 22, Last annotation update)
DE Telomerase catalytic subunit (Fragment).

```

```

OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Wong S., Gao S., Xu X., Yu H.;
RA "Rat telomerase catalytic subunit, rTERT.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF247818; AAF62177.1; -.
DR InterPro; IPR000477; RVTse.
DR InterPro; IPR003545; Telomerase_RT.
DR Pfam; PF00078; rvt; 1.
DR PRINTS; PR01365; TELOMERASERT.
DR RNA-directed DNA polymerase; Transferase.
FT NON TER 1
SQ SEQUENCE 575 AA; 65672 MW; F80C81BD7F6A91A3 CRC64;

Query Match 96.2%; Score 126; DB 11; Length 575;
Best Local Similarity 91.7%; Pred.No. 1.9e-11;
Matches 22; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 FFYVTTTQKNRLFFYRKSVWSK 24
DB 3 FFYVTTTQKNRLFFYRKSVWSK 26

RESULT 5
Q9QXZ4 PRELIMINARY; PRT; 1128 AA.
ID Q9QXZ4
AC Q9QXZ4;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Telomerase catalytic subunit.
OS Mesocricetus auratus (Golden hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Mesocricetus.
OX NCBI_TaxID=10036;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE-21240330; PubMed=11342218;
RA Guo W., Okamoto M., Lee Y.M., Baluda M.A., Park N.H.;
RA "Enhanced activity of cloned hamster TERT gene promoter in transformed
cells.";
RL Biochim. Biophys. Acta 1517:398-409(2001).
DR EMBL; AF149012; AAF17334.1; -.
DR InterPro; IPR000477; RVTse.
DR InterPro; IPR003545; Telomerase_RT.
DR Pfam; PF00078; rvt; 1.
DR PRINTS; PR01365; TELOMERASERT.
DR RNA-directed DNA polymerase; Transferase.
KW SEQUENCE 1128 AA; 128394 MW; 1D4F81249012174E CRC64;
SQ SEQUENCE 1128 AA; 128394 MW; 1D4F81249012174E CRC64;

Query Match 91.6%; Score 120; DB 11; Length 1128;
Best Local Similarity 87.5%; Pred.No. 3.2e-10;
Matches 21; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 FFYVTTTQKNRLFFYRKSVWSK 24
DB 554 FFYVTTTQKNRLFFYRKSVWSK 577

RESULT 6
Q9DE32 PRELIMINARY; PRT; 1191 AA.
ID Q9DE32
AC Q9DE32;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Telomerase reverse transcriptase.
GN TERT.

```

OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
 OC Xenopodinae; Xenopus.
 NCBI_TaxID=8355;
 [1] SEQUENCE FROM N.A.

RA Kuramoto M., Ishikawa F.;
 RA "Telomerase reverse transcriptase of Xenopus laevis";
 RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF212299; AAG43537.1; -
 DR InterPro; IPR000477; RVISE
 DR InterPro; IPR003545; Telomerase_RT.
 DR Pfam; PF00078; rvc; 2.
 DR PRINTS; PR01365; TELOMERASERT.
 KW RNA-directed DNA polymerase; Transferase.
 SQ SEQUENCE 1191 AA; 138016 MW; 9BD9D776869A57D6 CRC64;

Query Match 84.0%; Score 110; DB 13; Length 1191;
 Best Local Similarity 83.3%; Pred. NO. 1.3e-08;
 Matches 20; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 FFYVTTTFOKNRLLFFYRKSWSK 24
 ||||| ||||| ||||| ||||| |||||
 Db 615 FFYVTTTFOKNRLLFFYRKSWSK 638

RESULT 7

Q9R0B3 ID Q9R0B3 PRELIMINARY; PRT; 52 AA.
 AC Q9R0B3
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
 DE Telomerase catalytic subunit (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 [1] SEQUENCE FROM N.A.
 RA Drissi R., Cleveland J.L.;
 RA "Sequence of a Mus musculus telomerase catalytic subunit intron.";
 RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF090439; AAD54013.1; -
 FT NON TER 1
 FT NON TER 52
 SQ SEQUENCE 52 AA; 6479 MW; 41473425E44BDA9C CRC64;

Query Match 71.0%; Score 93; DB 11; Length 52;
 Best Local Similarity 100.0%; Pred. NO. 2.8e-07;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 TFOKNRLLFFYRKSWSK 24
 ||||| ||||| ||||| ||||| |||||
 Db 1 TFOKNRLLFFYRKSWSK 17

RESULT 8

Q81826 ID Q81826 PRELIMINARY; PRT; 1108 AA.
 AC Q81826
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Telomerase (Fragment).
 OS Sterkiella sp. Aspen.
 OC Eukaryota; Alveolata; Ciliophora; Spirotrichea; Stichotrichia;
 OC Stichotrichida; Oxytrichidae; Sterkiella.
 NCBI_TaxID=200599;
 [1] SEQUENCE FROM N.A.
 RA Marandi S.S., Prescott D.M.;

RT "The macronuclear telomerase gene in two closely related
 RT Stichotrichous ciliates.";
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY116502; AAN87867.1; -
 FT NON TER 1
 SQ SEQUENCE 1108 AA; 131535 MW; EC8262E01BBE0FAD CRC64;

Query Match 52.7%; Score 69; DB 5; Length 1108;
 Best Local Similarity 43.5%; Pred. NO. 0.033;
 Matches 10; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

QY 1 FFYVTTTFOKNRLLFFYRKSWWS 23
 ||||| ||||| ||||| ||||| |||||
 Db 535 FFYVTTTFOKNRLLFFYRKSWWS 557

RESULT 9

Q81827 ID Q81827 PRELIMINARY; PRT; 1135 AA.
 AC Q81827
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Telomerase.
 OS Sterkiella sp. Aspen.
 OC Eukaryota; Alveolata; Ciliophora; Spirotrichea; Stichotrichia;
 OC Stichotrichida; Oxytrichidae; Sterkiella.
 NCBI_TaxID=200599;
 [1] SEQUENCE FROM N.A.
 RA Marandi S.S., Prescott D.M.;
 RA "The macronuclear telomerase gene in two closely related
 RT Stichotrichous ciliates.";
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY116501; AAN87866.1; -
 SQ SEQUENCE 1135 AA; 134341 MW; 3661E5D9300A4942 CRC64;

Query Match 52.7%; Score 69; DB 5; Length 1135;
 Best Local Similarity 43.5%; Pred. NO. 0.033;
 Matches 10; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

QY 1 FFYVTTTFOKNRLLFFYRKSWWS 23
 ||||| ||||| ||||| ||||| |||||
 Db 562 FFYVTTTFOKNRLLFFYRKSWWS 584

RESULT 10

Q8SQ00 ID Q8SQ00 PRELIMINARY; PRT; 823 AA.
 AC Q8SQ00
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Telomerase reverse transcriptase.
 GN ECU09_0310.
 OS Encephalitozoon cuniculi.
 OC Eukaryota; Fungi; Microsporidia; Unikaryonidae; Encephalitozoon.
 NCBI_TaxID=6035;
 [1] SEQUENCE FROM N.A.
 RA STRAIN=GB-M1;
 RC Genoscope;
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 RN [2] SEQUENCE FROM N.A.
 RP STRAIN=GB-M1;
 RC MEDLINE=21576510; PubMed=11719806;
 RX Katinka M.D., Duprat S., Cornillot E., Metenier G., Thonarat F.,
 RA Prensier G., Barbe V., Peyretallade E., Brottier P., Wincker P.,
 RA Delbac F., El Alaoui H., Peyret P., Saurin W., Gouy M.,
 RA Weissenbach J., Vivares C.P.;
 RT "Genome sequence and gene compaction of the eukaryote parasite
 RT Encephalitozoon cuniculi.";

[illegible]

```

RN      SEQUENCE FROM N.A.
RP      Romero D.P., Ye A.J.;
RT      "A unique pause pattern during telomere addition by the error-prone
RT      telomerase from the ciliate Paramecium tetraurelia.";
RL      Gene 0:0-0(2002).
DR      EMBL; AF515460; AAN03860.1; -.
DR      InterPro; IPR000477; RVTse.
DR      InterPro; IPR003545; Telomerase_RT.
DR      Pfam; PF00078; rvt; 2.
DR      PRINTS; PR01365; TELOMERASERT.
KW      RNA-directed DNA polymerase; Transferrase.
SQ      SEQUENCE      896 AA;  107237 MW;  697031F9DD61A883 CRC64;

Query Match      48.1%; Score 63; DB 5; Length 896;
Best Local Similarity 45.5%; Pred. No. 0.23;
Matches 10; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY      2 FYVTETTFQKNRLFFYRKSVNS 23
      |||      :|||      :|
DB      392 FYITERMKDDWKLFFYRKEIWT 413

RESULT 15
Q9GRCS PRELIMINARY; PRT; 895 AA.
ID      Q9GRCS
AC      Q9GRCS;
DT      01-MAR-2001 (TEMBLrel. 16, Created)
DT      01-MAR-2001 (TEMBLrel. 16, Last sequence update)
DT      01-OCT-2002 (TEMBLrel. 22, Last annotation update)
DE      Telomerase reverse transcriptase.
GN      PCTER.
OS      Paramecium caudatum.
OC      Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Peniculida;
OC      Paramecium.
OX      NCBI_TaxID=5885;
RN      [1]
SEQUENCE FROM N.A.
RP      STRAIN=KNZ-5 and KNZ-2;
RX      MEDLINE=21147925; PubMed=11250070;
RA      Takenaka Y., Matsuura T., Hega N., Mitsui Y.;
RT      "Expression of telomerase reverse transcriptase and telomere
RT      elongation during sexual maturation in Paramecium caudatum.";
RL      Gene 264:153-161(2001).
DR      EMBL; AB035309; BAB18587.1; -.
DR      InterPro; IPR000477; RVTse.
DR      InterPro; IPR003545; Telomerase_RT.
DR      Pfam; PF00078; rvt; 2.
DR      PRINTS; PR01365; TELOMERASERT.
KW      RNA-directed DNA polymerase; Transferrase.
SQ      SEQUENCE      895 AA;  107086 MW;  130C0DB32FD11C76 CRC64;

Query Match      47.3%; Score 62; DB 5; Length 895;
Best Local Similarity 47.6%; Pred. No. 0.33;
Matches 10; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY      2 FYVTETTFQKNRLFFYRKSVW 22
      |||      :|||      :|
DB      388 FYITERMKDDWKLFFYRKEIW 408

Search completed: November 12, 2003, 19:50:44
Job time : 23.1101 secs

```

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 12, 2003, 19:47:20 ; Search time 21.566 Seconds
(without alignments)
215.025 Million cell updates/sec

Title: US-08-854-050-114

Perfect score: 130

Sequence: 1 ARTFREKRAERLTSRVKALFSLVLYE 27

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 644079 seqs, 17174922 residues

Total number of hits satisfying chosen parameters: 644079

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA.*

1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	130	100.0	27	10	US-09-843-676-114 Sequence 114, App
2	130	100.0	27	10	US-09-766-253-114 Sequence 114, App
3	130	100.0	27	11	US-09-438-486-114 Sequence 114, App
4	130	100.0	27	15	US-10-053-758-114 Sequence 114, App
5	130	100.0	27	15	US-10-054-295-114 Sequence 114, App
6	130	100.0	27	15	US-10-054-611-114 Sequence 114, App
7	130	100.0	27	15	US-10-044-692-115 Sequence 115, App
8	130	100.0	27	15	US-10-044-539-115 Sequence 115, App
9	130	100.0	129	10	US-09-843-676-67 Sequence 67, Appl
10	130	100.0	129	10	US-09-766-253-67 Sequence 67, Appl
11	130	100.0	129	11	US-09-438-486-67 Sequence 67, Appl
12	130	100.0	129	15	US-10-053-758-67 Sequence 67, Appl
13	130	100.0	129	15	US-10-054-295-67 Sequence 67, Appl
14	130	100.0	129	15	US-10-054-611-67 Sequence 67, Appl
15	130	100.0	129	15	US-10-044-692-13 Sequence 13, Appl

Sequence 13, Appl
Sequence 10, Appl
Sequence 10, Appl
Sequence 3, Appl
Sequence 2, Appl
Sequence 10, Appl
Sequence 81, Appl
Sequence 317, Appl
Sequence 317, Appl
Sequence 12, Appl
Sequence 5, Appl
Sequence 5, Appl
Sequence 217, App
Sequence 217, App
Sequence 217, App
Sequence 217, App
Sequence 217, App
Sequence 2, Appl
Sequence 31, Appl
Sequence 225, App
Sequence 2, Appl
Sequence 57, Appl
Sequence 225, App
Sequence 2, Appl
Sequence 225, App
Sequence 2, Appl
Sequence 2, Appl
Sequence 2, Appl
Sequence 323, App

16 130 100.0 129 15 US-10-044-539-13
17 130 100.0 259 15 US-10-044-692-10
18 130 100.0 259 15 US-10-044-539-10
19 130 100.0 291 12 US-10-282-960-3
20 130 100.0 437 15 US-10-294-778-2
21 130 100.0 438 15 US-10-294-778-10
22 130 100.0 438 15 US-10-282-960-81
23 130 100.0 530 15 US-10-044-692-317
24 130 100.0 530 15 US-10-044-539-317
25 130 100.0 622 15 US-10-294-778-12
26 130 100.0 807 15 US-10-044-692-5
27 130 100.0 807 15 US-10-044-539-5
28 130 100.0 1003 10 US-09-843-676-217
29 130 100.0 1003 11 US-09-438-486-217
30 130 100.0 1003 15 US-10-053-758-217
31 130 100.0 1003 15 US-10-054-295-217
32 130 100.0 1003 15 US-10-054-611-217
33 130 100.0 1132 10 US-09-990-080-2
34 130 100.0 1132 10 US-09-749-7288-31
35 130 100.0 1132 10 US-09-843-676-225
36 130 100.0 1132 10 US-09-953-052-2
37 130 100.0 1132 12 US-10-295-681-57
38 130 100.0 1132 15 US-10-053-758-225
39 130 100.0 1132 15 US-10-208-243-2
40 130 100.0 1132 15 US-10-054-295-225
41 130 100.0 1132 15 US-10-054-611-225
42 130 100.0 1132 15 US-10-105-963-2
43 130 100.0 1132 15 US-10-044-692-2
44 130 100.0 1132 15 US-10-044-539-2
45 130 100.0 1154 15 US-10-044-692-323

ALIGNMENTS

RESULT 1

US-09-843-676-114
; Sequence 114, Application US/09843676
; Patent No. US20020164786A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin
; Andrews, William H.
; TITLE OF INVENTION: NO. US20020164786A1el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/843,676
; FILING DATE: 26-APR-2001
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/724,643

```
;
; FILING DATE: 01-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002930US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 114:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 114:
US-09-843-676-114

Query Match 100.0%; Score 130; DB 10; Length 27;
Best Local Similarity 100.0%; Pred. No. 4.8e-13;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARTFREKRAERLTSRVKALFSVLNYE 27
Db 1 ARTFREKRAERLTSRVKALFSVLNYE 27

RESULT 2
US-09-766-253-114
; Sequence 114, Application US/09766253
; Publication No. US20020187471A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Linger, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin
; Andrews, William H.
; TITLE OF INVENTION: No. US20020187471A1 Telomerase
; NUMBER OF SEQUENCES: 171
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 19-Jan-2001
; APPLICATION NUMBER: US/09/766,253
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/846,017
; FILING DATE: 1997-04-25
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002920US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 114:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 amino acids
; TYPE: amino acid
; STRANDEDNESS:
```

```
;
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 114:
US-09-766-253-114

Query Match 100.0%; Score 130; DB 10; Length 27;
Best Local Similarity 100.0%; Pred. No. 4.8e-13;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARTFREKRAERLTSRVKALFSVLNYE 27
Db 1 ARTFREKRAERLTSRVKALFSVLNYE 27

RESULT 3
US-09-438-486-114
; Sequence 114, Application US/09438486
; Publication No. US20030009019A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Linger, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: No. US20030009019A1 Telomerase
; NUMBER OF SEQUENCES: 223
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/438,486
; FILING DATE: 12-NOV-1999
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002931US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 114:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 amino acids
; TYPE: amino acid
; STRANDEDNESS:
```

TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-438-486-114

Query Match 100.0%; Score 130; DB 11; Length 27;
Best Local Similarity 100.0%; Pred. No. 4.8e-13;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARTFREKRAERLTSRVKALFSLVNYE 27
Db 1 ARTFREKRAERLTSRVKALFSLVNYE 27

RESULT 4

US-10-053-758-114
Sequence 114, Application US/10053758
Publication No. US20030032075A1

GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
Andrews, William H.

TITLE OF INVENTION: No. US20030032075A1el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/053,758
FILING DATE: 18-Jan-2002
CLASSIFICATION: 536

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996

ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELEPHONE: (415) 576-0300
TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 114:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 amino acids
TYPE: amino acid
STRANDEDNESS: <unknown>
TOPOLOGY: linear

MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 114:
US-10-053-758-114

Query Match 100.0%; Score 130; DB 15; Length 27;
Best Local Similarity 100.0%; Pred. No. 4.8e-13;

Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ARTFREKRAERLTSRVKALFSLVNYE 27
Db 1 ARTFREKRAERLTSRVKALFSLVNYE 27

RESULT 5

US-10-054-295-114
Sequence 114, Application US/10054295
Publication No. US20030044953A1

GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
Andrews, William H.

TITLE OF INVENTION: No. US20030044953A1el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/054,295
FILING DATE: 18-Jan-2002
CLASSIFICATION: 536

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/854,050
FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996

ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 114:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 amino acids
TYPE: amino acid
STRANDEDNESS: <unknown>
TOPOLOGY: linear

MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 114:
US-10-054-295-114

Query Match 100.0%; Score 130; DB 15; Length 27;
Best Local Similarity 100.0%; Pred. No. 4.8e-13;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARTFREKRAERLTSRVKALFSLVNYE 27
Db 1 ARTFREKRAERLTSRVKALFSLVNYE 27

RESULT 6

US-10-054-611-114
; Sequence 114, Application US/10054611
; Publication No. US20030059787A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin
; Andrews, William H.
; TITLE OF INVENTION: NO. US20030059787A1el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/054,611
; FILING DATE: 18-Jan-2002
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/854,050
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002930US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 114:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 114:
US-10-054-611-114
Query Match 100.0%; Score 130; DB 15; Length 27;
Best Local Similarity 100.0%; Pred. No. 4.8e-13;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ARTFRREKRAERLTSRVKALFSLVNYE 27
Db 1 ARTFRREKRAERLTSRVKALFSLVNYE 27
RESULT 7
US-10-044-692-115
; Sequence 115, Application US/10044692
; Publication No. US20030096344A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin
; Andrews, William H.
; TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND
; NUMBER OF SEQUENCES: 335
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/044,692
; FILING DATE: 11-Jan-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/912,951
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002600US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 115:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 115:
US-10-044-692-115
Query Match 100.0%; Score 130; DB 15; Length 27;
Best Local Similarity 100.0%; Pred. No. 4.8e-13;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ARTFRREKRAERLTSRVKALFSLVNYE 27
Db 1 ARTFRREKRAERLTSRVKALFSLVNYE 27
RESULT 8
US-10-044-539-115
; Sequence 115, Application US/10044539
; Publication No. US20030100093A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin
; Andrews, William H.

TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND THERAPEUTIC METHODS
NUMBER OF SEQUENCES: 335
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/044,539
FILING DATE: 11-Jan-2002
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/912,951
FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002600US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 115:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 115:
US-10-044-539-115
Query Match 100.0%; Score 130; DB 15; Length 27;
Best Local Similarity 100.0%; Pred. No. 4.8e-13;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ARTFREKRAERLTSRVKALFSLVNYE 27
Db 1 ARTFREKRAERLTSRVKALFSLVNYE 27
RESULT 9
US-09-843-676-67
Sequence 67, Application US/09843676
Patent No. US20020164786A1
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: No. US20020164786A1el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/843,676
FILING DATE: 26-Apr-2001
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 67:
SEQUENCE CHARACTERISTICS:
LENGTH: 129 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..129
OTHER INFORMATION: /note= "TRT motifs from human"
SEQUENCE DESCRIPTION: SEQ ID NO: 67:
US-09-843-676-67
Query Match 100.0%; Score 130; DB 10; Length 129;
Best Local Similarity 100.0%; Pred. No. 2.9e-12;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ARTFREKRAERLTSRVKALFSLVNYE 27
Db 101 ARTFREKRAERLTSRVKALFSLVNYE 127
RESULT 10
US-09-766-253-67
Sequence 67, Application US/09766253
Publication No. US20020187471A1
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: No. US20020187471A1el Telomerase
NUMBER OF SEQUENCES: 171
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California

```

; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/766,253
; FILING DATE: 19-Jan-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/846,017
; FILING DATE: 1997-04-25
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002920US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 67:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 129 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..129
; OTHER INFORMATION: /note= "TRT motifs from human"
; SEQUENCE DESCRIPTION: SEQ ID NO: 67:
US-09-766-253-67

```

Query Match 100.0%; Score 130; DB 10; Length 129;
 Best Local Similarity 100.0%; Pred. No. 2.9e-12;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Qy 1 ARTFREKRAERLTSRVKALFSVLNVE 27
    |||||
Db 101 ARTFREKRAERLTSRVKALFSVLNVE 127
    |||||

```

```

RESULT 11
US-09-438-486-67
; Sequence 67, Application US/09438486
; Publication No. US2003000919A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: NO. US20030009019A1el Telomerase
; NUMBER OF SEQUENCES: 223
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:

```

```

; APPLICATION NUMBER: US/09/438,486
; FILING DATE: 12-NOV-1999
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002931US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 67:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 129 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..129
; OTHER INFORMATION: /note= "TRT motifs from human"
US-09-438-486-67

```

Query Match 100.0%; Score 130; DB 11; Length 129;
 Best Local Similarity 100.0%; Pred. No. 2.9e-12;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Qy 1 ARTFREKRAERLTSRVKALFSVLNVE 27
    |||||
Db 101 ARTFREKRAERLTSRVKALFSVLNVE 127
    |||||

```

```

RESULT 12
US-10-053-758-67
; Sequence 67, Application US/10053758
; Publication No. US20030032075A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: NO. US20030032075A1el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

```

SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/053,758
FILING DATE: 18-Jan-2002
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 67:
SEQUENCE CHARACTERISTICS:
LENGTH: 129 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..129
OTHER INFORMATION: /note= "TRT motifs from human"
SEQUENCE DESCRIPTION: SEQ ID NO: 67:
US-10-053-758-67

Query Match 100.0%; Score 130; DB 15; Length 129;
Best Local Similarity 100.0%; Pred. No. 2.9e-12;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARTFREKRAERLTSRVKALFSLVNYE 27
Db 101 ARTFREKRAERLTSRVKALFSLVNYE 127

RESULT 13
US-10-054-295-67
Sequence 67, Application US/10054295
Publication No. US20030044953A1
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: No. US20030044953A1el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/054,295
FILING DATE: 18-Jan-2002
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/854,050
FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 67:
SEQUENCE CHARACTERISTICS:
LENGTH: 129 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..129
OTHER INFORMATION: /note= "TRT motifs from human"
SEQUENCE DESCRIPTION: SEQ ID NO: 67:
US-10-054-295-67

Query Match 100.0%; Score 130; DB 15; Length 129;
Best Local Similarity 100.0%; Pred. No. 2.9e-12;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARTFREKRAERLTSRVKALFSLVNYE 27
Db 101 ARTFREKRAERLTSRVKALFSLVNYE 127

RESULT 14
US-10-054-611-67
Sequence 67, Application US/10054611
Publication No. US20030059787A1
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: No. US20030059787A1el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/054,611
FILING DATE: 18-Jan-2002
CLASSIFICATION: 536
PRIOR APPLICATION DATA:

```
APPLICATION NUMBER: 08/854,050
FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 67:
SEQUENCE CHARACTERISTICS:
LENGTH: 129 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..129
OTHER INFORMATION: /note= "TRT motifs from human"
SEQUENCE DESCRIPTION: SEQ ID NO: 67:
US-10-054-611-67

Query Match 100.0%; Score 130; DB 15; Length 129;
Best Local Similarity 100.0%; Pred. No. 2.9e-12;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARTFREKRAERLTSRVKALFSLVNYE 27
Db 101 ARTFREKRAERLTSRVKALFSLVNYE 127

RESULT 15
US-10-044-692-13
Sequence 13, Application US/10044692
Publication No. US20030096344A1
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND
THERAPEUTIC METHODS
NUMBER OF SEQUENCES: 335
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/044,692
FILING DATE: 11-Jan-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/912,951
FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/854,050
```

```
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002600US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 129 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..129
OTHER INFORMATION: /note= "TRT motifs from human"
SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-10-044-692-13

Query Match 100.0%; Score 130; DB 15; Length 129;
Best Local Similarity 100.0%; Pred. No. 2.9e-12;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARTFREKRAERLTSRVKALFSLVNYE 27
Db 101 ARTFREKRAERLTSRVKALFSLVNYE 127

Search completed: November 12, 2003, 19:55:47
Job time : 21.566 secs
```


GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model
Run on: November 12, 2003, 19:43:04 ; Search time 10.5283 Seconds
(without alignments)
246.626 Million cell updates/sec

Title: US-08-854-050-114
Perfect score: 130
Sequence: 1 ARTFRKEKAERLTSRVKALFSLVNYE 27
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues
Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 76:.*
1: Pir1:.*
2: Pir2:.*
3: Pir3:.*
4: Pir4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	130	100.0	1132	2 T03844	telomerase catalytic chain - human
2	51	39.2	98	2 B81120	hypothetical prote
3	49	37.7	331	2 T45089	pyruvate synthase
4	49	37.7	836	2 JE0248	ATP-binding casset
5	48	36.9	321	2 F81030	ABC transporter, p
6	48	36.9	321	2 F81976	probable ferric en
7	48	36.9	334	2 F71114	probable ferredoxi
8	48	36.9	631	2 AH0315	probable ABC trans
9	47.5	36.5	407	2 S53900	hypothetical prote
10	47	36.2	617	2 T49535	probable multifunc
11	46	35.4	135	2 D84730	60S ribosomal prot
12	46	35.4	200	2 D69500	molybdopterin-guan
13	46	35.4	462	2 T25544	hypothetical prote
14	46	35.4	474	1 IMBP4	site-specific reco
15	45	34.6	98	2 A81902	hypothetical prote
16	45	34.6	321	2 D90302	conserved hypotet
17	45	34.6	334	2 F75046	pyruvate synthase
18	45	34.6	436	2 H97270	thiamine biosynthe
19	44.5	34.2	335	2 E96799	probable carboxyph
20	44	33.8	40	2 C32338	hypothetical 4K pr
21	44	33.8	159	2 A70515	probable bIRA prot
22	44	33.8	172	1 MOCH2G	myosin regulatory
23	44	33.8	172	2 I51690	myosin II regulato
24	44	33.8	172	2 B37100	myosin regulatory
25	44	33.8	172	2 A61034	myosin regulatory
26	44	33.8	172	2 A37100	myosin regulatory
27	44	33.8	172	2 S45709	myosin regulatory
28	44	33.8	172	2 I52831	myosin regulatory
29	44	33.8	172	2 T20273	hypothetical prote

30	44	33.8	180	2 C64584	heat shock protein
31	44	33.8	180	2 E71929	heat shock protein
32	44	33.8	189	2 S11632	myosin regulatory
33	44	33.8	328	2 C45734	histidyl-tRNA synt
34	44	33.8	392	2 E88108	protein C46E10.3 f
35	44	33.8	520	2 F70350	recombination prot
36	44	33.8	534	2 H71069	probable nodulatio
37	44	33.8	594	2 B71893	exonuclease ABC c
38	44	33.8	4151	2 T13734	groovin gene prote
39	43	33.1	99	2 S03525	T-cell receptor al
40	43	33.1	104	2 H71204	hypothetical prote
41	43	33.1	111	2 S22899	T-cell receptor al
42	43	33.1	118	2 S21918	T-cell receptor al
43	43	33.1	128	2 B72230	hypothetical prote
44	43	33.1	167	2 T35494	probable bacteriof
45	43	33.1	174	2 A39932	myosin regulatory

ALIGNMENTS

RESULT 1
T03844
telomerase catalytic chain - human
N;Alternate names: telomerase reverse transcriptase
C;Species: Homo sapiens (man)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 08-Oct-1999
C;Accession: T03844
R;Nakamura, T.M.; Morin, G.B.; Chapman, K.B.; Weinrich, S.L.; Andrews, W.H.; Lingner, J.
S;Source 277, 955-959, 1997
A;Title: Telomerase catalytic subunit homologs from fission yeast and human.
A;Reference number: Z15111; MUID:97400623; PMID:9252327
A;Accession: T03844
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-1132 <NA>
A;Cross-references: EMBL:AF015950; NID:g2330016; PIDN:AAC51672.1; PID:g2330017
A;Experimental source: kidney
C;Genetics:
A;Gene: TRT
A;Map position: 5p

Query Match 100.0%; Score 130; DB 2; Length 1132;
Best Local Similarity 100.0%; Pred. No. 1.8e-11;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARTFRKEKAERLTSRVKALFSLVNYE 27
|||||
Db 642 ARTFRKEKAERLTSRVKALFSLVNYE 668

RESULT 2
B81120
hypothetical protein NM01120 [imported] - Neisseria meningitidis (strain MC58 serogroup
C;Species: Neisseria meningitidis
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001
C;Accession: B81120
R;Tetzelin, H.; Saunders, N.J.; Heideberg, J.; Jeffries, A.C.; Nelson, K.E.; Eiseen, J.
Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.
ri, H.; Qiu, H.; Vamathevan, J.; Gill, J.; Scariato, V.; Masignani, V.; Pizzi, M.
Science 287, 1809-1815, 2000
A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; V
A;Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
A;Reference number: A81000; MUID:20175755; PMID:10710307
A;Accession: B81120
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-98 <TET>
A;Cross-references: GB:AE002461; GB:AE002098; NID:g7226350; PIDN:AAF41510.1; PID:g72263
C;Genetics:
A;Gene: NM01120

```
Query Match      39.2%; Score 51; DB 2; Length 98;
Best Local Similarity 36.0%; Pred. No. 1.5;
Matches 9; Conservative 10; Mismatches 6; Indels 0; Gaps 0;

QY 1 ARTFRREKRAERLTSRVKALFSLVN 25
   :|||:| : : : :| :|||:|
Db 36 SRTYRRARLAQPKTRWKILYTLIN 60

RESULT 3
T45089
pyruvate synthase (EC 1.2.7.1) beta chain [validated] - Pyrococcus furiosus
C:Species: Pyrococcus furiosus
C>Date: 31-Jan-2000 #sequence_revision 31-Jan-2000 #text_change 03-May-2002
C:Accession: T45089
R:Kletzin, A.; Adams, M.W.
J. Bacteriol. 178, 248-257, 1996
A:Title: Molecular and phylogenetic characterization of pyruvate and 2-ketoisovalerate
A:Reference number: Z22508; MUID:96125254; PMID:8550425
A:Accession: T45089
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-331 <KLE>
A:Cross-references: EMBL:X85250; NID:g1197352; PIDN:CAA59506.1; PID:g1197364
A:Experimental source: DSM 3638
C:Genetics:
A:Gene: porB
C:Complex: homotetramer of alpha, beta, delta, and gamma chains
C:Function:
A:Description: EC 1.2.7.1 [validated, MUID:96125254; PMID:8550425]
A:Superfamily: pyruvate synthase beta chain
C:Keywords: coenzyme A; oxidoreductase
F:2-31/Product: 2-oxoisovalerate-ferredoxin oxidoreductase beta chain #status experimen

Query Match      37.7%; Score 49; DB 2; Length 331;
Best Local Similarity 41.7%; Pred. No. 10;
Matches 10; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY 4 FRREKRAERLTSRVKALFSLVNYE 27
   :| :| :| :| :| :| :| :|
Db 300 FKRPEATEELRNQVKAMKVLGVE 323

RESULT 4
JE0248
ATP-binding cassette half-transporter - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jul-2000
C:Accession: JE0248
R:Hirsch-Ernst, K.I.; Gaini-Rahimi, S.; Ernst, B.P.; Schmitz-Salue, C.; Blume, S.; Kahl,
Biochem. Biophys. Res. Commun. 249, 151-155, 1998
A:Title: Molecular cDNA cloning and tissue distribution of mRNA encoding a novel ATP-bin
A:Reference number: JE0248; MUID:98381042; PMID:9705847
A:Accession: JE0248
A:Molecule type: mRNA
A:Residues: 1-836 <HIR>
A:Cross-references: GB:A003004; NID:g2970020; PIDN:CAA05793.1; PID:g2982567
A:Superfamily: unassigned ATP-binding cassette proteins; ATP-binding cassette homology
C:Keywords: ATP
F:606-800/Domain: ATP-binding cassette homology <ABC>

Query Match      37.7%; Score 49; DB 2; Length 836;
Best Local Similarity 37.5%; Pred. No. 27;
Matches 9; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 4 FRREKRAERLTSRVKALFSLVNYE 27
   :| :| :| :| :| :| :| :|
Db 438 FRDWTQENATRAVDLSLNFE 461

RESULT 5
E81030
ABC transporter, periplasmic solute-binding protein, probable NMB1880 [imported] - Neis
```

```
C:Species: Neisseria meningitidis
C>Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001
C:Accession: F81030
R:Tetteelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.
Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.
xi, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Maignani, V.; Pizza, M.
Science 287, 1809-1815, 2000
A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; V
A:Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
A:Reference number: A81000; MUID:20175755; PMID:10710307
A:Accession: F81030
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-321 <TET>
A:Cross-references: GB:AE002538; GB:AE002098; NID:g7227136; PIDN:AAF42214.1; PID:g72271
A:Experimental source: serogroup B, strain MC58
C:Genetics:
A:Gene: NMB1880

Query Match      36.9%; Score 48; DB 2; Length 321;
Best Local Similarity 45.5%; Pred. No. 14;
Matches 10; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 1 ARTFRREKRAERLTSRVKALFS 22
   ||| :| :| :| :| :| :| :|
Db 155 ARIFGKEARAELKAQIDALFA 176

RESULT 6
F81976
probable ferric enterobactin transporter binding protein NMA0577 [imported] - Neisseria
C:Species: Neisseria meningitidis
C>Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001
C:Accession: F81976
R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; More
; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream
Nature 404, 502-506, 2000
A:Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.
A:Reference number: A81775; MUID:20222556; PMID:10761919
A:Accession: F81976
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-321 <PAR>
A:Cross-references: GB:AL162753; GB:AL157959; NID:g7379120; PIDN:CAB83868.1; PID:g73793
A:Experimental source: serogroup A, strain Z2491
C:Genetics:
A:Gene: fetB2; NMA0577

Query Match      36.9%; Score 48; DB 2; Length 321;
Best Local Similarity 45.5%; Pred. No. 14;
Matches 10; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 1 ARTFRREKRAERLTSRVKALFS 22
   ||| :| :| :| :| :| :| :|
Db 155 ARIFGKEARAELKAQIDALFA 176

RESULT 7
F71114
probable ferredoxin oxidoreductase beta subunit - Pyrococcus horikoshii
C:Species: Pyrococcus horikoshii
C>Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 20-Jun-2000
C:Accession: F71114
R:Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Seki
M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguch
DNA Res. 5, 55-76, 1998
A:Title: Complete sequence and gene organization of the genome of a hyper-thermophilic
A:Reference number: A71000; MUID:98344137; PMID:9679194
A:Accession: F71114
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-334 <KAW>
```

A;Cross-references: GB:AP000003; NID:g32361130; PIDN:BAA29776.1; PID:g3257093

A;Experimental source: strain OT3

A;Note: this accession replaces an interim accession for a sequence replaced by GenBank

C;Genetics:

A;Gene: PH0685

C;Superfamily: pyruvate synthase beta chain

Query Match 36.9%; Score 48; DB 2; Length 334;
Best Local Similarity 37.5%; Pred. No. 15;
Matches 9; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 4 FREKRAERLTSRVKALFSLVNYE 27

Db 303 FKPEALIELRNQIKAWKVLGVE 326

RESULT 8

AH0315

Probable ABC transport protein YPO2588 [imported] - Yersinia pestis (strain CO92)

C;Species: Yersinia pestis

C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 17-May-2002

C;Accession: AH0315

R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.; deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; et al. M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrall, Nature 413, 523-527, 2001

A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.

A;Reference number: AB0001; MUID:21470413; PMID:11586360

A;Accession: AH0315

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-631 <KUR>

A;Cross-references: GB:AL590842; PIDN:CAC91388.1; PID:g15980574; GSPDB:GN00175

A;Gene: YPO2588

C;Superfamily: unassigned ATP-binding cassette proteins; ATP-binding cassette homology

Query Match 36.9%; Score 48; DB 2; Length 631;
Best Local Similarity 41.7%; Pred. No. 28;
Matches 10; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

QY 4 FREKRAERLTSRVKALFSLVNYE 27

Db 229 FRRELKANADATKSIDSLVNYE 252

RESULT 9

S53900

hypothetical protein YNL078w - yeast (Saccharomyces cerevisiae)

N;Alternate names: hypothetical protein N2337

C;Species: Saccharomyces cerevisiae

C;Date: 08-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 19-Apr-2002

C;Accession: S53900; S63010; S63929

R;Poehlmann, R.; Philippsen, P.

submitted to the EMBL Data Library, April 1995

A;Reference number: S53896

A;Accession: S53900

A;Molecule type: DNA

A;Residues: 1-407 <POE>

A;Cross-references: EMBL:X86470; NID:g791101; PID:g791106

R;Poehlmann, R.; Philippsen, P.

submitted to the Protein Sequence Database, April 1996

A;Reference number: S62997

A;Accession: S63010

A;Molecule type: DNA

A;Residues: 1-407 <POW>

A;Cross-references: EMBL:Z71354; NID:g1301968; PID:e239687; PID:g1301969; MIPS:YNL078w

A;Experimental source: strain S288C

R;Poehlmann, R.; Philippsen, P.

yeast 12, 391-402, 1996

A;Title: Sequencing a cosmid clone of Saccharomyces cerevisiae chromosome XIV reveals 12

A;Reference number: S63925; MUID:96267764; PMID:8701611

A;Accession: S63929

A;Status: nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-407 <POF>

A;Cross-references: EMBL:X86470; NID:g791101; PIDN:CAA60180.1; PID:g791106

A;Note: the nucleotide sequence was submitted to the EMBL Data Library, April 1995

C;Genetics:

A;Gene: SGD:JIP1

A;Cross-references: SGD:S0005022

A;Map position: 14L

A;Note: YNL078w

Query Match 36.5%; Score 47.5; DB 2; Length 407;
Best Local Similarity 48.1%; Pred. No. 22;
Matches 13; Conservative 3; Mismatches 8; Indels 3; Gaps 1;

QY 3 TFRREKRAERLTSRV---KALFSLVNY 26

Db 170 SIRREDQAKVRSFRSKKELTSLVNY 196

RESULT 10

T49535

probable multifunctional folic acid synthesis protein [imported] - Neurospora crassa

N;Alternate names: protein B21J21.140

C;Species: Neurospora crassa

C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 28-Jul-2000

C;Accession: T49535

R;Schulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura

submitted to the Protein Sequence Database, May 2000

A;Reference number: Z25022

A;Accession: T49535

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-617 <SCH>

A;Cross-references: EMBL:AL355929; GSPDB:GN00116; NCSP:B21J21.140

A;Experimental source: BAC clone B21J21; strain OR74A

C;Genetics:

A;Gene: NCSP:B21J21.140

A;Map position: 6

A;Introns: 42/1; 222/3; 292/2

C;Superfamily: 2-amino-4-hydroxy-6-hydroxymethylidihydropteridine pyrophosphokinase homo

F;169-300/Domain: 2-amino-4-hydroxy-6-hydroxymethylidihydropteridine pyrophosphokinase h

Query Match 36.2%; Score 47; DB 2; Length 617;
Best Local Similarity 45.0%; Pred. No. 39;
Matches 9; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY 3 TFRREKRAERLTSRVKALFS 22

Db 48 TFRKKKAHQYQRLSEFSS 67

RESULT 11

D84730

60S ribosomal protein L27 [imported] - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cross)

C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 16-Feb-2001

C;Accession: D84730

R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.L.; Town, C.D.; Fujii, C.Y.;

M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, I.

euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter,

Nature 402, 761-768, 1999

A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A;Reference number: A84420; MUID:20083487; PMID:10617197

A;Accession: D84730

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-135 <STO>

A;Cross-references: GB:AE002093; NID:g4263697; PIDN:AAI5383.1; GSPDB:GN00139

C;Genetics:

A;Gene: At2g32220

A;Map position: 2

C;Superfamily: rat ribosomal protein L27

Query Match 35.4%; Score 46; DB 2; Length 135;
 Best Local Similarity 47.6%; Pred. No. 12;
 Matches 10; Conservative 5; Mismatches 4; Indels 2; Gaps 1;

Qy 7 EKRAERLTSRVKALFSLVNYE 27
 Db 60 KKTAKK--SRVKCFKVINQ 78
 :||:|||||:|:|:
 :||:|||||:|:|:

RESULT 12
 D69500
 molybdopterin-guanine dinucleotide biosynthesis protein A (moba) homolog - Archaeoglobus
 C:Species: Archaeoglobus fulgidus
 C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 21-Jul-2000
 C:Accession: D69500
 R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson
 ; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.
 Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
 Nature 390, 364-370, 1997
 A:Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.
 Smith, H.O.; Woese, C.R.; Venter, J.C.
 A:Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeo
 A:Reference number: A69250; MUID:98049343; PMID:9389475
 A:Accession: D69500
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-200 <KLE>
 A:Cross-references: GB:AE000964; GB:AE000782; MID:g2699287; PIDN:AAB89249.1; PID:g264853

Query Match 35.4%; Score 46; DB 2; Length 200;
 Best Local Similarity 58.8%; Pred. No. 18;
 Matches 10; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 5 RREKRAERLTSRVKALF 21
 Db 46 RDEKQAEKLSRVEAEF 62
 |||||:|:|:
 |||||:|:|:

RESULT 13
 T25544
 hypothetical protein C14A11.3 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
 C:Accession: T25544
 R;Wilson, R.; Greco, T.; Elliott, G.
 submitted to the EMBL Data Library, April 1997
 A:Description: The sequence of C. elegans cosmid C14A11.
 A:Reference number: Z20048
 A:Accession: T25544
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-462 <WTL>
 A:Cross-references: EMBL:U97592; PIDN:AAB52870.1; GSPDB:GN00028; CESP:C14A11.3
 A:Experimental source: strain Bristol N2; clone C14A11
 C:Genetics:
 A:Gene: CESP:C14A11.3
 A:Map position: X
 A:Introns: 38/3; 73/3; 153/2; 325/3; 440/3

Query Match 35.4%; Score 46; DB 2; Length 462;
 Best Local Similarity 50.0%; Pred. No. 42;
 Matches 12; Conservative 3; Mismatches 7; Indels 2; Gaps 1;

Qy 3 TFRREKRAERLTSRVKALFSLVNY 26
 Db 10 SFRFSKR--RLITSVSAPLIWNY 31
 :|||:|:|:|:|:
 :|||:|:|:|:|:

RESULT 14
 IMBP4
 site-specific recombinase for integration and excision - Bacillus phage phi-105
 N:Alternate names: immunity region protein 3, 4, 5, 6

C:Species: Bacillus phage phi-105
 C:Date: 31-Dec-1988 #sequence_revision 22-Oct-1999 #text_change 16-Jun-2000
 C:Accession: T13541; C24521; D24521; E24521; F24521
 R;Kobayashi, K.; Okamura, K.; Inoue, T.; Sato, T.; Kobayashi, Y.
 submitted to the EMBL Data Library, July 1998
 A:Description: Complete nucleotide sequence of Bacillus subtilis phage phi-105.
 A:Reference number: Z17688
 A:Accession: T13541
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-474 <KOB>
 A:Cross-references: EMBL:AB016282; PIDN:BAA36658.1
 R;Cully, D.F.; Garro, A.J.
 Gene 38, 153-164, 1985
 A:Title: Nucleotide sequence of the immunity region of Bacillus subtilis bacteriophage
 A:Reference number: A91535; MUID:86056972; PMID:3934047
 A:Accession: C24521
 A:Molecule type: DNA
 A:Residues: 1-78, 'MTHC' <CUL>
 A:Cross-references: GB:M11920; MID:g215477; PIDN:AAA88399.1; PID:g1196717
 A:Accession: D24521
 A:Molecule type: DNA
 A:Residues: 149-160, 'AR', '163', 'H', 'HSDSQRRVR', '381-383', 'RIQRRARS', '392 <CU2>
 A:Cross-references: GB:M11920; MID:g215477; PIDN:AAA88401.1; PID:g1196719
 A:Accession: E24521
 A:Molecule type: DNA
 A:Residues: 189-318, 'HAP', <CU3>
 A:Cross-references: GB:M11920
 A:Accession: F24521
 A:Molecule type: DNA
 A:Residues: 'MP', '319-376', 'RNTK', '381', 'PGPWS', <CU4>
 A:Cross-references: GB:M11920
 C:Superfamily: phage phi-105 site-specific recombinase
 C:Keywords: early protein

Query Match 35.4%; Score 46; DB 1; Length 474;
 Best Local Similarity 50.0%; Pred. No. 43;
 Matches 9; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 9 RAERLTSRVKALFSLVNY 26
 Db 86 RLDRLTSRVDRDYSLLDY 103
 |||||:|:|:
 |||||:|:|:

RESULT 15
 AB1902
 hypothetical protein NMA1329 [imported] - Neisseria meningitidis (strain Z2491 serogrou
 C:Species: Neisseria meningitidis
 C:Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001
 C:Accession: AB1902
 R;Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; More
 ; Holroyd, S.; Jageis, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream
 Nature 404, 502-506, 2000
 A:Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.
 A:Reference number: AB1775; MUID:20222556; PMID:10761919
 A:Accession: AB1902
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-98 <PAR>
 A:Cross-references: GB:AL162755; GB:AL157959; MID:g7379742; PIDN:CAB84580.1; PID:g738000
 A:Experimental source: serogroup A, strain Z2491
 C:Genetics:
 A:Gene: NMA1329

Query Match 34.6%; Score 45; DB 2; Length 98;
 Best Local Similarity 32.0%; Pred. No. 12;
 Matches 8; Conservative 10; Mismatches 7; Indels 0; Gaps 0;

Qy 1 ARTFREKRAERLTSRVKALFSLVNL 25
 Db 36 SRTYRGARLAQKPKTRKVLTYLIN 60
 :||:|:|:|:|:|:|:
 :||:|:|:|:|:|:|:

Search completed: November 12, 2003, 19:52:00
Job time : 10.5283 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 12, 2003, 19:41:59 ; Search time 5.60377 Seconds
(without alignments)
226.583 Million cell updates/sec

Title: US-08-854-050-114

Perfect score: 130

Sequence: 1 ARTFREKRAERLTSRVKALFSVLNVE 27

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	130	100.0	1132	1	TERT_HUMAN
2	73	56.2	1122	1	TERT_MOUSE
3	49	37.7	330	1	PORB_PYRFO
4	48	36.9	330	1	PORB_PYRFO
5	47.5	36.5	407	1	YNH8 YEAST
6	46	35.4	842	1	ABC6 HUMAN
7	45	34.6	330	1	PORB_PYRAB
8	45	34.6	337	1	REPL_ZYGBA
9	45	34.6	436	1	THIC_CLOAB
10	44.5	34.2	335	1	CPPM_ARATH
11	44	33.8	159	1	BFR_MYCTU
12	44	33.8	166	1	Y00F_BPT4
13	44	33.8	171	1	MLRB_RAT
14	44	33.8	171	1	MLRB_RAT
15	44	33.8	171	1	MLRN_CHICK
16	44	33.8	172	1	MLRH_CABEL
17	44	33.8	180	1	HSLV_HELPJ
18	44	33.8	180	1	HSLV_HELPJ
19	44	33.8	328	1	HISZ_LACLA
20	44	33.8	520	1	REC_N_AQUAE
21	44	33.8	594	1	UVRC_HELPJ
22	43	33.1	159	1	BFR_MYCAV
23	43	33.1	167	1	BFR_STRCO
24	43	33.1	174	1	MLRN_DROME
25	43	33.1	198	1	Y530_METJA
26	43	33.1	204	1	YFHI_YEAST
27	43	33.1	471	1	YX11_CABEL
28	43	33.1	488	1	PSD3_TOBAC
29	43	33.1	594	1	UVRC_HELPJ
30	43	33.1	1127	1	LONH_PYRHO
31	43	33.1	1170	1	DP3A_TREPA
32	42.5	32.7	868	1	TOPI_PASMU
33	42	32.3	112	1	Y668_AQUAE

34 42 32.3 227 1 NODW BRAJA
35 42 32.3 250 1 YBX4 SCHPO
36 42 32.3 285 1 AMPR CITDI
37 42 32.3 364 1 REC XFLEA
38 42 32.3 375 1 DJBC HUMAN
39 42 32.3 396 1 APA4 HUMAN
40 42 32.3 472 1 PLSB SPIOL
41 42 32.3 482 1 YSR2 CAEEL
42 42 32.3 491 1 NUOM RICPR
43 42 32.3 495 1 XKDE BACSU
44 42 32.3 644 1 YHOB DROME
45 42 32.3 693 1 YD01 SCHPO

ALIGNMENTS

RESULT 1
TERT_HUMAN STANDARD; PRT; 1132 AA.
AC O14746; O14783;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Telomerase reverse transcriptase (EC 2.7.7.-) (Telomerase catalytic subunit) (HEST2).
DE TERT OR TRT OR EST2 OR TCS1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=97400623; PubMed=9252327;
RA Nakamura T.M., Morin G.B., Chapman K.B., Weinrich S.L., Andrews W.H., Lingner J., Harley C.B., Cech T.R.;
RT "Telomerase catalytic subunit homologs from fission yeast and human."; Science 277:955-959(1997).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=97433088; PubMed=9288757;
RA Meyerson M., Counter C.M., Eaton E.N., Ellison L.W., Steiner P., Caddle S.D., Ziaugra L., Beijersbergen R.L., Davidoff M.J., Liu Q., Bacchetti S., Haber D.A., Weinberg R.A.;
RT "HEST2, the putative human telomerase catalytic subunit gene, is up-regulated in tumor cells and during immortalization."; Cell 90:785-795(1997).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=99267414; PubMed=10333526;
RA Wick M., Zubov D., Hagen G.;
RT "Genomic organization and promoter characterization of the gene encoding the human telomerase reverse transcriptase (hTERT)."; Gene 232:97-106(1999).
RN [4]
RP SEQUENCE FROM N.A.
RX Londono-Vallejo J.A.;
RT "Sequence of a BAC carrying the entire hTERT gene."; Submitted (Oct-2001) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: TELOMERASE IS A RIBONUCLEOPROTEIN ENZYME ESSENTIAL FOR THE REPLICATION OF CHROMOSOME TERMINI IN MOST EUKARYOTES. IT ELONGATES TELOMERES. IT IS A REVERSE TRANSCRIPTASE THAT ADDS SIMPLE SEQUENCE REPEATS TO CHROMOSOME ENDS BY COPYING A TEMPLATE SEQUENCE WITHIN THE RNA COMPONENT OF THE ENZYME.
CC -!- SUBUNIT: Interacts with PINX1.
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- DISEASE: ACTIVATION AND CANCER CELL PATHOGENESIS. IMMORTALIZATION BELONGS TO THE REVERSE TRANSCRIPTASE FAMILY.
CC -!- SIMILARITY: BELONGS TO THE REVERSE TRANSCRIPTASE FAMILY.

This SWISS-PROT entry is copyright. It is produced through a collaboration

P15940 bradyrhizob
Q10204 schizosacch
P52658 citrobacter
Q9phel xylella fas
Q9nxx2 homo sapien
F06727 homo sapien
Q43869 spinacia ol
Q09950 caenorhabdi
Q9zc90 rickettsia
P54325 bacillus su
P12258 drosophila
O14286 schizosacch

CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----

CC EMBL; AF015950; AAC51672.1; -;
 DR EMBL; AF018167; AAC51724.1; -;
 DR EMBL; AF128894; AAD30037.1; -;
 DR EMBL; AF128893; AAD30037.1; JOINED.
 DR EMBL; AY007685; AAG23289.1; -;
 DR PIR; T03844; T03844.
 DR Genew; HGNC:11730; TERT.
 DR MIM; 187270; -;
 DR GO; GO:000596; C:telomere; TAS.
 DR GO; GO:0003721; F:telomeric template RNA reverse transcriptase. . .; TAS.
 DR GO; GO:0007003; P:telomere binding; TAS.
 DR InterPro; IPR000477; RVTse.
 DR InterPro; IPR003545; Telomerase_RT.
 DR Pfam; PF000078; rvt; 1
 DR PRINTS; PRO1365; TLOMERASERT.
 DR Transferase; RNA-directed DNA polymerase; Telomere; Nuclear protein;
 KW DNA-binding.
 FT CONFLICT 516 516 D -> G (IN REF. 2).
 SQ SEQUENCE 1132 AA; 126956 MW; 94E35469C4CA33A0 CRC64;

Query Match 100.0%; Score 130; DB 1; Length 1132;
 Best Local Similarity 100.0%; Pred. No. 9.1e-12;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARTERREKRAERLTSRVKALFSLVNYE 27
 |||||
 Db 642 ARTERREKRAERLTSRVKALFSLVNYE 668

RESULT 2

TERT MOUSE
 ID TERT_MOUSE STANDARD; PRT; 1122 AA.
 AC 070372; G35432;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Telomerase reverse transcriptase (EC 2.7.7.-) (Telomerase catalytic
 DE subunit).
 GN TERT.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98241176; PubMed=9582020;
 RA Greenberg R.A., Allsopp R.C., Chin L., Morin G.B., Depinho R.A.;
 RT "Expression of mouse telomerase reverse transcriptase during
 RT development, differentiation and proliferation.";
 RL Oncogene 16:1723-1730(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98393668; PubMed=9724727;
 RA Martin-Rivera L., Herrera E., Albar J.P., Blasco M.A.;
 RT "Expression of mouse telomerase catalytic subunit in embryos and
 RT adult tissues.";
 RL Proc. Natl. Acad. Sci. U.S.A. 95:10471-10476(1998).
 RN [3]
 RP SEQUENCE OF 550-616 FROM N.A.
 RX Drissi R., Cleveland J.L.;
 RT "Partial sequence of Mus musculus telomerase catalytic subunit
 RT homolog.";
 RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.

CC -!- FUNCTION: TLOMERASE IS A RIBONUCLEOPROTEIN ENZYME ESSENTIAL FOR
 CC THE REPLICATION OF CHROMOSOME TERMINI IN MOST EUKARYOTES. IT
 CC ELONGATES TLOMERES. IT IS A REVERSE TRANSCRIPTASE THAT ADDS

CC SIMPLE SEQUENCE REPEATS TO CHROMOSOME ENDS BY COPYING A TEMPLATE
 CC SEQUENCE WITHIN THE RNA COMPONENT OF THE ENZYME.
 CC -!- SUBUNIT: Interacts with PINK1 (By similarity).
 CC -!- SUBCELLULAR LOCATION: Nuclear.
 CC -!- SIMILARITY: BELONGS TO THE REVERSE TRANSCRIPTASE FAMILY.
 CC TLOMERASE SUBFAMILY.
 CC -----

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----

DR EMBL; AF051911; AAC09323.1; -;
 DR EMBL; AF073311; AAC34821.1; -;
 DR EMBL; AF029235; AAB84200.1; -;
 DR MGD; MGI:1202709; Tert.
 DR InterPro; IPR000477; RVTse.
 DR InterPro; IPR003545; Telomerase_RT.
 DR Pfam; PF000078; rvt; 1
 DR PRINTS; PRO1365; TLOMERASERT.
 DR Transferase; RNA-directed DNA polymerase; Telomere; Nuclear protein;
 KW DNA-binding.
 FT CONFLICT 553 553 I -> V (IN REF. 3).
 SQ SEQUENCE 1122 AA; 127977 MW; F85266905DD6558C CRC64;

Query Match 56.2%; Score 73; DB 1; Length 1122;
 Best Local Similarity 53.8%; Pred. No. 0.0041;
 Matches 14; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 2 RTFRREKRAERLTSRVKALFSLVNYE 27
 |||||
 Db 633 RALGRRKQAHFTQRUKTLFSLVNYE 658

RESULT 3

PORB PYRFU
 ID PORB_PYRFU STANDARD; PRT; 330 AA.
 AC Q51805;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Pyruvate synthase subunit porB (EC 1.2.7.1) (Pyruvate oxidoreductase
 DE beta chain) (POR) (Pyruvic-ferredoxin oxidoreductase beta subunit).
 GN PORB OR PF0965.
 OS Pyrococcus furiosus.
 OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
 OC Pyrococcus.
 OX NCBI_TaxID=2261;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-23.
 RX STRAIN=Vc1 / DSM 3638 / ATCC 43587 / JCM 8422;
 RA MEDLINE=96125254; PubMed=8550425;
 RA Kletzin A., Adams M.W.W.;
 RT "Molecular and phylogenetic characterization of pyruvate and 2-
 RT ketoisovalerate ferredoxin oxidoreductases from Pyrococcus furiosus
 RT and pyruvate ferredoxin oxidoreductase from Thermotoga maritima.";
 RL J. Bacteriol. 178:248-257(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX STRAIN=Vc1 / DSM 3638 / ATCC 43587 / JCM 8422;
 RA Weiss R.B., Dunn D.M., Robb F.T., Brown J.R.;
 RT "The complete sequence of the Pyrococcus furiosus genome.";
 RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP CHARACTERIZATION.
 RX STRAIN=Vc1 / DSM 3638 / ATCC 43587 / JCM 8422;
 RA MEDLINE=93136227; PubMed=8380721;
 RA Blamey J.M., Adams M.W.W.;
 RT "Purification and characterization of pyruvate ferredoxin
 RT oxidoreductase from the hyperthermophilic archaeon Pyrococcus


```
RT furiosus."
RL Biochim. Biophys. Acta 1161:19-27(1993).
CC -!- CATALYTIC ACTIVITY: Pyruvate + CoA + oxidized ferredoxin = acetyl-
CC CoA + CO(2) + reduced ferredoxin.
CC -!- SUBUNIT: HETEROTETRAMER OF ONE ALPHA, ONE BETA, ONE DELTA AND ONE
CC GAMMA CHAIN.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X85250; CAA59506.1; -.
DR EMBL; AE010209; AAL81089.1; -.
DR PIR; T45089; T45089.
KW Oxidoreductase; Complete proteome.
FT INIT MET 0
SQ SEQUENCE 330 AA; 36130 MW; 2449203EFC20A7CB CRC64;
Query Match 37.7%; Score 49; DB 1; Length 330;
Best Local Similarity 41.7%; Pred. No. 4.9;
Matches 10; Conservative 6; Mismatches 8; Indels 0; Gaps 0;
QY 4 FRREKRAERLTSRVKALFSLVLYNE 27
Db 299 FRPEAIEELRNQIKAMKVLGV 322
RESULT 4
PORTB PYRHO STANDARD; PRT; 330 AA.
AC O58417;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DE Pyruvate synthase subunit porB (EC 1.2.7.1) (Pyruvate oxidoreductase
DE beta chain) (POR) (Pyruvic-ferredoxin oxidoreductase beta subunit).
GN PORB OR PH0685.
OS Pyrococcus horikoshii.
OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
OC Pyrococcus.
OX NCBI_TaxID=53953;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=OT3;
RX MEDLINE=98344137; PubMed=9679194;
RA Kawarabayashi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y.,
RA Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Nagai Y.,
RA Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Y.,
RA Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kishida N., Oguchi A.,
RA Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K.,
RA Masuchi Y., Shizuya H., Kikuchi H.;
RT "Complete sequence and gene organization of the genome of a hyper-
RT thermophilic archaeobacterium, Pyrococcus horikoshii OT3."
RT DNA Res. 5:55-76(1998).
CC -!- CATALYTIC ACTIVITY: Pyruvate + CoA + oxidized ferredoxin = acetyl-
CC CoA + CO(2) + reduced ferredoxin.
CC -!- SUBUNIT: HETEROTETRAMER OF ONE ALPHA, ONE BETA, ONE DELTA AND ONE
CC GAMMA CHAIN (BY SIMILARITY).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AP000003; BAA29776.1; ALU1 INIT;
KW Oxidoreductase; Complete proteome.
```

```
FT INIT MET 0 BY SIMILARITY.
SQ SEQUENCE 330 AA; 35987 MW; 1F3598D66BF2C6FC CRC64;
Query Match 36.9%; Score 48; DB 1; Length 330;
Best Local Similarity 37.5%; Pred. No. 7;
Matches 9; Conservative 7; Mismatches 8; Indels 0; Gaps 0;
QY 4 FRREKRAERLTSRVKALFSLVLYNE 27
Db 299 FRPEAIEELRNQIKAMKVLGV 322
RESULT 5
YNH8 YEAST STANDARD; PRT; 407 AA.
ID YNH8 YEAST
AC P53939;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Hypothetical 45.9 kDa protein in TPm1-MKSI intergenic region.
GN YNL078W OR N2337.
OS Saccharomyces cerevisiae (Baker's yeast)
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=S288c / FY1679;
RX MEDLINE=96267764; PubMed=8701611;
RA Poehlmann R., Philippsen P.;
RT "Sequencing a cosmid clone of Saccharomyces cerevisiae chromosome XIV
RT reveals 12 new open reading frames (ORFs) and an ancient duplication
RT of six ORFs."
RL Yeast 12:391-402(1996).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X86470; CAA60180.1; -.
DR EMBL; Z71354; CAA95952.1; -.
DR PIR; S53900; S53900.
DR SGD; S0005022; JIP1.
DR GO; GO:0005935; C:bud neck; IDA.
DR GO; GO:0005634; C:nucleus; IDA.
DR GO; GO:0007088; P:regulation of mitosis; IPI.
KW Hypothetical protein.
SQ SEQUENCE 407 AA; 45908 MW; 925C7B6063BCE4F1 CRC64;
Query Match 36.5%; Score 47.5; DB 1; Length 407;
Best Local Similarity 48.1%; Pred. No. 10;
Matches 13; Conservative 3; Mismatches 8; Indels 3; Gaps 1;
QY 3 TFREKRAERLTSRV---KALFSLVLYN 26
Db 170 SIRREDQAKVRSRPRSKELTSVLNY 196
RESULT 6
ABC6 HUMAN STANDARD; PRT; 842 AA.
ID ABC6 HUMAN
AC Q9NP58; O75542;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE ATP-binding cassette, sub-family B, member 6, mitochondrial precursor
DE (Mitochondrial ABC transporter 3) (Mt-ABC transporter 3) (ABC
DE transporter UMAT).
GN ABCB6 OR MTABC3.
```



```

RT archaeon Pyrococcus abyssi".
RL Mol. Microbiol. 47:1495-1512(2003).
CC -1- CATALYTIC ACTIVITY: Pyruvate + CoA + oxidized ferredoxin = acetyl-
CC CoA + CO(2) + reduced ferredoxin.
CC -1- SUBUNIT: HETEROTETRAMER OF ONE ALPHA, ONE BETA, ONE DELTA AND ONE
CC GAMMA CHAIN.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR ENBL; A2428287; CAB50267.1; ALT INIT.
KW Oxidoreductase; Complete proteome.
FT INIT MET 0 0 BY SIMILARITY.
SQ SEQUENCE 330 AA; 36065 MW; 50428984BDS9D99 CRC64;

Query Match 34.6%; Score 45; DB 1; Length 330;
Best Local Similarity 33.3%; Pred. No. 20;
Matches 8; Conservative 8; Mismatches 8; Indels 0; Gaps 0;

QY 4 FREKRAERLTSRVKALFVSVL 27
DB 299 FRPEAIDELRNOIKAMKVLGVE 322

RESULT 8
REPL_ZYGBA STANDARD; PRT; 357 AA.
ID REPL_ZYGBA
AC P13776;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 01-AUG-1990 (Rel. 15, Last annotation update)
DE Trans-acting factor B (REP1).
GN B.
OS Zygosaccharomyces baillii.
OG Plasmid pSB2.
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Zygosaccharomycetes.
OX NCBI_TaxID=4954;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IFO 1047;
RX MEDLINE=88058763; PubMed=3680169;
RA Utatsu I., Sakamoto S., Imura T., Toh-E A.;
RT "Yeast plasmids resembling 2 micron DNA: regional similarities and
RT diversities at the molecular level.";
RL J. Bacteriol. 169:5537-5545(1987).
CC -1- FUNCTION: PLASMID PARTITION REQUIRE REP1, REP2, AND A CIS-ACTING
CC DNA SEQUENCE (KNOWN AS STB). REP 1 MAY ACT BY INTERCALATING IN
CC THE YEAST NUCLEAR MATRIX AND BINDING STB EITHER DIRECTLY OR VIA
CC REP2.
CC -1- SIMILARITY: TO THE P GENE PRODUCT OF PSR1.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR ENBL; M18274; AAA35283.1; -.
KW Plasmid; Trans-acting factor.
SQ SEQUENCE 357 AA; 40752 MW; 7DF4C06359D4BA35 CRC64;

Query Match 34.6%; Score 45; DB 1; Length 357;
Best Local Similarity 50.0%; Pred. No. 22;
Matches 10; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

```

```

QY 5 FREKRAERLTSRVKALFVSVL 24
DB 4 REEVRASRPTKEMKMFVDVL 23

RESULT 9
THIC_CLOAB STANDARD; PRT; 436 AA.
ID THIC_CLOAB
AC Q97EU2;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Thiamine biosynthesis protein thic.
GN THIC OR CAC3014.
OS Clostridium acetobutylicum.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1488;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 824 / DSM 792 / VKM B-1787;
RX MEDLINE=21359325; PubMed=11466286;
RA Noelling J., Breton G., Omeichenko M.V., Makarova K.S., Zeng Q.,
RA Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I.,
RA Tatunov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J.,
RA Bennett G.N., Koonin E.V., Smith D.R.;
RT "Genome sequence and comparative analysis of the solvent-producing
RT bacterium Clostridium acetobutylicum.";
RL J. Bacteriol. 183:4823-4838(2001).
CC -1- FUNCTION: Required for the synthesis of the hydromethylpyrimidine
CC (HMP) moiety of thiamine (4-amino-2-methyl-5-
CC hydroxymethylpyrimidine) (By similarity).
CC -1- PATHWAY: Thiamine biosynthesis.
CC -1- SIMILARITY: BELONGS TO THE THIC FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR ENBL; AE007798; AAK80955.1; -.
DR PIR; H97270; H97270.
DR HAMAP; MF 00089; -; 1.
DR InterPro; IPR002817; Thic.
DR Pfam; PF01964; Thic; 1.
DR ProDom; PD007048; Thic; 1.
DR TIGRFAMs; TIGR00190; thic; 1.
KW Thiamine biosynthesis; Complete proteome.
SQ SEQUENCE 436 AA; 48495 MW; 60DE4DD880C92737 CRC64;

Query Match 34.6%; Score 45; DB 1; Length 436;
Best Local Similarity 56.2%; Pred. No. 27;
Matches 9; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 AETFKRAERLTSR 16
DB 171 AETFKRKRAMNIVSR 186

RESULT 10
CPPM_ARATH STANDARD; PRT; 335 AA.
ID CPPM_ARATH
AC O49290;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Putative carboxyvinyl-carboxyphosphonate phosphorylmutase
DE (EC 2.7.8.23) (Carboxyphosphonoethylpyruvate phosphonmutase)
DE phosphonmutase).
GN AT1G77060 OR F22K20.14.

```

OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RX MEDLINE=21016719; PubMed=11130712;
 RA Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,
 RA White O., Alonso J., Altati H., Araujo R., Bowman C.L., Brooks S.Y.,
 RA Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
 RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,
 RA Dunn P., Etgu P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y.,
 RA Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,
 RA Hunter J.B., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
 RA Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,
 RA Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,
 RA Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziani A.,
 RA Militecher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,
 RA Pai G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,
 RA Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,
 RA Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,
 RA Utterback T., Van Aken S., Vaysberg M., Vysotskaia V.S., Walker M.,
 RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;
 RT "Sequence and analysis of chromosome 1 of the plant Arabidopsis
 thaliana";
 RL Nature 408:816-820(2000).
 CC -!- CATALYTIC ACTIVITY: 1-carboxyvinyl carboxyphosphonate = 3-
 CC (hydroxyhydroxyphosphoryl)pyruvate + CO(2).
 CC -!- SIMILARITY: BELONGS TO THE ISOCITRATE LYASE FAMILY. CPEP MUTASE
 CC SUBFAMILY.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC EMBL; AC002291; AAC00621.1; -
 DR PIR; E96799; E96799.
 DR InterPro; IPR000918; Isocit_lyase_ph.
 DR Pfam; PF00463; ICL; 1
 DR ProDom; PD001857; Isocit_lyase_ph; 1.
 DR PROSITE; PS00161; ISOCITRATE_LYASE; 1.
 KW Transference.
 SQ SEQUENCE 335 AA; 36103 MW; 4390671598ADA83B CRC64;
 Query Match 34.2%; Score 44.5; DB 1; Length 335;
 Best Local Similarity 50.0%; Pred. No. 24;
 Matches 11; Conservative 3; Mismatches 5; Indels 3; Gaps 1;
 QY 3 TFRREKRAERL---TSRVKALF 21
 DB 20 TFRNPRAARLVNFTAIQTRF 41
 RESULT 11
 BFR_MYCTU STANDARD; PRT; 159 AA.
 AC 008465;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Bacterioferritin (BFR).
 GN BFR OR RV1876 OR MT1925 OR MTCV180.42C.
 OS Mycobacterium tuberculosis.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 NCBI_TaxID=1773;
 RN [1]

RP SEQUENCE FROM N.A.
 RC STRAIN=H37RV;
 RX MEDLINE=98295987; PubMed=9634230;
 RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
 RA Gordon S.V., Eigmeier K., Gas S., Barry C.E. III, Tekaa F.,
 RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
 RA Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
 RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
 RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
 RA Ruter S., Seeger K., Skelton S., Squares S., Squares R.,
 RA Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
 RT "Deciphering the biology of Mycobacterium tuberculosis from the
 complete genome sequence.";
 RL Nature 393:537-544(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CDC 1551 / Oshkosh;
 RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
 RA Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
 RA Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
 RA Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
 RA Bishai W.;
 RT "Whole genome comparison of Mycobacterium tuberculosis clinical and
 laboratory strains";
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: May perform analogous functions in iron detoxification
 CC and storage to that of animal ferritins (By similarity).
 CC -!- SUBUNIT: Oligomer of 24 identical subunits (By similarity).
 CC -!- MISCELLANEOUS: Bacterioferritin contains protoheme IX in addition
 CC to the non-haem iron core (By similarity).
 CC -!- SIMILARITY: Belongs to the bacterioferritin family.
 CC -!- SIMILARITY: Contains 1 ferritin-like diiron domain.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC EMBL; Z97193; CAB10050.1; -
 DR EMBL; AR007049; AAK46197.1; -
 DR PIR; A70515; A70515.
 DR HSP; P11056; 1BCF.
 DR TIGR; MT1925; -
 DR Tuberculin; Rv1876; -
 DR InterPro; IPR002024; Bacterioferritin.
 DR InterPro; IPR001519; Ferritin.
 DR Pfam; PF00210; ferritin; 1.
 DR PRINTS; PR00601; BACFERRITIN
 DR ProDom; PD002269; Bacterioferritin; 1.
 DR TIGRFAMS; TIGR00754; bfr; 1.
 DR PROSITE; PS00549; BACTERIOFERRITIN; 1.
 DR PROSITE; PS00905; FERRITIN LIKE; 1.
 KW Iron storage; Heme; Complete proteome.
 FT DOMAIN 1 145 FERRITIN-LIKE DIIRON.
 FT METAL 52 52 IRON (HEME AXIAL LIGAND) (POTENTIAL).
 SQ SEQUENCE 159 AA; 18341 MW; 098B6D7392A9CD60 CRC64;
 Query Match 33.8%; Score 44; DB 1; Length 159;
 Best Local Similarity 33.3%; Pred. No. 13;
 Matches 9; Conservative 6; Mismatches 12; Indels 0; Gaps 0;
 QY 1 ARTFREKRAERLTSRVKALFSLVNYE 27
 DB 46 AESFDEMRAHEITDRILLDGLPNYQ 72
 RESULT 12
 Y00F_BPT4
 ID Y00F_BPT4 STANDARD; PRT; 166 AA.
 AC P39416; P39417;


```

RC STRAIN=Sprague-Dawley; TISSUE=Brain, and Liver;
RX MEDLINE=90361739; PubMed=2391362;
RA Grant J.W., Taubman M.B., Church S.L., Johnson R., Nadal-Ginard B.;
RT "Mammalian, nonsarcomeric myosin regulatory light chains are encoded
RL by two differentially regulated and linked genes.";
RN J. Cell Biol. 111:1127-1135(1990).
RN [2]
RP REVISIONS.
RA Grant J.W.;
RL Submitted (OCT-1992) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: PLAYS AN IMPORTANT ROLE IN REGULATION OF BOTH SMOOTH
CC MUSCLE AND NONMUSCLE CELL CONTRACTION ACTIVITY.
CC -!- ENZYME REGULATION: PHOSPHORYLATION OF MLC-2 BY THE ENZYME MLC
CC KINASE IN THE PRESENCE OF CALCIUM AND CALMODULIN INCREASES THE
CC ACTIN-ACTIVATED MYOSIN ATPASE ACTIVITY AND THEREBY REGULATES THE
CC CONTRACTILE ACTIVITY.
CC -!- SUBUNIT: Myosin is an hexamer of 2 heavy chains and 4 light
CC chains.
CC -!- MISCELLANEOUS: THIS CHAIN BINDS CALCIUM.
CC -!- SIMILARITY: TO OTHER EF-HAND CALCIUM BINDING PROTEINS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X52840; CAA37024.1; -.
CC PIR; B37100; B37100.
CC HSP; P13543; LSCM.
CC InterPro; IPR002048; EF-hand.
CC Pfam; PF00036; ehand; 3.
CC ProDom; PD000012; EF-hand; 2.
CC SMART; SM00054; Eph; 2.
CC PROSITE; PS00018; EF HAND; 1.
CC Myosin; Calcium-binding; Muscle protein; Phosphorylation; Acetylation;
CC Multigene family.
CC INIT_MET 0 0 ACETYLATION (BY SIMILARITY).
CC MOD_RES 1 1 PHOSPHORYLATION (BY MLCK)
CC MOD_RES 18 18 (BY SIMILARITY).
CC MOD_RES 19 19 PHOSPHORYLATION (BY MLCK)
CC MOD_RES 41 52 EF-HAND.
CC CA_BIND 171 AA; AFD599E302314127 CRC64;
CC SEQUENCE 171 AA; 19707 MW; 479259E302314127 CRC64;

Query Match 33.8%; Score 44; DB 1; Length 171;
Best Local Similarity 47.6%; Pred. No. 14;
Matches 10; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 1 ARTFREKRAERLTSRVKALF 21
| : | : | : | : | : |
Db 5 AKTKTKRQPRATSNVFAMF 25

RESULT 15
MLRN CHICK STANDARD; PRT; 171 AA.
AC P24032;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Myosin regulatory light chain 2, smooth muscle minor isoform (G1)
DE (DTNB) (MLC-2) (isoform L20-B1).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.

```

```

RC TISSUE=Gizzard;
RX MEDLINE=89377832; PubMed=2776758;
RA Inoue A., Yanagisawa M., Takano-Ohmuro H., Masaki T.;
RT "Two isoforms of smooth muscle myosin regulatory light chain in
RT chicken gizzard.";
RL Eur. J. Biochem. 183:645-651(1989).
CC -!- FUNCTION: PLAYS AN IMPORTANT ROLE IN REGULATION OF BOTH SMOOTH
CC MUSCLE AND NONMUSCLE CELL CONTRACTION ACTIVITY.
CC -!- ENZYME REGULATION: PHOSPHORYLATION OF MLC-2 BY THE ENZYME MLC
CC KINASE IN THE PRESENCE OF CALCIUM AND CALMODULIN INCREASES THE
CC ACTIN-ACTIVATED MYOSIN ATPASE ACTIVITY AND THEREBY REGULATES THE
CC CONTRACTILE ACTIVITY.
CC -!- SUBUNIT: Myosin is an hexamer of 2 heavy chains and 4 light
CC chains.
CC -!- MISCELLANEOUS: THIS CHAIN BINDS CALCIUM.
CC -!- SIMILARITY: TO OTHER EF-HAND CALCIUM BINDING PROTEINS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X16532; CAA34535.1; -.
CC PIR; S05530; MOCH2G.
CC HSP; P13543; LSCM.
CC InterPro; IPR002048; EF-hand.
CC Pfam; PF00036; ehand; 3.
CC ProDom; PD000012; EF-hand; 2.
CC SMART; SM00054; Eph; 2.
CC PROSITE; PS00018; EF HAND; 1.
CC Myosin; Calcium-binding; Muscle protein; Phosphorylation; Acetylation;
CC Multigene family.
CC INIT_MET 0 0 BY SIMILARITY.
CC MOD_RES 1 1 ACETYLATION (BY SIMILARITY).
CC MOD_RES 18 18 PHOSPHORYLATION (BY MLCK)
CC MOD_RES 19 19 PHOSPHORYLATION (BY MLCK)
CC MOD_RES 41 52 EF-HAND.
CC CA_BIND 171 AA; 19780 MW; 47926518F95CC78 CRC64;
CC SEQUENCE 171 AA; 19780 MW; 47926518F95CC78 CRC64;

Query Match 33.8%; Score 44; DB 1; Length 171;
Best Local Similarity 47.6%; Pred. No. 14;
Matches 10; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 1 ARTFREKRAERLTSRVKALF 21
| : | : | : | : | : |
Db 5 AKTKTKRQPRATSNVFAMF 25

Search completed: November 12, 2003, 19:48:01
Job time : 6.60377 secs

```

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

QM protein - protein search, using sw model

Run on: November 12, 2003, 19:42:29 ; Search time 25.8113 Seconds
(without alignments)
269.937 Million cell updates/sec

Title: US-08-854-050-114
Perfect score: 130
Sequence: 1 ARTFRREKRAERLTSRVKALFSLVNYE 27

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: SPTRMBL 23:*
2: sp_archaea:*
3: sp_bacteria:*
4: sp_fungi:*
5: sp_human:*
6: sp_invertebrate:*
7: sp_mammal:*
8: sp_mhc:*
9: sp_organelle:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bactexiap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	130	100.0	795	4 Q8NG38	Q8ng38 homo sapien
2	130	100.0	807	4 Q8N6C3	Q8n6c3 homo sapien
3	130	100.0	1059	4 Q8NG46	Q8ng46 homo sapien
4	73	56.2	575	11 Q9UK99	Q9uk99 rattus norv
5	69	53.1	1128	11 Q9QXZ4	Q9qxz4 mesocricetu
6	61	46.9	1191	13 Q9DE32	Q9de32 xenopus lae
7	51.5	39.6	164	2 Q9EU10	Q9eu10 salmonella
8	51.5	39.6	554	16 Q93GR0	Q93gr0 salmonella
9	51	39.2	98	16 Q9JZC0	Q9jzc0 neisseria m
10	50.5	38.8	189	16 Q9KJX7	Q9kjsx7 streptomyce
11	49	37.7	190	2 Q8KKV1	Q8kkv1 rhizobium e
12	49	37.7	601	16 Q8F5K1	Q8f5k1 leptospira
13	49	37.7	836	11 Q70595	Q70595 rattus norv
14	49	37.7	842	11 Q9DC29	Q9dc29 mus musculus
15	48	36.9	81	15 Q9ORH2	Q9orh2 human immun
16	48	36.9	321	16 Q9JXU5	Q9jxu5 neisseria m

17	48	36.9	321	16 Q9JW24	Q9jw24 neisseria m
18	48	36.9	596	16 Q8D129	Q8d129 versinia pe
19	48	36.9	631	16 Q8ZD10	Q8zdi0 versinia pe
20	48	36.9	738	2 Q59490	Q59490 lactobacill
21	47	36.2	183	5 Q96737	Q96737 plasmodium
22	47	36.2	231	2 Q9RHB7	Q9rnb7 bradyrhizob
23	47	36.2	592	16 Q9KDK8	Q9kdk8 streptomyce
24	46.5	35.8	455	6 Q9XS78	Q9xs78 delphinapte
25	46	35.4	135	10 Q9SKX8	Q9skx8 arabidopsis
26	46	35.4	192	5 Q9GUA2	Q9gua2 riftia pach
27	46	35.4	200	17 Q28274	Q28274 archaeoglob
28	46	35.4	454	17 Q8TR29	Q8tr29 methanosarc
29	46	35.4	462	5 Q02134	Q02134 caenorhabdi
30	46	35.4	474	9 Q9GME8	Q9gme8 bacterioph
31	46	35.4	766	4 Q96FW1	Q96fw1 abies sapien
32	46	35.4	853	10 Q38710	Q38710 abies grand
33	46	35.4	868	10 Q38710	Q38710 abies grand
34	46	35.4	896	4 Q9HAQ7	Q9haq7 homo sapien
35	46	35.4	910	5 Q8IN05	Q8in05 drosophila
36	45	34.6	81	15 Q91JR3	Q91jr3 human immun
37	45	34.6	98	16 Q9JUF9	Q9juf9 neisseria m
38	45	34.6	321	17 Q97Y91	Q97y91 sulfolobus
39	45	34.6	341	17 Q96Y98	Q96y98 sulfolobus
40	45	34.6	437	16 Q8G6T2	Q8g6t2 bifidobacte
41	45	34.6	450	12 Q9EMU0	Q9emu0 amaecta moo
42	45	34.6	454	17 Q8PUD3	Q8puj3 methanosarc
43	45	34.6	777	5 Q8SVW7	Q8svw7 encephalito
44	45	34.6	1422	16 Q8EFU3	Q8efu3 shewanella
45	44.5	34.2	329	17 Q8ZWS9	Q8zws9 pyrobaculum

ALIGNMENTS

RESULT 1

Q8NG38 Q8NG38 PRELIMINARY; PRT; 795 AA.
AC Q8NG38;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE ABG-deleted variant of telomerase reverse transcriptase.
GN TERT.

OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Stomach;
RA Hisatomi H., Nagao K., Kanamaru T., Hirata H., Miyachi K., Hikiiji H.;
RT "Exon 11 deleted variant of human reverse transcriptase."
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB086950; BAC11015.1; -
DR InterPro; IPR003545; Telomerase RT.
DR PRINTS; PR01365; TELOMERASERT.
KW RNA-directed DNA polymerase.
SQ SEQUENCE 795 AA; 88965 MW; 6BEAC8A6D1A2E8CB CRC64;

Query Match 100.0%; Score 130; DB 4; Length 795;
Best Local Similarity 100.0%; Pred. No. 1.1e-11;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARTFRREKRAERLTSRVKALFSLVNYE 27
|||||

Db 642 ARTFRREKRAERLTSRVKALFSLVNYE 668
|||||

RESULT 2

Q8N6C3 Q8N6C3 PRELIMINARY; PRT; 807 AA.
ID Q8N6C3;
AC Q8N6C3;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)

```
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Beta and gamma deletion isoform of telomerase reverse
DE transcriptase.
GN HTERT.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Stomach cancer;
RA Hisatomi H., Nagao K., Kanamaru T., Sumida H., Hirata H., Yamamoto M.,
RA Kazumasa H.;
RT "Both beta and gamma deletion isoform of human telomerase reverse
RT transcriptase.";
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB086379; BAC11014.1; -.
DR InterPro; IPR003545; Telomerase_RT.
DR PRINTS; PR01365; TELOMERASERT.
SQ SEQUENCE 807 AA; 90225 MW; 199664460CB6D763 CRC64;

Query Match 100.0%; Score 130; DB 4; Length 807;
Best Local Similarity 100.0%; Pred. No. 1.1e-11;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARTFRREKRAERLTSRVKALFSLVNYE 27
Db 642 ARTFRREKRAERLTSRVKALFSLVNYE 668

RESULT 3
Q8NG46 PRELIMINARY; PRT; 1069 AA.
AC Q8NG46;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Telomerase reverse transcriptase.
GN HTERT.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Hisatomi H., Nagao K., Hirata H., Hikiji K., Kanamaru T.;
RT "Exon 11 deleted variant of the human telomerase reverse
RT transcriptase.";
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB085628; BAC11010.1; -.
DR InterPro; IPR003545; Telomerase_RT.
DR PRINTS; PR01365; TELOMERASERT.
KW RNA-directed DNA polymerase.
SQ SEQUENCE 1069 AA; 120047 MW; BE1E77A653B1C666 CRC64;

Query Match 100.0%; Score 130; DB 4; Length 1069;
Best Local Similarity 100.0%; Pred. No. 1.1e-11;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARTFRREKRAERLTSRVKALFSLVNYE 27
Db 642 ARTFRREKRAERLTSRVKALFSLVNYE 668

RESULT 4
Q9JK99 PRELIMINARY; PRT; 575 AA.
AC Q9JK99;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Telomerase catalytic subunit (Fragment).
```

```
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Wong S., Gao S., Xu X., Yu H.;
RT "Rat telomerase catalytic subunit, rTERT.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF247818; AAF62177.1; -.
DR InterPro; IPR000477; RVTse.
DR InterPro; IPR003545; Telomerase_RT.
DR Pfam; PF00078; rvt; 1.
DR PRINTS; PR01365; TELOMERASERT.
KW RNA-directed DNA polymerase; Transferase.
FT NON_TER 1
SQ SEQUENCE 575 AA; 65672 MW; F80C81BD7F6A91A3 CRC64;

Query Match 56.2%; Score 73; DB 11; Length 575;
Best Local Similarity 53.8%; Pred. No. 0.0068;
Matches 14; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

Qy 2 RTFRREKRAERLTSRVKALFSLVNYE 27
Db 86 RALGRKQAQHFQRLKTLFSLVNYE 111

RESULT 5
Q9QX24 PRELIMINARY; PRT; 1128 AA.
AC Q9QX24;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Telomerase catalytic subunit.
OS Mesocricetus auratus (Golden hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Mesocricetus.
OX NCBI_TaxID=10036;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=21240330; PubMed=11342218;
RX Guo W., Okamoto M., Lee Y.M., Baluda M.A., Park N.H.;
RT "Enhanced activity of cloned hamster TERT gene promoter in transformed
RT cells.";
RL Blochim. Biophys. Acta 1517:398-409(2001).
DR EMBL; AF149012; AAF17334.1; -.
DR InterPro; IPR000477; RVTse.
DR InterPro; IPR003545; Telomerase_RT.
DR Pfam; PF00078; rvt; 1.
DR PRINTS; PR01365; TELOMERASERT.
KW RNA-directed DNA polymerase; Transferase.
SQ SEQUENCE 1128 AA; 128394 MW; 1D4F81249012174E CRC64;

Query Match 53.1%; Score 69; DB 11; Length 1128;
Best Local Similarity 53.8%; Pred. No. 0.058;
Matches 14; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

Qy 2 RTFRREKRAERLTSRVKALFSLVNYE 27
Db 636 RALGRKQAQHFQRLKTLFSLVNYE 661

RESULT 6
Q9DE32 PRELIMINARY; PRT; 1191 AA.
AC Q9DE32;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Telomerase reverse transcriptase.
GN TERT.
```



```

OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipiloidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA Kuramoto M., Ishikawa F.;
RT "Telomerase reverse transcriptase of Xenopus laevis.";
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF212299; AAG43537.1; -
DR InterPro; IPR000477; RVTse.
DR InterPro; IPR003545; Telomerase_RT.
DR Pfam; PF00078; rvt; 2.
DR PRINTS; PR01365; TELOMERASERT.
DR RNA-directed DNA polymerase; Transferase.
SQ SEQUENCE 1191 AA; 138016 MW; 98D9D776869A57D6 CRC64;

Query Match 46.9%; Score 61; DB 13; Length 1191;
Best Local Similarity 50.0%; Pred. No. 1.1;
Matches 11; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY 6 REKRAERLTSRVKALFSLVNYE 27
   :||: |||||
Db 704 QEKKIHFSSQIRNLFSLVNYE 725

RESULT 7
Q9EUI0
ID Q9EUI0 PRELIMINARY; PRT; 164 AA.
AC Q9EUI0
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Orf47.
OS Salmonella enterica subsp. enterica serovar Choleraesuis.
OG Plasmid 50k virulence plasmid.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCBI_TaxID=119912;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PE-1.
RX MEDLINE=21153631; PubMed=11254626;
RA Haneda T., Okada N., Nakazawa N., Kawakami T., Danbara H.;
RT "Complete DNA Sequence and Comparative Analysis of the 50-Kilobase
RT Virulence Plasmid of Salmonella enterica Serovar Choleraesuis.";
RL Infect. Immun. 69:2612-2620(2001).
RL EMBL; AB040415; BAB20554.1; -
RW Plasmid.
SQ SEQUENCE 164 AA; 18678 MW; BE1414258D07EBAE CRC64;

Query Match 39.6%; Score 51.5; DB 2; Length 164;
Best Local Similarity 58.3%; Pred. No. 4.4;
Matches 14; Conservative 1; Mismatches 8; Indels 1; Gaps 1;

QY 2 RTFRREKRAERLTSRVKALFSLVNL 25
   ||||| |||||
Db 42 RTFRGKAAER-ADRIHALARQLN 64

RESULT 8
Q93GR0
ID Q93GR0 PRELIMINARY; PRT; 554 AA.
AC Q93GR0
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Putative integrase protein.
DE ILGA OR PSLT044.
GN Salmonella typhimurium.
OS Salmonella typhimurium.
OG Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;

```

```

OC Enterobacteriaceae; Salmonella.
OX NCBI_TaxID=602;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=LT2 / SGSC1412 / ATCC 700720;
RX MEDLINE=21534948; PubMed=11677609;
RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
RA Courtnay L., Porwollik S., Ali J., Dante M., Du P., Hou S., Layman D.,
RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
RA Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
RA Waterston R., Wilson R.K.;
RT "Complete genome sequence of Salmonella enterica serovar Typhimurium
RT LT2.";
RL Nature 413:852-856(2001).
RL EMBL; AE006471; AAL23534.1; -
DR InterPro; IPR001584; Rve.
DR Pfam; PF00665; rve; 1.
KW Plasmid; Complete proteome.
SQ SEQUENCE 554 AA; 63738 MW; A0DB885C18031190 CRC64;

Query Match 39.6%; Score 51.5; DB 16; Length 554;
Best Local Similarity 58.3%; Pred. No. 15;
Matches 14; Conservative 1; Mismatches 8; Indels 1; Gaps 1;

QY 2 RTFRREKRAERLTSRVKALFSLVNL 25
   ||||| |||||
Db 432 RTFRGKAAER-ADRIHALARQLN 454

RESULT 9
Q9JZC0
ID Q9JZC0 PRELIMINARY; PRT; 98 AA.
AC Q9JZC0
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Hypothetical protein NMB1120.
GN NMB1120.
OS Neisseria meningitidis (serogroup B).
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=491;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MC58 / Serogroup B;
RX MEDLINE=20175755; PubMed=10710307;
RA Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E.,
RA Eisen J.A., Ketchum K.A., Hood D.W., Feden J.F., Dodson R.J.,
RA Nelson W.C., Winn M.L., DeBoy R., Peterson J.D., Hickey E.K.,
RA Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A.,
RA Mason T., Ciecko A., Parksey D.S., Blair E., Ciftone H., Clark E.B.,
RA Cotton M.D., Utterback T.R., Khouri H., Qin H., Vamathevan J.,
RA Gill J., Scarlato V., Maignani V., Pizza M., Grandi G., Sun L.,
RA Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C.;
RT "Complete genome sequence of Neisseria meningitidis serogroup B strain
RT MC58.";
RL Science 287:1809-1815(2000).
RL EMBL; AE002461; AAF41510.1; -
DR TIGR; NMB1120; -
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 98 AA; 11432 MW; E5DC7F0CF6115EA3 CRC64;

Query Match 39.2%; Score 51; DB 16; Length 98;
Best Local Similarity 36.0%; Pred. No. 3.1;
Matches 9; Conservative 10; Mismatches 6; Indels 0; Gaps 0;

QY 1 ARTFRREKRAERLTSRVKALFSLVNL 25
   :||: |||||
Db 36 SNTYRRARLAQPKTRWKLYTLIN 60

RESULT 10
Q9RJX7

```

```

ID Q9RJK7 PRELIMINARY; PRT; 189 AA.
AC Q9RJK7;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Putative tetR-family transcriptional regulator.
GN SC01193 OR SCG11A.24C.
OS Streptomyces coelicolor.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OC NCBI_TaxID=1902;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RA Oliver K., Harris D.;
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RA Cerdano A.M., Parkhill J., Barrell B.G., Rajandream M.A.;
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
[3]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RX MEDLINE=97000351; PubMed=8843436;
RA Redenbach M., Kieser H.M., Denapante D., Eichner A., Cullum J.,
RA Kinashi H., Hopwood D.A.;
RT "A set of ordered cosmids and a detailed genetic and physical map for
RT the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
RL Mol. Microbiol. 21:77-96(1996).
[4]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2) / M145;
RX MEDLINE=21996410; PubMed=12000953;
RA Bentley S.D., Chater K.F., Cerdano-Tarraga A.-M., Challis G.L.,
RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
RA Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S.,
RA Rabinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,
RA Seeger K., Saunders D., Sharp S., Squares S., Taylor K.,
RA Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
RA Hopwood D.A.;
RT "Complete genome sequence of the model actinomycete Streptomyces
RT coelicolor A3(2).";
RL Nature 417:141-147(2002).
CC -!- SIMILARITY: BELONGS TO THE TETR/ACRR FAMILY OF TRANSCRIPTIONAL
CC REGULATORS.
DR EMBL; AL939108; CAB61605.1; -.
DR InterPro; IPR001647; HTH_Tetr.
DR Pfam; PF00440; tetr; 1.
DR PRINTS; PR00455; HTHTEPR.
KW DNA-binding; Transcription regulation; Complete proteome.
SQ SEQUENCE 189 AA; 20687 MW; 2EC75D53C59259B8 CRC64;

Query Match 38.8%; Score 50.5; DB 16; Length 189;
Best Local Similarity 54.2%; Pred. No. 7.3; Mismatches 3; Indels 1; Gaps 1;
Matches 13; Conservative 3;

QY 5 RREKRAERLTSRVKAL-FSVLNYE 27
DB 140 RGEARPERLTGRVSLPFDLLRQE 163

RESULT 11
Q8KKV1
ID Q8KKV1 PRELIMINARY; PRT; 190 AA.
AC Q8KKV1;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein.
GN YP085.

```

```

OS Rhizobium etli.
OG Plasmid symbiotic plasmid p42d.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Rhizobium.
OX NCBI_TaxID=29449;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CFN42;
RX MEDLINE=91193195; PubMed=2013564;
RA Girard M.L., Flores M., Brom S., Romero D., Palacios R., Davila G.;
RT "Structural complexity of the symbiotic plasmid of Rhizobium
RT leguminosarum bv. phaseoli.";
RL J. Bacteriol. 173:2411-2419(1991).
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=CFN42;
RX MEDLINE=97419521; PubMed=9274036;
RA Ramirez-Romero M.A., Bustos P., Girard L., Rodriguez O.,
RA Cevallos M.A., Davila G.;
RT "Sequence, localization and characteristics of the replicator region
RT of the symbiotic plasmid of Rhizobium etli.";
RL Microbiology 143:2825-2831(1997).
[3]
RP SEQUENCE FROM N.A.
RC STRAIN=CFN42;
RA Quintero V., Cevallos M.A., Davila G.;
RT "A site-specific recombinase and RecA are required to exert
RT incompatibility towards the symbiotic plasmid of Rhizobium etli.";
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; U80928; AAMS5029.1; -.
KW Hypothetical protein; Plasmid.
SQ SEQUENCE 190 AA; 21230 MW; 448E0069C5DF232D CRC64;

Query Match 37.7%; Score 49; DB 2; Length 190;
Best Local Similarity 50.0%; Pred. No. 13;
Matches 10; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 1 ARTERREKRAERLTSRVKAL 20
DB 64 ARTYAEKDAERVSRVKG 83

RESULT 12
Q8F5K1 PRELIMINARY; PRT; 601 AA.
ID Q8F5K1;
AC Q8F5K1;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Aspartyl-tRNA synthetase (EC 6.1.1.12).
GN ASPS OR LA1680.
OS Leptospira interrogans.
OC Bacteria; Spirochaetes; Spirochaetales; Leptospiraceae; Leptospira.
OX NCBI_TaxID=173;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=56601 / Serogroup Icterohaemorrhagiae / Serovar lai;
RA Ren S.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE011345; AAN48879.1; -.
KW Aminoacyl-tRNA synthetase; Ligase; Complete proteome.
SQ SEQUENCE 601 AA; 69124 MW; 59A5A4DFD3AD845 CRC64;

Query Match 37.7%; Score 49; DB 16; Length 601;
Best Local Similarity 39.1%; Pred. No. 42;
Matches 9; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY 4 FREKRAERLTSRVKALFSVLNY 26
DB 141 FREELKNRMKXHEFIFAIRNY 163

RESULT 13

```

```

070595
ID 070595 PRELIMINARY; PRT; 836 AA.
AC 070595;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE ABC transporter.
DE Rattus norvegicus (Rat).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98381042; PubMed=9705847;
RA Hirsch-Ernst K.I., Gaini-Rahimi S., Ernst B.P., Schmitz-Salve C.,
RA Blume S., Kahl G.F.;
RT "Molecular cDNA cloning and tissue distribution of mRNA encoding a
RT novel ATP-binding cassette (ABC) half-transporter.";
RL Biochem. Biophys. Res. Commun. 249:151-155(1998).
CC -i- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY.
DR EMBL; AJ003004; CAA05793.1; -.
DR InterPro; IPR003593; AAAATPase.
DR InterPro; IPR001140; ABC_TM_transp.
DR InterPro; IPR003439; ABC_transport.
DR Pfam; PF00664; ABC_membrane; 1.
DR Pfam; PF00005; ABC_tran; 1.
DR ProDom; PD000006; ABC_transporter; 1.
DR SMART; SM00382; AAA; 1.
DR PROSITE; PS00211; ABC_TRANSPORTER; 1.
DR ATP-binding; Transport.
KW ABC TRANSPORTER.
SQ SEQUENCE 836 AA; 93304 MW; 40EC2C32E865522B CRC64;

Query Match 37.7%; Score 49; DB 11; Length 836;
Best Local Similarity 37.5%; Pred. No. 58;
Matches 9; Conservative 7; Mismatches 8; Indels 0; Gaps

Qy 4 FRREKRAERLTSRVKALFSLVNYE 27
|||: : : : : : : : : : : : :
Db 438 FRDMNTQENATRAVAVDLSLNF 461

RESULT 14
Q9DC29 PRELIMINARY; PRT; 842 AA.
AC Q9DC29;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE I200005B17Rik protein (RIKEN CDNA I200005B17 gene).
GN ABCB6 OR I200005B17RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=C57BL/6J; TISSUE=Lung;
RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojohori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Giesi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schirni L.M., Staebli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bernaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

```

RA	Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA	Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohetsuki S.,
RA	Hayashizaki Y.;
RL	"Functional annotation of a full-length mouse cDNA collection.";
RL	Nature 409:685-690(2001).
RP	(2)
RP	SEQUENCE FROM N.A.
RA	Strausberg R.;
CC	Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
CC	-1- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY.
DR	EMBL; AK004605; BAB23404.1; -
DR	EMBL; BC006634; AAH06634.1; -
DR	MED; MGI-1921354; Abcb6
DR	InterPro; IPR003593; AAA_ATPase.
DR	InterPro; IPR001140; ABC_TM_transpt.
DR	InterPro; IPR003439; ABC transporter.
DR	Pfam; PF00664; ABC membrane; 1.
DR	Pfam; PF00005; ABC tran; 1.
DR	ProDom; PD000006; ABC transporter; 1.
DR	SMART; SM03382; AAA_1.
DR	PROSITE; PS00211; ABC_TRANSPORTER; 1.
KW	ATP-binding; Transport.
SQ	SEQUENCE 842 AA; 93770 MW; 5B8E1653011AA4C0D CRC64;
	Query Match 37.7%; Score 49; DB 11; Length 842;
	Best Local Similarity 37.5%; Pred.No. 59;
	Matches 9; Conservative 7; Mismatches 8; Indels 0; Gaps 0;
Qy	4 FRRKRAELTSRVKALFSVINYE 27
	: : : : :: :
Dd	438 FRDMNTQENATRARAVIDSLNFE 461
RESULT 15	
ID	Q9ORH2 PRELIMINARY; PRT; 81 AA.
AC	Q9ORH2;
DT	01-DEC-2001 (T-EMBLrel. 19, Created)
DT	01-DEC-2001 (T-EMBLrel. 19, Last sequence update)
DT	01-OCT-2002 (T-EMBLrel. 22, Last annotation update)
DE	Vpu protein.
GN	VPU.
OS	Human immunodeficiency virus 1.
OC	Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX	NCBI_TaxID=11676;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAN=96CGI7;
RA	Taniguchi Y., Takehisa J., Bikandou B., Mboudjeka I.,
RA	N'Doundou-N'Kodia M.-Y., Obengui, M'Pele P., Harada Y.,
RA	Havami M., Ichimura H., Parra J.H.;
RT	"Genetic Subtypes of HIV Type 1 Based on the vpu/env Sequences in
RT	Republic of Congo-Brazzaville.";
RL	Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
RL	EMBL; AF127546; AAK84902.1; -
DR	InterPro; IPR002094; Vpu.
DR	Pfam; PF00558; Vpu; 1.
SQ	SEQUENCE 81 AA; 9199 MW; A174A88987FE5119 CRC64;
	Query Match 36.9%; Score 48; DB 15; Length 81;
	Best Local Similarity 52.9%; Pred.No. 7.5;
	Matches 9; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

```

Qy      2  RTFRKRAERLTSRVK 18
      |  |||||  |||  ::
Db     31  RKIRREKIERLDRIR 47

```

Search completed: November 12, 2003, 19:50:45
Job time : 26.978 secs

Search completed: November 12, 2003, 19:50:45
Job time : 26.978 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 12, 2003, 19:43:50 ; Search time 13.0314 Seconds
(without alignments)
90.911 Million cell updates/sec

Title: US-08-854-050-115
Perfect score: 146
Sequence: 1 AKFLHLMVSYYVVELLSFFYTTFQ 28

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA*
1: /cgn2_6/ptodata/1/iaa/5A-COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/5B-COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/6A-COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B-COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PTUS-COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	146	100.0	28	3	US-08-851-843A-115 Sequence 115, App
2	146	100.0	28	3	US-08-851-843A-115 Sequence 235, App
3	146	100.0	28	3	US-08-854-050-115 Sequence 115, App
4	146	100.0	28	4	US-09-430-323-115 Sequence 115, App
5	146	100.0	129	3	US-08-851-843A-67 Sequence 67, Appl
6	146	100.0	129	3	US-08-851-843A-13 Sequence 13, Appl
7	146	100.0	129	3	US-08-854-050-67 Sequence 67, Appl
8	146	100.0	129	4	US-09-430-323-67 Sequence 67, Appl
9	146	100.0	129	4	US-08-912-951-13 Sequence 13, Appl
10	146	100.0	364	4	US-09-417-485D-40 Sequence 40, Appl
11	146	100.0	807	4	US-08-974-549A-5 Sequence 5, Appli
12	146	100.0	807	4	US-08-912-951-5 Sequence 5, Appli
13	146	100.0	1003	3	US-08-851-843A-217 Sequence 217, App
14	146	100.0	1003	3	US-08-854-050-336 Sequence 336, App
15	146	100.0	1003	3	US-08-854-050-217 Sequence 217, App
16	146	100.0	1003	4	US-09-430-323-217 Sequence 217, App
17	146	100.0	1132	3	US-08-851-843A-225 Sequence 225, App
18	146	100.0	1132	3	US-08-854-050-225 Sequence 225, App
19	146	100.0	1132	3	US-08-974-549A-2 Sequence 2, Appli
20	146	100.0	1132	3	US-08-854-050-344 Sequence 344, App
21	146	100.0	1132	3	US-08-854-050-225 Sequence 225, App
22	146	100.0	1132	4	US-09-430-323-225 Sequence 225, App
23	146	100.0	1132	4	US-09-128-354-2 Sequence 2, Appli
24	146	100.0	1132	4	US-09-675-321-2 Sequence 2, Appli
25	146	100.0	1132	4	US-09-052-919-2 Sequence 2, Appli
26	146	100.0	1132	4	US-08-912-951-2 Sequence 2, Appli
27	146	100.0	1154	4	US-08-974-549A-611 Sequence 611, App
					US-08-912-951-323 Sequence 323, App

check for double post

28	146	100.0	1189	3	US-08-974-549A-613 Sequence 613, App
29	146	100.0	1189	4	US-08-912-951-325 Sequence 325, App
30	146	100.0	1200	3	US-08-974-549A-612 Sequence 612, App
31	146	100.0	1200	4	US-08-912-951-324 Sequence 324, App
32	146	100.0	1285	3	US-08-974-549A-600 Sequence 600, App
33	146	100.0	1285	4	US-08-912-951-314 Sequence 314, App
34	146	100.0	1407	3	US-08-974-549A-628 Sequence 628, App
35	146	100.0	1407	4	US-08-912-951-334 Sequence 334, App
36	119	81.5	43	3	US-08-974-549A-72 Sequence 72, Appl
37	119	81.5	43	4	US-08-912-951-72 Sequence 72, Appl
38	119	81.5	48	3	US-08-974-549A-30 Sequence 30, Appl
39	119	81.5	48	4	US-08-912-951-30 Sequence 30, Appl
40	115	78.8	364	4	US-09-417-485D-41 Sequence 41, Appl
41	104	71.2	259	3	US-08-974-549A-10 Sequence 10, Appl
42	104	71.2	259	4	US-08-912-951-10 Sequence 10, Appl
43	104	71.2	515	3	US-08-974-549A-604 Sequence 604, App
44	104	71.2	515	4	US-08-912-951-318 Sequence 318, App
45	104	71.2	530	3	US-08-974-549A-603 Sequence 603, App

ALIGNMENTS

RESULT 1
US-08-851-843A-115
; Sequence 115, Application US/08851843A
; Patent No. 6093809
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: No. 6093809el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/851,843A
; FILING DATE: 06-MAY-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002930US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 115:

```
;
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-851-843A-115

Query Match 100.0%; Score 146; DB 3; Length 28;
Best Local Similarity 100.0%; Pred. No. 9e-16; Mismatches 0; Indels 0; Gaps 0;
Matches 28; Conservative 0;

QY 1 AKFLHMLSVYVVELLSFFVYVTTTFQ 28
| | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1 AKFLHMLSVYVVELLSFFVYVTTTFQ 28
| | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 2
; US-08-974-549A-235
; Sequence 235, Application US/08974549A
; Patent No. 6166178
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin B.
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 727
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,549A
; FILING DATE: 19-NOV-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION DATA:
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; APPLICATION DATA:
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION DATA:
; APPLICATION NUMBER: US 08/911,312
; FILING DATE: 14-AUG-1997
; APPLICATION DATA:
; APPLICATION NUMBER: US 08/912,951
; FILING DATE: 14-AUG-1997
; APPLICATION DATA:
; APPLICATION NUMBER: US 08/915,503
; FILING DATE: 14-AUG-1997
; APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/17618

;
; FILING DATE: 01-OCT-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/17885
; FILING DATE: 01-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph Ted
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002610US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 235:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-974-549A-235

Query Match 100.0%; Score 146; DB 3; Length 28;
Best Local Similarity 100.0%; Pred. No. 9e-16; Mismatches 0; Indels 0; Gaps 0;
Matches 28; Conservative 0;

QY 1 AKFLHMLSVYVVELLSFFVYVTTTFQ 28
| | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1 AKFLHMLSVYVVELLSFFVYVTTTFQ 28
| | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 3
; US-08-854-050-115
; Sequence 115, Application US/08854050
; Patent No. 6261836
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: No. 6261836el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/854,050
; FILING DATE: 09-MAY-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION DATA:
; APPLICATION NUMBER: US 08/915,503
; FILING DATE: 14-AUG-1997
; APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
```

; FILING DATE: 01-OCT-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002930US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 115:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-854-050-115

Query Match 100.0%; Score 146; DB 3; Length 28;
Best Local Similarity 100.0%; Pred. No. 9e-16;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Caps 0;

Qy 1 AKFLHMLMSVYVVELLSFFYVTTTFQ 28
Db 1 AKFLHMLMSVYVVELLSFFYVTTTFQ 28

RESULT 4

US-09-430-323-115
; Sequence 115, Application US/09430323
; Patent No. 6309867
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; LIngner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin
; Andrews, William H.
; TITLE OF INVENTION: No. 6309867el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/430,323
; FILING DATE: 29-Oct-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002930US
; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 115:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 115:
; US-09-430-323-115

Query Match 100.0%; Score 146; DB 4; Length 28;
Best Local Similarity 100.0%; Pred. No. 9e-16;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Caps 0;

Qy 1 AKFLHMLMSVYVVELLSFFYVTTTFQ 28
Db 1 AKFLHMLMSVYVVELLSFFYVTTTFQ 28

RESULT 5

US-08-851-843A-67
; Sequence 67, Application US/08851843A
; Patent No. 6093809
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: No. 6093809el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/851,843A
; FILING DATE: 06-MAY-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002930US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 67:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 129 amino acids

```
;
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..129
; OTHER INFORMATION: /note= "TRT motifs from human"
US-08-851-843A-67

Query Match 100.0%; Score 146; DB 3; Length 129;
Best Local Similarity 100.0%; Pred. No. 4.9e-15;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKFLHMLSVVYVVELLSFFVYVTTTFQ 28
Db 1 AKFLHMLSVVYVVELLSFFVYVTTTFQ 28

RESULT 6
US-08-974-549A-13
; Sequence 13, Application US/08974549A
; Patent No. 6166178
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin B.
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 727
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,549A
; FILING DATE: 19-NOV-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/911,312
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/912,951
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/915,503
; FILING DATE: 14-AUG-1997

;
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..129
; OTHER INFORMATION: /note= "TRT motifs from human"
US-08-851-843A-67

Query Match 100.0%; Score 146; DB 3; Length 129;
Best Local Similarity 100.0%; Pred. No. 4.9e-15;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKFLHMLSVVYVVELLSFFVYVTTTFQ 28
Db 1 AKFLHMLSVVYVVELLSFFVYVTTTFQ 28

RESULT 7
US-08-854-050-67
; Sequence 67, Application US/08854050
; Patent No. 6261836
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: No. 6261836el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/854,050
; FILING DATE: 09-MAY-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; CLASSIFICATION: 536
```



```

; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; FILING DATE: 25-APR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; FILING DATE: 18-APR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; FILING DATE: 01-OCT-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002600US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 129 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..129
; OTHER INFORMATION: /note= "TRT motifs from human"
;
US-08-912-951-13
Query Match 100.0%; Score 146; DB 4; Length 129;
Best Local Similarity 100.0%; Pred. No. 4.9e-15;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKFLHLMMSVYVVELLSFFVYVTTTQ 28
DB 1 AKFLHLMMSVYVVELLSFFVYVTTTQ 28

RESULT 10
; Sequence 40, Application US/09417485D
; Patent No. 6541202
; GENERAL INFORMATION:
; APPLICANT: Long, David M.
; APPLICANT: Metz, Anneke M.
; APPLICANT: Love, Ruschelle A.
; TITLE OF INVENTION: Telomerase Reverse Transcriptase (TERT) Genes
; FILE REFERENCE: 47714-5009-US
; CURRENT APPLICATION NUMBER: US/09/417,485D
; CURRENT FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 40
; LENGTH: 364
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Partial TERT sequence
;
US-09-417-485D-40
Query Match 100.0%; Score 146; DB 4; Length 364;
Best Local Similarity 100.0%; Pred. No. 1.5e-14;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKFLHLMMSVYVVELLSFFVYVTTTQ 28
DB 79 AKFLHLMMSVYVVELLSFFVYVTTTQ 106

RESULT 11
US-08-974-549A-5
; Sequence 5, Application US/08974549A
; Patent No. 6166178
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin B.
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 727
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,549A
; FILING DATE: 19-NOV-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; PRIOR APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/911,312
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/912,951
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/915,503
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/17618
; FILING DATE: 01-OCT-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/17885
; FILING DATE: 01-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph Ted
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002610US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 807 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
```

US-08-974-549A-5

Query Match 100.0%; Score 146; DB 3; Length 807;
Best Local Similarity 100.0%; Pred. No. 3.7e-14;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKFLHLMSSVVVVELLSRFFVYVTTTFQ 28
|||||
Db 542 AKFLHLMSSVVVVELLSRFFVYVTTTFQ 569

RESULT 12

US-08-912-951-5
; Sequence 5, Application US/08912951
; Patent No. 6475789
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND
; TITLE OF INVENTION: THERAPEUTIC METHODS
; NUMBER OF SEQUENCES: 335
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/912,951
; FILING DATE: 14-AUG-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002600US
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 807 amino acids
; TYPE: amino acid

; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-912-951-5

Query Match 100.0%; Score 146; DB 4; Length 807;
Best Local Similarity 100.0%; Pred. No. 3.7e-14;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AKFLHLMSSVVVVELLSRFFVYVTTTFQ 28
|||||
Db 542 AKFLHLMSSVVVVELLSRFFVYVTTTFQ 569

RESULT 13

US-08-851-843A-217
; Sequence 217, Application US/08851843A
; Patent No. 6093809
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: No. 6093809el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/851,843A
; FILING DATE: 06-MAY-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002930US
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 217:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1003 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-851-843A-217

Query Match 100.0%; Score 146; DB 3; Length 1003;
Best Local Similarity 100.0%; Pred. No. 4.7e-14;


```
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 1003 amino acids
;   TYPE: amino acid
;   STRANDEDNESS:
;   TOPOLOGY: linear
;   MOLECULE TYPE: peptide
US-08-854-050-217

Query Match      100.0%; Score 146; DB 3; Length 1003;
Best Local Similarity 100.0%; Pred. No. 4.7e-14;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AKFLHLMMSVYVVELLRSPFYVTTTFQ 28
Db      413 AKFLHLMMSVYVVELLRSPFYVTTTFQ 440

Search completed: November 12, 2003, 19:53:27
Job time : 13.0314 secs
```

THIS PAGE BLANK (USPTO)

Result No.	Score	Query Match	Length	DB	ID	Description
1	146	100.0	28	10	US-09-843-676-115	Sequence 115, App
2	146	100.0	28	10	US-09-766-253-67	Sequence 115, App
3	146	100.0	28	11	US-09-438-486-115	Sequence 115, App
4	146	100.0	28	15	US-10-053-758-115	Sequence 115, App
5	146	100.0	28	15	US-10-054-295-115	Sequence 115, App
6	146	100.0	28	15	US-10-054-641-115	Sequence 115, App
7	146	100.0	129	10	US-09-843-676-67	Sequence 67, Appl
8	146	100.0	129	10	US-09-766-253-67	Sequence 67, Appl
9	146	100.0	129	11	US-09-438-486-67	Sequence 67, Appl
10	146	100.0	129	15	US-10-053-758-67	Sequence 67, Appl
11	146	100.0	129	15	US-10-054-295-67	Sequence 67, Appl
12	146	100.0	129	15	US-10-054-611-67	Sequence 67, Appl
13	146	100.0	129	15	US-10-044-692-13	Sequence 13, Appl
14	146	100.0	129	15	US-10-044-539-13	Sequence 13, Appl
15	146	100.0	291	12	US-10-282-960-3	Sequence 3, Appl

```
;
; FILING DATE: 01-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002930US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 115:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; MOLECULE TYPE: linear
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 115:
US-09-843-676-115

Query Match 100.0%; Score 146; DB 10; Length 28;
Best Local Similarity 100.0%; Pred. No. 4.9e-14;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKFLHLMSSVYVVELLSFFVYVTTTFQ 28
| | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1 AKFLHLMSSVYVVELLSFFVYVTTTFQ 28

RESULT 2
US-09-766-253-115
; Sequence 115, Application US/09766253
; Publication No. US20020187471A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Linger, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin
; Andrews, William H.
; TITLE OF INVENTION: No. US20020187471A1 Telomerase
; NUMBER OF SEQUENCES: 171
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/766,253
; FILING DATE: 19-Jan-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/846,017
; FILING DATE: 1997-04-25
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002920US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 115:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
```

```
;
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 115:
US-09-766-253-115

Query Match 100.0%; Score 146; DB 10; Length 28;
Best Local Similarity 100.0%; Pred. No. 4.9e-14;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKFLHLMSSVYVVELLSFFVYVTTTFQ 28
| | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1 AKFLHLMSSVYVVELLSFFVYVTTTFQ 28

RESULT 3
US-09-438-486-115
; Sequence 115, Application US/09438486
; Publication No. US20030009019A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Linger, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: No. US20030009019A1 Telomerase
; NUMBER OF SEQUENCES: 223
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/438,486
; FILING DATE: 12-NOV-1999
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002931US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 115:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
```



```
;          TOPOLOGY: linear
;          MOLECULE TYPE: peptide
US-09-438-486-115

Query Match          100.0%; Score 146; DB 11; Length 28;
Best Local Similarity 100.0%; Pred. No. 4.9e-14;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKFLHMLMSVYVVELLSFFYVTTTFQ 28
Db 1 AKFLHMLMSVYVVELLSFFYVTTTFQ 28

RESULT 4
US-10-053-758-115
; Sequence 115, Application US/10053758
; Publication No. US20030032075A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin
; Andrews, William H.
; TITLE OF INVENTION: No. US20030032075A1el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; STREET: Townsend and Townsend and Crew LLP
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/053,758
; FILING DATE: 18-Jan-2002
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002930US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0300
; TELEFAX: (415) 576-0200
; INFORMATION FOR SEQ ID NO: 115:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid
; STRANDEDNESS: <unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 115:
US-10-053-758-115

Query Match          100.0%; Score 146; DB 15; Length 28;
Best Local Similarity 100.0%; Pred. No. 4.9e-14;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKFLHMLMSVYVVELLSFFYVTTTFQ 28
Db 1 AKFLHMLMSVYVVELLSFFYVTTTFQ 28

RESULT 5
US-10-054-295-115
; Sequence 115, Application US/10054295
; Publication No. US20030044953A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin
; Andrews, William H.
; TITLE OF INVENTION: No. US20030044953A1el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; STREET: Townsend and Townsend and Crew LLP
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/054,295
; FILING DATE: 18-Jan-2002
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/854,050
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002930US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 115:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 115:
US-10-054-295-115

Query Match          100.0%; Score 146; DB 15; Length 28;
Best Local Similarity 100.0%; Pred. No. 4.9e-14;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKFLHMLMSVYVVELLSFFYVTTTFQ 28
Db 1 AKFLHMLMSVYVVELLSFFYVTTTFQ 28

RESULT 6
```

US-10-054-611-115
; Sequence 115, Application US/10054611
; Publication No. US20030059787A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin
; Andrews, William H.

; TITLE OF INVENTION: No. US20030059787A1el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/054,611
; FILING DATE: 18-Jan-2002
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/854,050
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996

; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002930US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 115:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; NAME/KEY: peptide
; LOCATION: 1..115

; OTHER INFORMATION: /note= "TRT motifs from human"
; SEQUENCE DESCRIPTION: SEQ ID NO: 115:
US-10-054-611-115

Query Match 100.0%; Score 146; DB 15; Length 28;
Best Local Similarity 100.0%; Pred. No. 4.9e-14;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKFLHLMMSVYVVELLSFFVYTTTFQ 28
Db 1 AKFLHLMMSVYVVELLSFFVYTTTFQ 28

RESULT 7
US-09-843-676-67
; Sequence 67, Application US/09843676
; Patent No. US20020164786A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.

; Morin, Gregg B.
; Harley, Calvin
; Andrews, William H.
; TITLE OF INVENTION: No. US20020164786A1el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/843,676
; FILING DATE: 26-APR-2001
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996

; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002930US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 67:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 129 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..129

; OTHER INFORMATION: /note= "TRT motifs from human"
; SEQUENCE DESCRIPTION: SEQ ID NO: 67:
US-09-843-676-67

Query Match 100.0%; Score 146; DB 10; Length 129;
Best Local Similarity 100.0%; Pred. No. 2.3e-13;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKFLHLMMSVYVVELLSFFVYTTTFQ 28
Db 1 AKFLHLMMSVYVVELLSFFVYTTTFQ 28

RESULT 8
US-09-766-253-67
; Sequence 67, Application US/09766253
; Publication No. US20020187471A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin
; Andrews, William H.
; TITLE OF INVENTION: No. US20020187471A1el Telomerase

NUMBER OF SEQUENCES: 171
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/766,253
FILING DATE: 19-Jan-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/846,017
FILING DATE: 1997-04-25
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002920US
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 67:
SEQUENCE CHARACTERISTICS:
LENGTH: 129 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
MOLECULE TYPE: linear
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..129
OTHER INFORMATION: /note= "TRT motifs from human"
SEQUENCE DESCRIPTION: SEQ ID NO: 67:
US-09-766-253-67

Query Match 100.0%; Score 146; DB 10; Length 129;
Best Local Similarity 100.0%; Pred. No. 2.3e-13;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKFLHLMMSVYVVELLSFFYVTTTFQ 28
Db 1 AKFLHLMMSVYVVELLSFFYVTTTFQ 28

RESULT 9
US-09-438-486-67
; Sequence 67, Application US/09438486
; Publication No. US20030009019A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: No. US20030009019A1el Telomerase
; NUMBER OF SEQUENCES: 223
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111-3834

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/438,486
FILING DATE: 12-NOV-1999
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002931US
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 67:
SEQUENCE CHARACTERISTICS:
LENGTH: 129 amino acids
TYPE: amino acid
STRANDEDNESS:
MOLECULE TYPE: linear
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..129
OTHER INFORMATION: /note= "TRT motifs from human"
US-09-438-486-67

Query Match 100.0%; Score 146; DB 11; Length 129;
Best Local Similarity 100.0%; Pred. No. 2.3e-13;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKFLHLMMSVYVVELLSFFYVTTTFQ 28
Db 1 AKFLHLMMSVYVVELLSFFYVTTTFQ 28

RESULT 10
US-10-053-758-67
; Sequence 67, Application US/10053758
; Publication No. US20030032075A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: No. US20030032075A1el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California

COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/053,758
FILING DATE: 18-Jan-2002
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US/08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US/08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US/08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US/08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 67:
SEQUENCE CHARACTERISTICS:
LENGTH: 129 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..129
OTHER INFORMATION: /note= "TRT motifs from human"
SEQUENCE DESCRIPTION: SEQ ID NO: 67:
US-10-053-758-67
Query Match 100.0%; Score 146; DB 15; Length 129;
Best Local Similarity 100.0%; Pred. No. 2.3e-13;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 AKFLHLMVSVVVELLSFFVYVTTTFQ 28
Db 1 AKFLHLMVSVVVELLSFFVYVTTTFQ 28
RESULT 11
US-10-054-295-67
Sequence 67, Application US/10054295
Publication No. US20030044953A1
GENERAL INFORMATION:
APPLICANT: Cecch, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: No. US20030044953A1el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/054,295
FILING DATE: 18-Jan-2002
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/854,050
FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 67:
SEQUENCE CHARACTERISTICS:
LENGTH: 129 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..129
OTHER INFORMATION: /note= "TRT motifs from human"
SEQUENCE DESCRIPTION: SEQ ID NO: 67:
US-10-054-295-67
Query Match 100.0%; Score 146; DB 15; Length 129;
Best Local Similarity 100.0%; Pred. No. 2.3e-13;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 AKFLHLMVSVVVELLSFFVYVTTTFQ 28
Db 1 AKFLHLMVSVVVELLSFFVYVTTTFQ 28
RESULT 12
US-10-054-611-67
Sequence 67, Application US/10054611
Publication No. US20030059787A1
GENERAL INFORMATION:
APPLICANT: Cecch, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: No. US20030059787A1el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/054,611
FILING DATE: 18-Jan-2002
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/854,050
FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 67:
SEQUENCE CHARACTERISTICS:
LENGTH: 129 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..129
OTHER INFORMATION: /note= "TRT motifs from human"
SEQUENCE DESCRIPTION: SEQ ID NO: 67:
US-10-054-611-67

Query Match 100.0%; Score 146; DB 15; Length 129;
Best Local Similarity 100.0%; Pred. No. 2.3e-13;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKFLHMLMSVYVVELLSFFVYVTTTFQ 28
Db 1 AKFLHMLMSVYVVELLSFFVYVTTTFQ 28

RESULT 13
US-10-044-692-13
Sequence 13, Application US/10044692
Publication No. US20030096344A1
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND THERAPEUTIC METHODS
NUMBER OF SEQUENCES: 335
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/044,692

FILING DATE: 11-Jan-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/912,951
FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002600US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 129 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..129
OTHER INFORMATION: /note= "TRT motifs from human"
SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-10-044-692-13

Query Match 100.0%; Score 146; DB 15; Length 129;
Best Local Similarity 100.0%; Pred. No. 2.3e-13;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKFLHMLMSVYVVELLSFFVYVTTTFQ 28
Db 1 AKFLHMLMSVYVVELLSFFVYVTTTFQ 28

RESULT 14
US-10-044-539-13
Sequence 13, Application US/10044539
Publication No. US20030100093A1
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND THERAPEUTIC METHODS
NUMBER OF SEQUENCES: 335
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/044,692

APPLICATION NUMBER: US/10/044,539
FILING DATE: 11-Jan-2002
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/912,951
FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002600US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 129 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..129
OTHER INFORMATION: /note= "TRT motifs from human"
SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-10-044-539-13

Query Match 100.0%; Score 146; DB 15; Length 129;
Best Local Similarity 100.0%; Pred. No. 2.3e-13; Indels 0; Gaps 0;
Matches 28; Conservative 0; Mismatches 0;

Qy 1 AKFLHLMMSVYVVELLSFFYVTTTFQ 28
Db 1 AKFLHLMMSVYVVELLSFFYVTTTFQ 28

RESULT 15
US-10-282-960-3
Sequence 3, Application US/10282960
Publication No. US20030143228A1
GENERAL INFORMATION:
APPLICANT: Chen, Si-Yi
APPLICANT: Zhaoyang, You
APPLICANT: Schroers, Roland
TITLE OF INVENTION: Human Telomerase Reverse Transcriptase as a Class-II Restricted T
FILE REFERENCE: P02193US1
CURRENT APPLICATION NUMBER: US/10/282,960
CURRENT FILING DATE: 2002-10-29
PRIOR APPLICATION NUMBER: US 60/345,012
PRIOR FILING DATE: 2001-10-29
NUMBER OF SEQ ID NOS: 100
SOFTWARE: PatentIn version 3.1
SEQ ID NO 3
LENGTH: 291
TYPE: PRT
ORGANISM: Human
US-10-282-960-3

Query Match 100.0%; Score 146; DB 12; Length 291;
Best Local Similarity 100.0%; Pred. No. 5.1e-13; Indels 0; Gaps 0;
Matches 28; Conservative 0; Mismatches 0;

Qy 1 AKFLHLMMSVYVVELLSFFYVTTTFQ 28
Db 3 AKFLHLMMSVYVVELLSFFYVTTTFQ 30
Search completed: November 12, 2003, 19:55:47
Job time : 22.3648 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 12, 2003, 19:41:04 ; Search time 37.3585 Seconds
(without alignments)
127.462 Million cell updates/sec

Title: US-08-854-050-116

Perfect score: 152

Sequence: 1 LFYRKSVWSKLSIGIRQHLLKRVQLRDVS 30

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_19Jun03:*

1: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1980.DAT:*

2: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:*

3: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:*

4: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1983.DAT:*

5: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1984.DAT:*

6: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1985.DAT:*

7: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1986.DAT:*

8: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1987.DAT:*

9: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1988.DAT:*

10: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1989.DAT:*

11: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1990.DAT:*

12: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1991.DAT:*

13: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1992.DAT:*

14: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1993.DAT:*

15: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1994.DAT:*

16: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1995.DAT:*

17: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1996.DAT:*

18: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1997.DAT:*

19: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1998.DAT:*

20: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1999.DAT:*

21: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:*

22: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*

23: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*

24: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	152	100.0	30	19	AAW57395 Human telomerase r
2	152	100.0	131	20	AAW57385 Amino acid sequenc
3	145	95.4	100	23	ABG71627 hTERT fragment wit
4	145	95.4	259	19	AAW46998 Human telomerase r
5	145	95.4	283	20	AAV43128 Human telomerase r
6	145	95.4	437	20	AAV25461 Human CRT-1 protei
7	145	95.4	438	20	AAV25462 Human CRT-1 protei
8	145	95.4	564	19	AAW56109 Human telomerase r
9	145	95.4	591	20	AAW57384 A catalytic telome

10	145	95.4	622	20	AAV25463 Human CRT-1 protei
11	145	95.4	807	19	AAW46997 Human telomerase r
12	145	95.4	807	20	AAV00637 N-terminal truncat
13	145	95.4	807	20	AAV00646 Truncated telomera
14	145	95.4	936	20	AAV00642 Truncated telomera
15	145	95.4	936	20	AAV00651 Truncated telomera
16	145	95.4	948	20	AAV00639 N-terminal truncat
17	145	95.4	948	20	AAV00648 Truncated telomera
18	145	95.4	949	19	AAW61349 Human telomerase p
19	145	95.4	1041	20	AAV00643 Altered C-terminus
20	145	95.4	1041	20	AAV00652 Altered C-terminus
21	145	95.4	1053	20	AAV00640 Altered C-terminus
22	145	95.4	1093	20	AAV00649 Altered C-terminus
23	145	95.4	1120	20	AAV00641 Telomerase protein
24	145	95.4	1120	20	AAV00650 Telomerase (ver. 2
25	145	95.4	1132	19	AAW71376 Human telomerase c
26	145	95.4	1132	19	AAW46957 Human telomerase r
27	145	95.4	1132	20	AAV43621 A human telomerase
28	145	95.4	1132	20	AAV28881 Human telomerase r
29	145	95.4	1132	20	AAV32090 Human telomerase r
30	145	95.4	1132	20	AAV28401 Human EST2 protein
31	145	95.4	1132	20	AAV26580 Human telomerase r
32	145	95.4	1132	20	AAV00627 Human telomerase p
33	145	95.4	1132	20	AAV00638 Truncated telomera
34	145	95.4	1132	20	AAW90251 Human catalytic te
35	145	95.4	1132	21	AAV96566 hEST2, a human tel
36	145	95.4	1132	22	AAW82765 Human telomerase r
37	145	95.4	1132	22	AAW99930 Human telomerase p
38	145	95.4	1132	22	AAW64329 Human protein #2
39	145	95.4	1132	22	AAW64859 Heart muscle cell
40	145	95.4	1132	23	AAE29226 Human telomerase r
41	145	95.4	1132	23	AAU2735 Human telomerase r
42	145	95.4	1132	24	ABP56676 Glutathione-S-tran
43	145	95.4	1150	19	AAW47006 Human telomerase p
44	145	95.4	1154	19	AAW61350 Human telomerase p
45	145	95.4	1166	20	AAV00647 Telomerase (ver. 2

ALIGNMENTS

RESULT 1

AAW57395

ID AAW57395 standard; peptide; 30 AA.

XX

AC AAW57395;

XX

XX

DT 13-AUG-1998 (first entry)

XX

DE Human telomerase reverse transcriptase antigenic peptide A-2.

XX

XX Human; telomerase reverse transcriptase; hTERT; diagnosis; prognosis; cell proliferation; cancer; ageing; ribonucleoprotein.

XX

OS Synthetic.

OS Homo sapiens.

XX

PN GB2317891-A.

XX

PD 08-APR-1998.

XX

PF 01-OCT-1997; 97GB-0020890.

XX

PR 14-AUG-1997; 97US-0915503.

PR 01-OCT-1996; 96US-0724643.

PR 18-APR-1997; 97US-0844419.

PR 25-APR-1997; 97US-0846017.

PR 06-MAY-1997; 97US-0851843.

PR 09-MAY-1997; 97US-0854050.

PR 14-AUG-1997; 97US-0911312.

PR 14-AUG-1997; 97US-0912951.

XX

PA (GERO-) GERON CORP.

(UYTE-) UNIV TECHNOLOGY CORP.

Andrews WH, Cech TR, Chapman KB, Harley C, Lingner J;
Morin GB, Nakamura T, Harley CB;

WPI; 1998-171633/16.

Pure and recombinant human Telomerase Reverse Transcriptase and its
variants - are useful in the diagnosis, prognosis and treatment of
cell proliferation conditions especially cancer and ageing

Example 8; Fig 54; 387pp; English.

The present sequence represents an antigenic peptide from human
telomerase reverse transcriptase (hTERT), from the present invention. The
present invention also describes the following methods: (A) determining
whether a test compound is a modulator of hTERT, by detecting the change
in hTERT recombinant protein or polynucleotide, on administration of the
compound; (B) preparation of recombinant telomerase by contacting a
protein preparation of hTERT with a telomerase RNA component; (C)
detection of the hTERT RNA or protein in a sample by binding a relevant
probe to the sample and detecting the complex formed or in the case of
RNA detection, amplifying the product and correlating the presence of
complex or amplification product with presence of hTERT in the sample;
and (D) increasing the proliferation of a vertebrate cell by increasing
hTERT expression; and (E) the use of an agent that causes an increase in
cell vertebrate cell proliferation to create a medicament that inhibits
ageing. A protein preparation of hTERT and the polynucleotide encoding
hTERT can be used in the manufacture of medicaments for inhibiting the
effect of ageing or cancer. Inhibitors of telomerase activity can be
used to treat conditions that are associated with high telomerase
activity. A protein preparation of hTERT can also be used in the new
methods.

Sequence 30 AA;

Query Match 100.0%; Score 152; DB 19; Length 30;
Best Local Similarity 100.0%; Pred. No. 2.4e-16;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 LFFYKSVWSKLSQIGIRQHLKRVQLRDVS 30

1 LFFYKSVWSKLSQIGIRQHLKRVQLRDVS 30

RESULT 2

AAW97385
ID AAW97385 standard; Protein; 131 AA.

AAW97385;

14-MAY-1999 (first entry)

Amino acid sequence of the specification.

Catalytic telomerase; diagnosis; disease; telomerase activity.

Homo sapiens.

JP11046768-A.

23-FEB-1999.

01-AUG-1997; 97JP-0207708.

01-AUG-1997; 97JP-0207708.

(MITU) MITSUBISHI CHEM CORP.

WPI; 1999-208111/18.

N-PSDB; AAX15924.

New catalytic protein of telomerase of a higher animal and a gene

coding it - useful for diagnosis of diseases caused by the change in
activity of a telomerase

Example 1; Page 14; 18pp; Japanese.

The specification describes a human catalytic telomerase protein.

The products are useful in drug compositions for the diagnosis

of diseases caused by the change in activity of telomerase. The

present sequence appears in the specification.

Sequence 131 AA;

Query Match 100.0%; Score 152; DB 20; Length 131;
Best Local Similarity 100.0%; Pred. No. 1.2e-15;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 LFFYKSVWSKLSQIGIRQHLKRVQLRDVS 30

32 LFFYKSVWSKLSQIGIRQHLKRVQLRDVS 61

RESULT 3

ABG71627

ID ABG71627 standard; protein; 100 AA.

ABG71627;

09-JAN-2003 (first entry)

hTERT fragment with HLA containing polypeptide at its N-terminus.

Human; telomerase catalytic subunit; hTERT; human leukocyte antigen;

human telomerase reverse transcriptase; HLA epitope; cancer;

HLA profile; breast cancer; pancreatic cancer; colorectal cancer;

lung cancer; ovarian cancer; cervical cancer; malignant melanoma;

leukaemia; lymphoma; biliary tract carcinoma; anti-cancer; mutant;

cytostatic; HLA class I epitope; HLA class II epitope; mutein.

Homo sapiens.

Synthetic.

WO200270679-A2.

12-SEP-2002.

19-FEB-2002; 2002WO-NO00069.

02-MAR-2001; 2001GB-0005238.

(GEMV-) GEMVAX AS.

Eriksen JA, Gaudernack G, Moller M;

WPI; 2002-750459/81.

New polypeptide with an additional C-terminal and/or N-terminal

sequence, useful for preparing anti-cancer vaccines

Disclosure; Fig 1; 62pp; English.

The present invention relates to a polypeptide comprising a 20 amino
acid sequence derived from human telomerase catalytic subunit

(or human telomerase reverse transcriptase, hTERT) amino acid residues

537-556, or fragments thereof comprising at least 10 amino acids and

at least two human leukocyte antigen (HLA) class I or class II

epitopes. The invention also describes a polypeptide having the above

20 amino acid peptide sequence as additional C- and/or N-terminal

sequences on a fragment of hTERT which is not more than 100 amino

acids of hTERT. The polypeptides of the invention are useful in a

pharmaceutical composition or in a vaccine for preventing or treating

cancer in populations of individuals having varying HLA profiles.

The polypeptides are also useful in a diagnostic kit for diagnosing

cancers such as breast, pancreatic, colorectal, lung, ovarian or

CC cervical cancer, malignant melanoma, leukaemia, lymphoma or biliary
 CC tract carcinoma. The polypeptides or encoding polynucleotide
 CC sequences are useful for performing identity, sequence homology
 CC and/or hybridisation studies, for predicting structure and/or
 CC function (e.g. anti-cancer activity), or for screening methods in
 CC drug development or drug screening procedures. The present sequence
 CC represents a hTERT fragment with the 20 amino acid HLA epitope
 CC containing polypeptide at its N-terminus.

XX Sequence 100 AA;

Query Match 95.4%; Score 145; DB 23; Length 100;
 Best Local Similarity 93.3%; Pred. No. 1.1e-14;
 Matches 28; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LFFYRKSVMSKLSQSIGIRQHLKRVQLRDVS 30
 |||||
 Db 37 LFFYRKSVMSKLSQSIGIRQHLKRVQLRELS 66
 |||||

RESULT 4
 AAW46998
 ID AAW46998 standard; Protein; 259 AA.

XX AAW46998;

DT 13-AUG-1998 (first entry)

XX Human telomerase reverse transcriptase protein from cDNA clone 712562.

XX Human; telomerase reverse transcriptase; hTERT; TRT; diagnosis;
 KW prognosis; cell proliferation; cancer; ageing; ribonucleoprotein.

XX Homo sapiens.

XX GB2317891-A.

XX 08-APR-1998.

XX 01-OCT-1997; 97GB-0020890.

XX 14-AUG-1997; 97US-0915503.

XX 01-OCT-1996; 96US-0724643.

XX 18-APR-1997; 97US-0844419.

XX 25-APR-1997; 97US-0846017.

XX 06-MAY-1997; 97US-0851843.

XX 09-MAY-1997; 97US-0854050.

XX 14-AUG-1997; 97US-0911312.

XX 14-AUG-1997; 97US-0912951.

XX (GERO-) GERON CORP.

XX (UYTE-) UNIV TECHNOLOGY CORP.

XX Andrews WH, Cech TR, Chapman KB, Harley C, Lingner J;

XX Morin GB, Nakamura T, Harley CB;

XX WPI; 1998-171633/16.

XX N-PSDB; AAW22379.

XX Pure and recombinant human Telomerase Reverse Transcriptase and its
 PT variants - are useful in the diagnosis, prognosis and treatment of
 PT cell proliferation conditions especially cancer and ageing
 XX Example 1; Fig 19; 387pp; English.

XX The present sequence represents a human telomerase reverse transcriptase
 CC (hTERT) protein from a cDNA clone from the present invention. The present
 CC invention also describes the following methods: (A) determining whether
 CC a test compound is a modulator of hTERT, by detecting the change in hTERT
 CC recombinant protein or polynucleotide, on administration of the compound;
 CC (B) preparation of recombinant telomerase by contacting a protein
 CC preparation of hTERT with a telomerase RNA component; (C) detection of
 CC the hTERT RNA or protein in a sample by binding a relevant probe to the

CC sample and detecting the complex formed or in the case of RNA detection,
 CC amplifying the product and correlating the presence of complex or
 CC amplification product with presence of hTERT in the sample; and (D)
 CC increasing the proliferation of a vertebrate cell by increasing hTERT
 CC expression; and (E) the use of an agent that causes an increase in cell
 CC vertebrate cell proliferation to create a medicament that inhibits
 CC ageing. A protein preparation of hTERT and the polynucleotide encoding
 CC hTERT can be used in the manufacture of medicaments for inhibiting the
 CC effect of ageing or cancer. Inhibitors of telomerase activity can be
 CC used to treat conditions that are associated with high telomerase
 CC activity. A protein preparation of hTERT can also be used in the new
 CC methods.

XX Sequence 259 AA;

Query Match 95.4%; Score 145; DB 19; Length 259;
 Best Local Similarity 93.3%; Pred. No. 3.2e-14;

Matches 28; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LFFYRKSVMSKLSQSIGIRQHLKRVQLRDVS 30
 |||||
 Db 25 LFFYRKSVMSKLSQSIGIRQHLKRVQLRELS 54
 |||||

RESULT 5

AA43128

ID AAY43128 standard; Protein; 283 AA.

XX AAY43128;

XX 20-DEC-1999 (first entry)

XX Human telomerase reverse transcriptase.

XX Human telomerase reverse transcriptase; hTERT; antibody; diagnosis;
 KW telomerase-related disease; cancer.

XX Homo sapiens.

XX WO9950407-A1.

XX 07-OCT-1999.

XX 26-MAR-1999; 99WO-JP01557.

XX 26-MAR-1998; 98JP-0098486.

XX (KYOW) KYOWA HAKKO KOGYO KK.

XX Hanai N, Yamasaki M, Shibata K, Furuya A, Mikuni O, Anazawa H;

XX WPI; 1999-591316/50.

XX New monoclonal antibody recognizing human telomerase catalytic subunit
 PT (hTERT) useful for treating and diagnosing cancer -
 XX Claim 2; Page 72-73; 78pp; Japanese.

XX This sequence represents the human telomerase reverse transcriptase
 CC (hTERT). The invention relates to a monoclonal antibody recognising the
 CC hTERT. The antibody can be used for the investigation, diagnosis and
 CC treatment of telomerase-related diseases, especially diseases in which
 CC telomerase expression is up-regulated e.g. cancers.

XX Sequence 283 AA;

Query Match 95.4%; Score 145; DB 20; Length 283;
 Best Local Similarity 93.3%; Pred. No. 3.5e-14;

Matches 28; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LFFYRKSVMSKLSQSIGIRQHLKRVQLRDVS 30
 |||||
 Db 25 LFFYRKSVMSKLSQSIGIRQHLKRVQLRELS 54
 |||||

CRT-1; reverse transcriptase; telomerase; inhibitor; detection;
telomerase activity; cancer cell; screening; human.

RESULT 6
AAV25461
ID AAY25461 standard; Protein; 437 AA.

XX
AC AAY25461;

DT 22-SEP-1999 (first entry)

XX Human CRT-1 protein #1.

XX CRT-1; reverse transcriptase; telomerase; inhibitor; detection;
telomerase activity; cancer cell; screening; human.

OS Homo sapiens.

XX Key Location/Qualifiers
FH Protein 1..437

FT /label= CRT-1
FT /note= "Partial sequence, no stop codon given"

XX WO9935261-A1.

XX 15-JUL-1999.

XX 08-JAN-1999; 99WO-JP00039.

XX 06-MAY-1998; 98JP-0139177.

XX 08-JAN-1998; 98JP-0013232.

XX 30-JAN-1998; 98JP-0033584.

XX (CHUS) CHUGAI SEIYAKU KK.

XX Teuchiya M, Yoshida K;

XX WPI; 1999-430393/36.

XX N-PSDB; AAX88243.

XX Novel gene, useful in detection of telomerase activity and cancer
cells as well as screening telomerase inhibitors for treatment of
cancers

XX Claim 2; Page 31-32; 44pp; Japanese.

XX This invention describes novel human CRT-1 genes and their encoded
proteins containing a reverse transcriptase motif, which act as
telomerase inhibitors. The gene, its encoded protein and derived
antibodies can be used to provide base sequence information, detect
telomerase activity and cancer cells, and to screen telomerase
inhibitors. The detection method is simple and effective.

XX Sequence 437 AA;

Query Match 95.4%; Score 145; DB 20; Length 437;

Best Local Similarity 93.3%; Pred. No. 5.7e-14;

Matches 28; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LFFYRKSVWSKLSQIGIRQHLKRVQLRDVS 30

DB 63 LFFYRKSVWSKLSQIGIRQHLKRVQLRELS 92

RESULT 7

AAV25462

ID AAY25462 standard; Protein; 438 AA.

XX
AC AAY25462;

DT 22-SEP-1999 (first entry)

XX Human CRT-1 protein #2.

XX

KW CRT-1; reverse transcriptase; telomerase; inhibitor; detection;
telomerase activity; cancer cell; screening; human.

XX Homo sapiens.

XX OS

XX Key Location/Qualifiers

FH Protein 1..438

FT /label= CRT-1

FT /note= "Partial sequence, no stop codon given"

XX WO9935261-A1.

XX 15-JUL-1999.

XX 08-JAN-1999; 99WO-JP00039.

XX 06-MAY-1998; 98JP-0139177.

XX 08-JAN-1998; 98JP-0013232.

XX 30-JAN-1998; 98JP-0033584.

XX (CHUS) CHUGAI SEIYAKU KK.

XX Teuchiya M, Yoshida K;

XX WPI; 1999-430393/36.

XX N-PSDB; AAX88250.

XX Novel gene, useful in detection of telomerase activity and cancer
cells as well as screening telomerase inhibitors for treatment of
cancers

XX Example 1; Page 35-36; 44pp; Japanese.

XX This invention describes novel human CRT-1 genes and their encoded
proteins containing a reverse transcriptase motif, which act as
telomerase inhibitors. The gene, its encoded protein and derived
antibodies can be used to provide base sequence information, detect
telomerase activity and cancer cells, and to screen telomerase
inhibitors. The detection method is simple and effective.

XX Sequence 438 AA;

Query Match 95.4%; Score 145; DB 20; Length 438;

Best Local Similarity 93.3%; Pred. No. 5.7e-14;

Matches 28; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LFFYRKSVWSKLSQIGIRQHLKRVQLRDVS 30

DB 63 LFFYRKSVWSKLSQIGIRQHLKRVQLRELS 92

RESULT 8

AAW56109

ID AAW56109 standard; Protein; 564 AA.

XX
AC AAW56109;

DT 13-AUG-1998 (first entry)

XX Human telomerase reverse transcriptase 63 kDa clone 712562 protein.

XX Human; telomerase reverse transcriptase; hTRT; TRT; diagnosis;
prognosis; cell proliferation; cancer; ageing; ribonucleoprotein.

XX Synthetic.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Misc-difference 102

FT /label= encoded by ARG

XX GB2317891-A.

XX

PD 08-APR-1998.
 XX
 PF 01-OCT-1997; 97GB-0020890.
 XX
 PR 14-AUG-1997; 97US-0915503.
 PR 01-OCT-1996; 96US-0724643.
 PR 18-APR-1997; 97US-0844419.
 PR 25-APR-1997; 97US-0846017.
 PR 06-MAY-1997; 97US-0851843.
 PR 09-MAY-1997; 97US-0854050.
 PR 14-AUG-1997; 97US-0911312.
 PR 14-AUG-1997; 97US-0912951.
 XX
 PA (GERO-) GERON CORP.
 PA (UYTE-) UNIV TECHNOLOGY CORP.
 XX
 PI Andrews WH, Cech TR, Chapman KB, Harley C, Lingner J;
 PI Morin GB, Nakamura T, Harley CB;
 DR WPI; 1998-171633/16.
 DR N-PSDB; AAV22426.
 XX
 PT Pure and recombinant human Telomerase Reverse Transcriptase and its
 PT variants - are useful in the diagnosis, prognosis and treatment of
 PT cell proliferation conditions especially cancer and ageing
 XX
 XX Example 1; Fig 68; 387pp; English.
 XX
 CC The present sequence is a human telomerase reverse transcriptase (hTERT)
 CC clone protein from the present invention. The present invention also
 CC describes the following methods: (A) determining whether a test compound
 CC is a modulator of hTERT, by detecting the change in hTERT recombinant
 CC protein or polynucleotide, on administration of the compound; (B)
 CC preparation of recombinant telomerase by contacting a protein
 CC preparation of hTERT with a telomerase RNA component; (C) detection of
 CC the hTERT RNA or protein in a sample by binding a relevant probe to the
 CC sample and detecting the complex formed or in the case of RNA detection,
 CC amplifying the product and correlating the presence of complex or
 CC amplification product with presence of hTERT in the sample; and (D)
 CC increasing the proliferation of a vertebrate cell by increasing hTERT
 CC expression; and (E) the use of an agent that causes an increase in cell
 CC vertebrate cell proliferation to create a medicament that inhibits
 CC ageing. A protein preparation of hTERT and the polynucleotide encoding
 CC hTERT can be used in the manufacture of medicaments for inhibiting the
 CC effect of ageing or cancer. Inhibitors of telomerase activity can be
 CC used to treat conditions that are associated with high telomerase
 CC activity. A protein preparation of hTERT can also be used in the new
 CC methods.
 XX
 SQ Sequence 564 AA;
 Query Match 95.4%; Score 145; DB 19; Length 564;
 Best Local Similarity 93.3%; Pred. No. 7.5e-14;
 Matches 28; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LFFYRKSVMSKLSIGIRQLKRVQLRDVS 30
 DB 25 LFFYRKSVMSKLSIGIRQLKRVQLRELS 54
 RESULT 9
 AAW97384
 ID AAW97384 standard; Protein; 591 AA.
 XX
 AC AAW97384;
 XX
 DT 14-MAY-1999 (first entry)
 XX
 DE A catalytic telomerase protein.
 XX
 KW Catalytic telomerase; diagnosis; disease; telomerase activity.
 XX
 OS Homo sapiens.

XX JPI1046768-A.
 PN 23-FEB-1999.
 XX
 PD 01-AUG-1997; 97JP-0207708.
 PF
 PR 01-AUG-1997; 97JP-0207708.
 PR
 PA (MITU) MITSUBISHI CHEM CORP.
 XX
 XX WPI; 1999-208111/18.
 DR N-PSDB; AAX15923.
 XX
 PT New catalytic protein of telomerase of a higher animal and a gene
 PT coding it - useful for diagnosis of diseases caused by the change in
 PT activity of a telomerase
 XX
 XX Claim 1; Page 11-14; 18pp; Japanese.
 XX
 CC The present sequence represents a catalytic telomerase protein.
 CC The products are useful in drug compositions for the diagnosis
 CC of diseases caused by the change in activity of telomerase.
 XX
 SQ Sequence 591 AA;
 Query Match 95.4%; Score 145; DB 20; Length 591;
 Best Local Similarity 93.3%; Pred. No. 7.9e-14;
 Matches 28; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LFFYRKSVMSKLSIGIRQLKRVQLRDVS 30
 DB 32 LFFYRKSVMSKLSIGIRQLKRVQLRELS 61
 RESULT 10
 AAY25463
 ID AAY25463 standard; Protein; 622 AA.
 XX
 AC AAY25463;
 XX
 DT 22-SEP-1999 (first entry)
 XX
 DE Human CRT-1 protein #3.
 XX
 KW CRT-1; reverse transcriptase; telomerase; inhibitor; detection;
 KW telomerase activity; cancer cell; screening; human.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Protein 1..622
 FT /label= CRT-1
 FT /note= "Partial sequence, no stop codon given"
 XX
 PN WO9935261-A1.
 XX
 PD 15-JUL-1999.
 XX
 XX 08-JAN-1999; 99WO-JP000039.
 XX
 PR 06-MAY-1998; 98JP-0139177.
 PR 08-JAN-1998; 98JP-0013232.
 PR 30-JAN-1998; 98JP-0033584.
 XX
 PA (CHUS) CHUGAI SEIYAKU KK.
 XX
 PI Tsuchiya M, Yoshida K;
 XX
 DR WPI; 1999-430393/36.
 DR N-PSDB; AAX88251.
 XX
 PT Novel gene, useful in detection of telomerase activity and cancer

PT cells as well as screening telomerase inhibitors for treatment of
 PT cancers

PS Example 1; Page 37-39; 44pp; Japanese.

XX This invention describes novel human CRT-1 genes and their encoded
 CC proteins containing a reverse transcriptase motif, which act as
 CC telomerase inhibitors. The gene, its encoded protein and derived
 CC antibodies can be used to provide base sequence information, detect
 CC telomerase activity and cancer cells, and to screen telomerase
 CC inhibitors. The detection method is simple and effective.

XX Sequence 622 AA;

Query Match 95.4%; Score 145; DB 20; Length 622;
 Best Local Similarity 93.3%; Pred. No. 8.4e-14;
 Matches 28; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LFFYRKSVWSKLSIGIRQHLKRVQLRDVS 30
 |||||
 Db 63 LFFYRKSVWSKLSIGIRQHLKRVQLRELS 92
 |||||

RESULT 11
 AAW46997
 ID AAW46997 standard; Protein; 807 AA.

AC AAW46997;

XX 13-AUG-1998 (first entry)

DE Human telomerase reverse transcriptase Delta182 variant.

XX Human; telomerase reverse transcriptase; hTERT; TRT; diagnosis;
 KW prognosis; cell proliferation; cancer; ageing; ribonucleoprotein.

XX Synthetic.

OS Homo sapiens.

XX GB2317891-A.

XX 08-APR-1998.

XX 01-OCT-1997; 97GB-0020890.

XX 14-AUG-1997; 97US-0915503.

PR 01-OCT-1996; 96US-0724643.

PR 18-APR-1997; 97US-0844419.

PR 25-APR-1997; 97US-0846017.

PR 06-MAY-1997; 97US-0851843.

PR 09-MAY-1997; 97US-0854050.

PR 14-AUG-1997; 97US-0911312.

PR 14-AUG-1997; 97US-0912951.

XX (GERO-) GERON CORP.

PA (UYTE-) UNIV TECHNOLOGY CORP.

XX Andrews WH, Cech TR, Chapman KB, Harley C, Lingner J;

PI Morin GB, Nakamura T, Harley CB;

XX WPI; 1998-171633/16.

XX N-PSDB; AAV22382.

XX Pure and recombinant human Telomerase Reverse Transcriptase and its

PT variants - are useful in the diagnosis, prognosis and treatment of

PT cell proliferation conditions especially cancer and ageing

XX Disclosure; Fig 20; 387pp; English.

CC protein or polynucleotide, on administration of the compound; (B)
 CC preparation of recombinant telomerase by contacting a protein
 CC preparation of hTERT with a telomerase RNA component; (C) detection of
 CC the hTERT RNA or protein in a sample by binding a relevant probe to the
 CC sample and detecting the complex formed or in the case of RNA detection,
 CC amplifying the product and correlating the presence of complex or
 CC amplification product with presence of hTERT in the sample; and (D)
 CC increasing the proliferation of a vertebrate cell by increasing hTERT
 CC expression; and (E) the use of an agent that causes an increase in cell
 CC vertebrate cell proliferation to create a medicament that inhibits
 CC ageing. A protein preparation of hTERT and the polynucleotide encoding
 CC hTERT can be used in the manufacture of medicaments for inhibiting the
 CC effect of ageing or cancer. Inhibitors of telomerase activity can be
 CC used to treat conditions that are associated with high telomerase
 CC activity. A protein preparation of hTERT can also be used in the new
 CC methods.

SQ Sequence 807 AA;

Query Match 95.4%; Score 145; DB 19; Length 807;
 Best Local Similarity 93.3%; Pred. No. 1.1e-13;
 Matches 28; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LFFYRKSVWSKLSIGIRQHLKRVQLRDVS 30
 |||||
 Db 573 LFFYRKSVWSKLSIGIRQHLKRVQLRELS 602
 |||||

RESULT 12
 AAY00637
 ID AAY00637 standard; Protein; 807 AA.

XX AAY00637;

XX 26-JUL-1999 (first entry)

XX N-terminal truncated telomerase protein sequence.

XX Telomerase; human; cancer; diagnosis; melanoma; skin cancer; leukaemia;
 KW neuroblastoma; breast carcinoma; colon carcinoma; lymphoma; osteosarcoma;
 KW smooth muscle cell hyperplasia; stem cell proliferation; Wilms' tumour;
 KW stem cell differentiation; organ regeneration; organ differentiation.

XX Homo sapiens.

OS Synthetic.

XX WO9901560-A1.

XX 14-JAN-1999.

XX 01-JUL-1998; 98WO-US13835.

XX 09-SEP-1997; 97US-0058287.

PR 01-JUL-1997; 97US-0051410.

PR 21-JUL-1997; 97US-0053018.

PR 21-JUL-1997; 97US-0053329.

PR 04-AUG-1997; 97US-0054642.

XX (CAMB-) CAMBIA BIOSYSTEMS LLC.

XX Bowtell D, Kilian A;

XX WPI; 1999-106060/09.

XX N-PSDB; AAX18265.

XX New isolated vertebrate telomerase genes - used to develop products

XX for treating cancers or for organ regeneration, nerve cell or brain

XX cell growth following injury or bone marrow transplantation

XX Claim 4; Fig 11d-e; 134pp; English.

XX This sequence is a truncated human telomerase of the
 CC invention. Primers that amplify the telomerase coding sequence can be

CC used in a method for diagnosing cancer in a patient. The telomerase can
 CC be used for detection, diagnosis and drug screening. Inhibitors of
 CC telomerase activity can be used to treat cancers such as melanomas, other
 CC skin cancers, neuroblastomas, breast carcinomas, colon carcinomas,
 CC leukaemias, lymphomas, osteosarcomas or smooth muscle cell hyperplasias
 CC or skin growths. Enhancers of telomerase may be used to stimulate stem
 CC cell proliferation and differentiation (expansion of haematopoietic stem
 CC cells could be administered in the bone marrow transplant context). As
 CC well, many tissues have stem cells. Proliferation of these cells may be
 CC useful in wound healing, hair growth, treatment of disease such as Wilms
 CC tumour, organ regeneration or differentiation after injury or diseases,
 CC nerve cell or brain cell growth following injury.

SQ . Sequence 807 AA;
 Query Match 95.4%; Score 145; DB 20; Length 807;
 Best Local Similarity 93.3%; Pred. NO. 1.1e-13;
 Matches 28; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LFFYRKSVMSKLSIGIRQHLKRVQLRDVS 30
 |||||
 Db 573 LFFYRKSVMSKLSIGIRQHLKRVQLRELS 602

RESULT 13
 AAY00646
 ID AAY00646 standard; Protein; 807 AA.

XX AAY00646;
 XX 26-JUL-1999 (first entry)
 DT Truncated telomerase (ver. 2) protein sequence.
 DE
 XX Telomerase; human; cancer; diagnosis; melanoma; skin cancer; leukaemia;
 KW neuroblastoma; breast carcinoma; colon carcinoma; lymphoma; osteosarcoma;
 KW smooth muscle cell hyperplasia; stem cell proliferation; Wilms' tumour;
 KW stem cell differentiation; organ regeneration; organ differentiation.

XX Homo sapiens.
 OS Synthetic.
 XX WO9901560-A1.
 XX 14-JAN-1999.
 XX 01-JUL-1998; 98WO-US13835.
 XX 09-SEP-1997; 97US-0058287.
 XX 01-JUL-1997; 97US-0051410.
 XX 21-JUL-1997; 97US-0053018.
 XX 21-JUL-1997; 97US-0053329.
 XX 04-AUG-1997; 97US-0054642.
 XX (CAMB-) CAMBIA BIOSYSTEMS LLC.

XX Bowtell D, Kilian A;
 XX WPI; 1999-106060/09.
 XX N-PSDB; AAX18274.
 XX New isolated vertebrate telomerase genes - used to develop products
 PT for treating cancers or for organ regeneration, nerve cell or brain
 PT cell growth following injury or bone marrow transplantation
 XX Claim 4; Fig 11x-Y; 134pp; English.

XX This sequence is a truncated human telomerase of the
 CC invention. Primers that amplify the telomerase coding sequence can be
 CC used in a method for diagnosing cancer in a patient. The telomerase can
 CC be used for detection, diagnosis and drug screening. Inhibitors of
 CC telomerase activity can be used to treat cancers such as melanomas,
 CC other skin cancers, neuroblastomas, breast carcinomas, colon carcinomas,

CC leukaemias, lymphomas, osteosarcomas or smooth muscle cell hyperplasias
 CC or skin growths. Enhancers of telomerase may be used to stimulate stem
 CC cell proliferation and differentiation (expansion of haematopoietic stem
 CC cells could be administered in the bone marrow transplant context). As
 CC well, many tissues have stem cells. Proliferation of these cells may be
 CC useful in wound healing, hair growth, treatment of disease such as
 CC Wilms' tumour, organ regeneration or differentiation after injury or
 CC diseases, nerve cell or brain cell growth following injury.
 CC Note: The N-terminus of this sequence can be replaced by the sequences
 CC shown in AAY00656-Y00658.

SQ . Sequence 807 AA;
 Query Match 95.4%; Score 145; DB 20; Length 807;
 Best Local Similarity 93.3%; Pred. NO. 1.1e-13;
 Matches 28; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LFFYRKSVMSKLSIGIRQHLKRVQLRDVS 30
 |||||
 Db 573 LFFYRKSVMSKLSIGIRQHLKRVQLRELS 602

RESULT 14
 AAY00642
 ID AAY00642 standard; Protein; 936 AA.

XX AAY00642;
 XX 26-JUL-1999 (first entry)
 DT Truncated telomerase protein sequence lacking motif A.
 DE
 XX Telomerase; human; cancer; diagnosis; melanoma; skin cancer; leukaemia;
 KW neuroblastoma; breast carcinoma; colon carcinoma; lymphoma; osteosarcoma;
 KW smooth muscle cell hyperplasia; stem cell proliferation; Wilms' tumour;
 KW stem cell differentiation; organ regeneration; organ differentiation.

XX Homo sapiens.
 OS Synthetic.
 XX WO9901560-A1.
 XX 14-JAN-1999.
 XX 01-JUL-1998; 98WO-US13835.
 XX 09-SEP-1997; 97US-0058287.
 XX 01-JUL-1997; 97US-0051410.
 XX 21-JUL-1997; 97US-0053018.
 XX 21-JUL-1997; 97US-0053329.
 XX 04-AUG-1997; 97US-0054642.
 XX (CAMB-) CAMBIA BIOSYSTEMS LLC.

XX Bowtell D, Kilian A;
 XX WPI; 1999-106060/09.
 XX N-PSDB; AAX18270.
 XX New isolated vertebrate telomerase genes - used to develop products
 PT for treating cancers or for organ regeneration, nerve cell or brain
 PT cell growth following injury or bone marrow transplantation
 XX Claim 4; Fig 11p-q; 134pp; English.

XX This sequence is a truncated human telomerase of the
 CC invention. Primers that amplify the telomerase coding sequence can be
 CC used in a method for diagnosing cancer in a patient. The telomerase can
 CC be used for detection, diagnosis and drug screening. Inhibitors of
 CC telomerase activity can be used to treat cancers such as melanomas, other
 CC skin cancers, neuroblastomas, breast carcinomas, colon carcinomas,
 CC leukaemias, lymphomas, osteosarcomas or smooth muscle cell hyperplasias
 CC or skin growths. Enhancers of telomerase may be used to stimulate stem

CC cell proliferation and differentiation (expansion of haematopoietic stem
CC cells could be administered in the bone marrow transplant context). As
CC well, many tissues have stem cells. Proliferation of these cells may be
CC useful in wound healing, hair growth, treatment of disease such as Wilm's
CC tumour, organ regeneration or differentiation after injury or diseases,
CC nerve cell or brain cell growth following injury.
XX

SQ Sequence 936 AA;
Query Match 95.4%; Score 145; DB 20; Length 936;
Best Local Similarity 93.3%; Pred. No. 1.3e-13;
Matches 28; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 LFFYRKSVWSKLSIGIRQHLKRVQLRDVS 30
|||||
Db 573 LFFYRKSVWSKLSIGIRQHLKRVQLRELS 602
|||||

RESULT 15
AAY00651
ID AAY00651 standard; Protein; 936 AA.
XX
AC AAY00651;
XX
DT 26-JUL-1999 (first entry)
XX
DE Truncated telomerase (ver. 2) protein sequence lacking motif A.
XX
KW Telomerase; human; cancer; diagnosis; melanoma; skin cancer; leukaemia;
KW neuroblastoma; breast carcinoma; colon carcinoma; lymphoma; osteosarcoma;
KW smooth muscle cell hyperplasia; stem cell proliferation; Wilm's tumour;
KW stem cell differentiation; organ regeneration; organ differentiation.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO9901560-A1.
XX
PD 14-JAN-1999.
XX
PF 01-JUL-1998; 98WO-US13835.
XX
PR 09-SEP-1997; 97US-0058287.
PR 01-JUL-1997; 97US-0051410.
PR 21-JUL-1997; 97US-0053018.
PR 21-JUL-1997; 97US-0053329.
PR 04-AUG-1997; 97US-0054642.
XX
(CAMB-) CAMBIA BIOSYSTEMS LLC.
XX
PI Bowtell D, Kilian A;
XX
DR WPI; 1999-106060/09.
DR N-PSDB; AAX18279.
XX

PT New isolated vertebrate telomerase genes - used to develop products
PT for treating cancers or for organ regeneration, nerve cell or brain
PT cell growth following injury or bone marrow transplantation
XX
PS Claim 4; Fig 11ak-al; 134pp; English.
XX
CC This sequence is a truncated human telomerase of the
CC invention. Primers that amplify the telomerase coding sequence can be
CC used in a method for diagnosing cancer in a patient. The telomerase can
CC be used for detection, diagnosis and drug screening. Inhibitors of
CC telomerase activity can be used to treat cancers such as melanomas,
CC other skin cancers, neuroblastomas, breast carcinomas, colon carcinomas,
CC leukaemias, lymphomas, osteosarcomas or smooth muscle cell hyperplasias
CC or skin growths. Enhancers of telomerase may be used to stimulate stem
CC cell proliferation and differentiation (expansion of haematopoietic stem
CC cells could be administered in the bone marrow transplant context). As
CC well, many tissues have stem cells. Proliferation of these cells may be
CC useful in wound healing, hair growth, treatment of disease such as

CC Wilm's tumour, organ regeneration or differentiation after injury or
CC diseases, nerve cell or brain cell growth following injury.
CC Note: The N-terminus of this sequence can be replaced by the sequences
CC shown in AAY00656-Y00658.
XX
SQ Sequence 936 AA;
Query Match 95.4%; Score 145; DB 20; Length 936;
Best Local Similarity 93.3%; Pred. No. 1.3e-13;
Matches 28; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 LFFYRKSVWSKLSIGIRQHLKRVQLRDVS 30
|||||
Db 573 LFFYRKSVWSKLSIGIRQHLKRVQLRELS 602
|||||
Search completed: November 12, 2003, 19:47:14
Job time : 37.3585 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 12, 2003, 19:43:50 ; Search time 13.9623 Seconds
(without alignments)
90.911 Million cell updates/sec

Title: US-08-854-050-116

Perfect score: 152

Sequence: 1 LFFYKRVSVKLSIGIRHKLKRVQURDVS 30

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*
1: /cgn2_6/ptodata/1/iaa/5A-COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/5B-COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/6A-COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B-COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PCTUS-COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	152	100.0	30	3	US-08-851-843A-116
2	152	100.0	30	3	US-08-851-843A-116
3	152	100.0	30	3	US-08-851-843A-116
4	152	100.0	30	4	US-08-851-843A-116
5	145	95.4	129	3	US-08-851-843A-67
6	145	95.4	129	3	US-08-851-843A-67
7	145	95.4	129	3	US-08-851-843A-67
8	145	95.4	129	4	US-08-851-843A-67
9	145	95.4	129	4	US-08-851-843A-67
10	145	95.4	259	3	US-08-851-843A-10
11	145	95.4	259	4	US-08-851-843A-10
12	145	95.4	564	3	US-08-851-843A-101
13	145	95.4	564	3	US-08-851-843A-101
14	145	95.4	564	3	US-08-851-843A-101
15	145	95.4	564	4	US-08-851-843A-101
16	145	95.4	807	3	US-08-851-843A-5
17	145	95.4	807	4	US-08-851-843A-5
18	145	95.4	1003	3	US-08-851-843A-217
19	145	95.4	1003	3	US-08-851-843A-217
20	145	95.4	1003	3	US-08-851-843A-217
21	145	95.4	1003	4	US-08-851-843A-217
22	145	95.4	1132	3	US-08-851-843A-225
23	145	95.4	1132	3	US-08-851-843A-225
24	145	95.4	1132	3	US-08-851-843A-225
25	145	95.4	1132	4	US-08-851-843A-225
26	145	95.4	1132	4	US-08-851-843A-225
27	145	95.4	1132	4	US-08-851-843A-225

Sequence 2, Appli
Sequence 2, Appli
Sequence 611, App
Sequence 323, App
Sequence 613, App
Sequence 325, App
Sequence 612, App
Sequence 600, App
Sequence 314, App
Sequence 604, App
Sequence 604, App
Sequence 604, App
Sequence 603, App
Sequence 317, App
Sequence 344, App
Sequence 628, App
Sequence 334, App
Sequence 40, Appli

ALIGNMENTS

RESULT 1
US-08-851-843A-116
; Sequence 116, Application US/08851843A
; Patent No. 6093809
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: No. 6093809el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/851,843A
; FILING DATE: 06-MAY-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002930US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 116:

```
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-851-843A-116

Query Match 100.0%; Score 152; DB 3; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.7e-16; Indels 0; Gaps 0;
Matches 30; Conservative 0; Mismatches 0;

QY 1 LFFYRKSVMSKLSIGIRQHLKRVQLRDVS 30
| | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1 LFFYRKSVMSKLSIGIRQHLKRVQLRDVS 30
| | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 2
US-08-974-549A-236
; Sequence 236, Application US/08974549A
; Patent No. 6166178
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin B.
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 727
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,549A
; FILING DATE: 19-NOV-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/911,312
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/912,951
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/915,503
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/17618

; FILING DATE: 01-OCT-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/17885
; FILING DATE: 01-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph Ted
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002610US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 236:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-974-549A-236

Query Match 100.0%; Score 152; DB 3; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.7e-16; Indels 0; Gaps 0;
Matches 30; Conservative 0; Mismatches 0;

QY 1 LFFYRKSVMSKLSIGIRQHLKRVQLRDVS 30
| | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1 LFFYRKSVMSKLSIGIRQHLKRVQLRDVS 30
| | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 3
US-08-854-050-116
; Sequence 116, Application US/08854050
; Patent No. 6261836
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: No. 6261836el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/854,050
; FILING DATE: 09-MAY-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 536
; APPLICATION NUMBER: US 08/724,643
```


;; FILING DATE: 01-OCT-1996
;; CLASSIFICATION: 536
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Apple, Randolph T.
;; REGISTRATION NUMBER: 36,429
;; REFERENCE/DOCKET NUMBER: 015389-002930US
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (415) 576-0200
;; TELEFAX: (415) 576-0300
;; INFORMATION FOR SEQ ID NO: 116:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 30 amino acids
;; TYPE: amino acid
;; STRANDEDNESS:
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
US-08-854-050-116

Query Match 100.0%; Score 152; DB 3; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.7e-16;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LFFYKSVMSKLSIGIRQHLKRVQLRDVS 30
Db 1 LFFYKSVMSKLSIGIRQHLKRVQLRDVS 30

RESULT 4

US-09-430-323-116
; Sequence 116, Application US/09430323
; Patent No. 6309867

GENERAL INFORMATION:

;; APPLICANT: Cech, Thomas R.
;; Lingner, Joachim
;; Nakamura, Toru
;; Chapman, Karen B.
;; Morin, Gregg B.
;; Harley, Calvin
;; Andrews, William H.
;; TITLE OF INVENTION: No. 6309867el Telomerase

;; NUMBER OF SEQUENCES: 225

;; CORRESPONDENCE ADDRESS:

;; ADDRESSEE: Townsend and Townsend and Crew LLP
;; STREET: Two Embarcadero Center, 8th Floor
;; CITY: San Francisco
;; STATE: California
;; COUNTRY: United States of America
;; ZIP: 94111

COMPUTER READABLE FORM:

;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/430,323
;; FILING DATE: 29-Oct-1999
;; CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

;; APPLICATION NUMBER: US 08/854,050
;; FILING DATE: 09-MAY-1997
;; APPLICATION NUMBER: US 08/851,843
;; FILING DATE: 06-MAY-1997
;; APPLICATION NUMBER: US 08/846,017
;; FILING DATE: 25-APR-1997
;; APPLICATION NUMBER: US 08/844,419
;; FILING DATE: 18-APR-1997
;; APPLICATION NUMBER: US 08/724,643
;; FILING DATE: 01-OCT-1996

ATTORNEY/AGENT INFORMATION:

;; NAME: Apple, Randolph T.
;; REGISTRATION NUMBER: 36,429
;; REFERENCE/DOCKET NUMBER: 015389-002930US
;; TELECOMMUNICATION INFORMATION:

;; TELEPHONE: (415) 576-0200
;; TELEFAX: (415) 576-0300
;; INFORMATION FOR SEQ ID NO: 116:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 30 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: <Unknown>
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; SEQUENCE DESCRIPTION: SEQ ID NO: 116:
US-09-430-323-116

Query Match 100.0%; Score 152; DB 4; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.7e-16;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LFFYKSVMSKLSIGIRQHLKRVQLRDVS 30
Db 1 LFFYKSVMSKLSIGIRQHLKRVQLRDVS 30

RESULT 5

US-08-851-843A-67
; Sequence 67, Application US/08851843A
; Patent No. 6093809

GENERAL INFORMATION:

;; APPLICANT: Cech, Thomas R.
;; APPLICANT: Lingner, Joachim
;; APPLICANT: Nakamura, Toru
;; APPLICANT: Chapman, Karen B.
;; APPLICANT: Morin, Gregg B.
;; APPLICANT: Harley, Calvin
;; APPLICANT: Andrews, William H.
;; TITLE OF INVENTION: No. 6093809el Telomerase

;; NUMBER OF SEQUENCES: 225

;; CORRESPONDENCE ADDRESS:

;; ADDRESSEE: Townsend and Townsend and Crew LLP
;; STREET: Two Embarcadero Center, 8th Floor
;; CITY: San Francisco
;; STATE: California
;; COUNTRY: United States of America
;; ZIP: 94111

COMPUTER READABLE FORM:

;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/851,843A
;; FILING DATE: 06-MAY-1997

CLASSIFICATION:

;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/846,017
;; FILING DATE: 25-APR-1997

CLASSIFICATION:

;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/844,419
;; FILING DATE: 18-APR-1997

CLASSIFICATION:

;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/724,643
;; FILING DATE: 01-OCT-1996

CLASSIFICATION:

;; ATTORNEY/AGENT INFORMATION:
;; NAME: Apple, Randolph T.
;; REGISTRATION NUMBER: 36,429
;; REFERENCE/DOCKET NUMBER: 015389-002930US
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (415) 576-0200
;; TELEFAX: (415) 576-0300
;; INFORMATION FOR SEQ ID NO: 67:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 129 amino acids

```

; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..129
; OTHER INFORMATION: /note= "TRT motifs from human"
US-08-851-843A-67

Query Match 95.4%; Score 145; DB 3; Length 129;
Best Local Similarity 93.3%; Pred. No. 1.1e-14;
Matches 28; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LFFYRKSVWSKLSIGIRQHLKRVQLRDVS 30
Db 32 LFFYRKSVWSKLSIGIRQHLKRVQLRELS 61

RESULT 6
US-08-974-549A-13
; Sequence 13, Application US/08974549A
; Patent No. 6166178
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin B.
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 727
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,549A
; FILING DATE: 19-NOV-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/911,312
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/912,951
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/915,503
; FILING DATE: 14-AUG-1997
```

```

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/17618
; FILING DATE: 01-OCT-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/17885
; FILING DATE: 01-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph Ted
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002610US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 129 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..129
; OTHER INFORMATION: /note= "TRT motifs from human"
US-08-974-549A-13

Query Match 95.4%; Score 145; DB 3; Length 129;
Best Local Similarity 93.3%; Pred. No. 1.1e-14;
Matches 28; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LFFYRKSVWSKLSIGIRQHLKRVQLRDVS 30
Db 32 LFFYRKSVWSKLSIGIRQHLKRVQLRELS 61

RESULT 7
US-08-854-050-67
; Sequence 67, Application US/08854050
; Patent No. 6261836
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: No. 6261836el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/854,050
; FILING DATE: 09-MAY-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; CLASSIFICATION: 536
```

```

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002930US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0300
; TELEFAX: (415) 576-0200
; INFORMATION FOR SEQ ID NO: 67:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 129 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..129
; OTHER INFORMATION: /note= "TRT motifs from human"
;
; US-08-854-050-67
;
Query Match 95.4%; Score 145; DB 3; Length 129;
Best Local Similarity 93.3%; Pred. No. 1.1e-14;
Matches 28; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LFFYRKSVMSKLSIGIRQHLKRVQLRDVS 30
Db 32 LFFYRKSVMSKLSIGIRQHLKRVQLRELS 61

RESULT 8
US-09-430-323-67
; Sequence 67, Application US/09430323
; Patent No. 6309867
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; LINGNER, JOACHIM
; NAKAMURA, TORU
; CHAPMAN, KAREN B.
; MORIN, GREGG B.
; HARLEY, CALVIN
; ANDREWS, WILLIAM H.
; TITLE OF INVENTION: No. 6309867el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/430,323
; FILING DATE: 29-Oct-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; APPLICATION NUMBER: US 08/846,017

```

```

; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002930US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 67:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 129 amino acids
; TYPE: amino acid
; STRANDEDNESS: <unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..129
; OTHER INFORMATION: /note= "TRT motifs from human"
;
; US-09-430-323-67
;
Query Match 95.4%; Score 145; DB 4; Length 129;
Best Local Similarity 93.3%; Pred. No. 1.1e-14;
Matches 28; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LFFYRKSVMSKLSIGIRQHLKRVQLRDVS 30
Db 32 LFFYRKSVMSKLSIGIRQHLKRVQLRELS 61

RESULT 9
US-08-912-951-13
; Sequence 13, Application US/08912951
; Patent No. 6475789
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND
; NUMBER OF SEQUENCES: 335
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/912,951
; FILING DATE: 14-AUG-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997

```


;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Townsend and Townsend and Crew LLP
;; STREET: Two Embarcadero Center, 8th Floor
;; CITY: San Francisco
;; STATE: California
;; COUNTRY: United States of America
;; ZIP: 94111
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/912,951
;; FILING DATE: 14-AUG-1997
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/854,050
;; FILING DATE: 09-MAY-1997
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/846,017
;; FILING DATE: 25-APR-1997
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/851,843
;; FILING DATE: 06-MAY-1997
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/844,419
;; FILING DATE: 18-APR-1997
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/724,643
;; FILING DATE: 01-OCT-1996
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Apple, Randolph T.
;; REGISTRATION NUMBER: 36,429
;; REFERENCE/DOCKET NUMBER: 015389-002600US
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (415) 576-0200
;; TELEFAX: (415) 576-0300
;; INFORMATION FOR SEQ ID NO: 10:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 259 amino acids
;; TYPE: amino acid
;; STRANDEDNESS:
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; FEATURE:
;; NAME/KEY: Protein
;; LOCATION: 1..259
;; OTHER INFORMATION: /note= "protein encoded by clone 712562"
;;
US-08-912-951-10

Query Match 95.4%; Score 145; DB 4; Length 259;
Best Local Similarity 93.3%; Pred. No. 2.3e-14;
Matches 28; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LFFYRKSVWSKLSIGIRQHLKRVQLRDVS 30
|||
DB 25 LFFYRKSVWSKLSIGIRQHLKRVQLRELS 54

RESULT 12
US-08-851-843A-101
; Sequence 101, Application US/08851843A
; Patent No. 6093809
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru

;; APPLICANT: Chapman, Karen B.
;; APPLICANT: Morin, Gregg B.
;; APPLICANT: Harley, Calvin
;; APPLICANT: Andrews, William H.
;; TITLE OF INVENTION: No. 6093809el Telomerase
;; NUMBER OF SEQUENCES: 225
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Townsend and Townsend and Crew LLP
;; STREET: Two Embarcadero Center, 8th Floor
;; CITY: San Francisco
;; STATE: California
;; COUNTRY: United States of America
;; ZIP: 94111
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/851,843A
;; FILING DATE: 06-MAY-1997
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/846,017
;; FILING DATE: 25-APR-1997
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/844,419
;; FILING DATE: 18-APR-1997
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/724,643
;; FILING DATE: 01-OCT-1996
;; CLASSIFICATION:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Apple, Randolph T.
;; REGISTRATION NUMBER: 36,429
;; REFERENCE/DOCKET NUMBER: 015389-002930US
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (415) 576-0200
;; TELEFAX: (415) 576-0300
;; INFORMATION FOR SEQ ID NO: 101:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 564 amino acids
;; TYPE: amino acid
;; STRANDEDNESS:
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; FEATURE:
;; NAME/KEY: Protein
;; LOCATION: 1..564
;; OTHER INFORMATION: /note= "63 kDa telomerase protein
;; OTHER INFORMATION: encoded by ORF of EcoRI-No. 6093809I insert of
;; OTHER INFORMATION: clone 712562"
;;
US-08-851-843A-101

Query Match 95.4%; Score 145; DB 3; Length 564;
Best Local Similarity 93.3%; Pred. No. 5.6e-14;
Matches 28; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LFFYRKSVWSKLSIGIRQHLKRVQLRDVS 30
|||
DB 25 LFFYRKSVWSKLSIGIRQHLKRVQLRELS 54

RESULT 13
US-08-974-549A-267
; Sequence 267, Application US/08974549A
; Patent No. 6166178
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru

APPLICANT: Chapman, Karen B.
 APPLICANT: Morin, Gregg B.
 APPLICANT: Harley, Calvin B.
 APPLICANT: Andrews, William H.
 TITLE OF INVENTION: Human Telomerase Catalytic Subunit
 NUMBER OF SEQUENCES: 727
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend and Crew LLP
 STREET: Two Embarcadero Center, Eighth Floor
 CITY: San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94111-3834
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/974,549A
 FILING DATE: 19-NOV-1997
 CLASSIFICATION: 536
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/724,643
 FILING DATE: 01-OCT-1996
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/844,419
 FILING DATE: 18-APR-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/846,017
 FILING DATE: 25-APR-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/851,843
 FILING DATE: 06-MAY-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/854,050
 FILING DATE: 09-MAY-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/911,312
 FILING DATE: 14-AUG-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/912,951
 FILING DATE: 14-AUG-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/915,503
 FILING DATE: 14-AUG-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: WO PCT/US97/17618
 FILING DATE: 01-OCT-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: WO PCT/US97/17885
 FILING DATE: 01-OCT-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Apple, Randolph Ted
 REGISTRATION NUMBER: 36,429
 REFERENCE/DOCKET NUMBER: 015389-002610US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 576-0200
 TELEFAX: (415) 576-0300
 INFORMATION FOR SEQ ID NO: 267:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 564 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 FEATURE:
 NAME/KEY: Protein
 LOCATION: 1..564
 OTHER INFORMATION: /note= "63 kDa telomerase protein
 OTHER INFORMATION: encoded by ORF of ECORI-No. 61661781 insert of
 OTHER INFORMATION: clone 712562"
 US-08-974-549A-267

Query Match 95.4%; Score 145; DB 3; Length 564;
 Best Local Similarity 93.3%; Pred. No. 5.6e-14;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LFFYRKSVWSKLSQSGIRHQLKRVQLRDVS 30
 Db 25 LFFYRKSVWSKLSQSGIRHQLKRVQLRELS 54
 RESULT 14
 US-08-854-050-101
 ; Sequence 101, Application US/08854050
 ; Patent No. 6261836
 ; GENERAL INFORMATION:
 ; APPLICANT: Cech, Thomas R.
 ; APPLICANT: Lingner, Joachim
 ; APPLICANT: Nakamura, Toru
 ; APPLICANT: Chapman, Karen B.
 ; APPLICANT: Morin, Gregg B.
 ; APPLICANT: Harley, Calvin
 ; APPLICANT: Andrews, William H.
 ; TITLE OF INVENTION: No. 6261836el Telomerase
 ; NUMBER OF SEQUENCES: 225
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Townsend and Townsend and Crew LLP
 ; STREET: Two Embarcadero Center, 8th Floor
 ; CITY: San Francisco
 ; STATE: California
 ; COUNTRY: United States of America
 ; ZIP: 94111
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/854,050
 ; FILING DATE: 09-MAY-1997
 ; CLASSIFICATION: 536
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/851,843
 ; FILING DATE: 06-MAY-1997
 ; CLASSIFICATION: 536
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/846,017
 ; FILING DATE: 25-APR-1997
 ; CLASSIFICATION: 536
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/844,419
 ; FILING DATE: 18-APR-1997
 ; CLASSIFICATION: 536
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/724,643
 ; FILING DATE: 01-OCT-1996
 ; CLASSIFICATION: 536
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Apple, Randolph T.
 ; REGISTRATION NUMBER: 36,429
 ; REFERENCE/DOCKET NUMBER: 015389-002930US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 576-0200
 ; TELEFAX: (415) 576-0300
 ; INFORMATION FOR SEQ ID NO: 101:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 564 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS:
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; FEATURE:
 ; NAME/KEY: Protein
 ; LOCATION: 1..564

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 12, 2003, 19:47:20 ; Search time 23.9623 Seconds
(without alignments)
215.025 Million cell updates/sec

Title: US-08-854-050-116
Perfect score: 152
Sequence: 1 LFFYKSVMSKLSIGIRHKLKRVQRDVS 30

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 644079 seqs, 171749292 residues

Total number of hits satisfying chosen parameters: 644079

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	152	100.0	30	10	US-09-843-676-116 Sequence 116, App
2	152	100.0	30	10	US-09-766-253-67 Sequence 116, App
3	152	100.0	30	11	US-09-438-486-116 Sequence 116, App
4	152	100.0	30	15	US-10-053-758-116 Sequence 116, App
5	152	100.0	30	15	US-10-054-295-116 Sequence 116, App
6	152	100.0	30	15	US-10-054-611-116 Sequence 116, App
7	145	95.4	129	10	US-09-843-676-67 Sequence 67, Appl
8	145	95.4	129	10	US-09-766-253-67 Sequence 67, Appl
9	145	95.4	129	11	US-09-438-486-67 Sequence 67, Appl
10	145	95.4	129	15	US-10-053-758-67 Sequence 67, Appl
11	145	95.4	129	15	US-10-054-295-67 Sequence 67, Appl
12	145	95.4	129	15	US-10-054-611-67 Sequence 67, Appl
13	145	95.4	129	15	US-10-044-692-13 Sequence 13, Appl
14	145	95.4	129	15	US-10-044-539-13 Sequence 13, Appl
15	145	95.4	259	15	US-10-044-692-15 Sequence 10, Appl

16	145	95.4	259	15	US-10-044-539-10	Sequence 10, Appl
17	145	95.4	291	12	US-10-282-960-3	Sequence 3, Appl
18	145	95.4	437	15	US-10-294-778-2	Sequence 2, Appl
19	145	95.4	438	15	US-10-294-778-10	Sequence 10, Appl
20	145	95.4	500	12	US-10-282-960-81	Sequence 81, Appl
21	145	95.4	564	10	US-09-843-676-101	Sequence 101, App
22	145	95.4	564	10	US-09-766-253-101	Sequence 101, App
23	145	95.4	564	11	US-09-438-486-101	Sequence 101, App
24	145	95.4	564	15	US-10-053-758-101	Sequence 101, App
25	145	95.4	564	15	US-10-054-295-101	Sequence 101, App
26	145	95.4	564	15	US-10-054-611-101	Sequence 101, App
27	145	95.4	622	15	US-10-294-778-12	Sequence 12, Appl
28	145	95.4	807	15	US-10-044-692-5	Sequence 5, Appl
29	145	95.4	807	15	US-10-044-539-5	Sequence 5, Appl
30	145	95.4	1003	10	US-09-843-676-217	Sequence 217, App
31	145	95.4	1003	11	US-09-438-486-217	Sequence 217, App
32	145	95.4	1003	15	US-10-053-758-217	Sequence 217, App
33	145	95.4	1003	15	US-10-054-295-217	Sequence 217, App
34	145	95.4	1003	15	US-10-054-611-217	Sequence 217, App
35	145	95.4	1132	10	US-09-990-080-2	Sequence 2, Appl
36	145	95.4	1132	10	US-09-749-728B-31	Sequence 31, Appl
37	145	95.4	1132	10	US-09-843-676-225	Sequence 225, App
38	145	95.4	1132	10	US-09-953-052-2	Sequence 2, Appl
39	145	95.4	1132	12	US-10-295-681-57	Sequence 57, Appl
40	145	95.4	1132	15	US-10-053-758-225	Sequence 225, App
41	145	95.4	1132	15	US-10-208-243-2	Sequence 2, Appl
42	145	95.4	1132	15	US-10-054-295-225	Sequence 225, App
43	145	95.4	1132	15	US-10-054-611-225	Sequence 225, App
44	145	95.4	1132	15	US-10-105-963-2	Sequence 2, Appl
45	145	95.4	1132	15	US-10-044-692-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-09-843-676-116
; Sequence 116, Application US/09843676
; Patent No. US20020164786A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; ; Lingner, Joachim
; ; Nakamura, Toru
; ; Chapman, Karen B.
; ; Morin, Gregg B.
; ; Harley, Calvin
; ; Andrews, William H.
; ;
; TITLE OF INVENTION: No. US20020164786A1el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; ;
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; ;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/843,676
; FILING DATE: 26-APR-2001
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/724,643

```
;
; FILING DATE: 01-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002930US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 116:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; MOLECULE TYPE: linear
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 116:
US-09-843-676-116

Query Match 100.0%; Score 152; DB 10; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.5e-15;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LFFYRKSVWSKLSQIGIRQHKLKRVQLRDVS 30
Db 1 LFFYRKSVWSKLSQIGIRQHKLKRVQLRDVS 30

RESULT 2
US-09-766-253-116
; Sequence 116, Application US/09766253
; Publication No. US20020187471A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; LINGNER, JOACHIM
; NAKAMURA, TORU
; CHAPMAN, KAREN B.
; MORIN, GREGG B.
; HARLEY, CALVIN
; ANDREWS, WILLIAM H.
; TITLE OF INVENTION: No. US20020187471A1el Telomerase
; NUMBER OF SEQUENCES: 171
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/766,253
; FILING DATE: 19-Jan-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/846,017
; FILING DATE: 1997-04-25
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002920US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 116:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 amino acids
; TYPE: amino acid
; STRANDEDNESS:
;
;
```

```
;
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 116:
US-09-766-253-116

Query Match 100.0%; Score 152; DB 10; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.5e-15;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LFFYRKSVWSKLSQIGIRQHKLKRVQLRDVS 30
Db 1 LFFYRKSVWSKLSQIGIRQHKLKRVQLRDVS 30

RESULT 3
US-09-438-486-116
; Sequence 116, Application US/09438486
; Publication No. US2003009019A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; LINGNER, JOACHIM
; NAKAMURA, TORU
; CHAPMAN, KAREN B.
; MORIN, GREGG B.
; HARLEY, CALVIN
; ANDREWS, WILLIAM H.
; TITLE OF INVENTION: No. US2003009019A1el Telomerase
; NUMBER OF SEQUENCES: 223
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/438,486
; FILING DATE: 12-NOV-1999
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002931US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 116:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 amino acids
; TYPE: amino acid
; STRANDEDNESS:
;
;
```

```
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-438-486-116
Query Match 100.0%; Score 152; DB 11; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.5e-15;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LFFYRKSVWSKLSIGIRQHLKRVQLRDVS 30
Db 1 LFFYRKSVWSKLSIGIRQHLKRVQLRDVS 30

RESULT 4
US-10-053-758-116
; Sequence 116, Application US/10053758
; Publication No. US20030032075A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin
; Andrews, William H.
; TITLE OF INVENTION: No. US20030032075A1el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; STREET: Townsend and Townsend and Crew LLP
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/053,758
; FILING DATE: 18-Jan-2002
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002930US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 116:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 116:
US-10-053-758-116
Query Match 100.0%; Score 152; DB 15; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.5e-15;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LFFYRKSVWSKLSIGIRQHLKRVQLRDVS 30
Db 1 LFFYRKSVWSKLSIGIRQHLKRVQLRDVS 30

RESULT 5
US-10-054-295-116
; Sequence 116, Application US/10054295
; Publication No. US20030044953A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin
; Andrews, William H.
; TITLE OF INVENTION: No. US20030044953A1el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; STREET: Townsend and Townsend and Crew LLP
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/054,295
; FILING DATE: 18-Jan-2002
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/854,050
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002930US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 116:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 116:
US-10-054-295-116
Query Match 100.0%; Score 152; DB 15; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.5e-15;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LFFYRKSVWSKLSIGIRQHLKRVQLRDVS 30
Db 1 LFFYRKSVWSKLSIGIRQHLKRVQLRDVS 30

RESULT 6
US-10-054-295-116
Query Match 100.0%; Score 152; DB 15; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.5e-15;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LFFYRKSVWSKLSIGIRQHLKRVQLRDVS 30
Db 1 LFFYRKSVWSKLSIGIRQHLKRVQLRDVS 30
```

US-10-054-611-116
; Sequence 116, Application US/10054611
; Publication No. US20030059787A1
; GENERAL INFORMATION:

APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin
; Andrews, William H.

TITLE OF INVENTION: NO. US20030059787A1el Telomerase

NUMBER OF SEQUENCES: 225

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/054,611

FILING DATE: 18-Jan-2002

CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/854,050

FILING DATE: <Unknown>

APPLICATION NUMBER: US 08/846,017

FILING DATE: 25-APR-1997

APPLICATION NUMBER: US 08/844,419

FILING DATE: 18-APR-1997

APPLICATION NUMBER: US 08/724,643

FILING DATE: 01-OCT-1996

ATTORNEY/AGENT INFORMATION:

NAME: Apple, Randolph T.

REGISTRATION NUMBER: 36,429

REFERENCE/DOCKET NUMBER: 015389-002930US

TELEPHONE: (415) 576-0200

TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 116:

SEQUENCE CHARACTERISTICS:

LENGTH: 30 amino acids

TYPE: amino acid

STRANDEDNESS: <Unknown>

TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 116:

US-10-054-611-116

Query Match 100.0%; Score 152; DB 15; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.5e-15;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LFFYKSVWSKLQSIGIRQHLKRVQLRDVS 30

Db 1 LFFYKSVWSKLQSIGIRQHLKRVQLRDVS 30

RESULT 7
US-09-843-676-67
; Sequence 67, Application US/09843676
; Patent No. US20020164786A1

GENERAL INFORMATION:

APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.

Morin, Gregg B.
; Harley, Calvin
; Andrews, William H.

TITLE OF INVENTION: No. US20020164786A1el Telomerase

NUMBER OF SEQUENCES: 225

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/843,676

FILING DATE: 26-Apr-2001

CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/854,050

FILING DATE: 09-MAY-1997

APPLICATION NUMBER: US 08/846,017

FILING DATE: 25-APR-1997

APPLICATION NUMBER: US 08/844,419

FILING DATE: 18-APR-1997

APPLICATION NUMBER: US 08/724,643

FILING DATE: 01-OCT-1996

ATTORNEY/AGENT INFORMATION:

NAME: Apple, Randolph T.

REGISTRATION NUMBER: 36,429

REFERENCE/DOCKET NUMBER: 015389-002930US

TELEPHONE: (415) 576-0200

TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 67:

SEQUENCE CHARACTERISTICS:

LENGTH: 129 amino acids

TYPE: amino acid

STRANDEDNESS: <Unknown>

TOPOLOGY: linear

MOLECULE TYPE: peptide

FEATURE:

NAME/KEY: Peptide

LOCATION: 1..129

OTHER INFORMATION: /note= "TRT motifs from human"

SEQUENCE DESCRIPTION: SEQ ID NO: 67:

US-09-843-676-67

Query Match 95.4%; Score 145; DB 10; Length 129;
Best Local Similarity 93.3%; Pred. No. 7.7e-14;
Matches 28; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LFFYKSVWSKLQSIGIRQHLKRVQLRDVS 30

Db 32 LFFYKSVWSKLQSIGIRQHLKRVQLRELS 61

RESULT 8

US-09-766-253-67

; Sequence 67, Application US/09766253

; Publication No. US20020187471A1

GENERAL INFORMATION:

APPLICANT: Cech, Thomas R.

; Lingner, Joachim

; Nakamura, Toru

; Chapman, Karen B.

; Morin, Gregg B.

; Harley, Calvin

; Andrews, William H.

TITLE OF INVENTION: No. US20020187471A1el Telomerase

```

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/438,486
FILING DATE: 12-NOV-1999
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 536
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002931US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 67:
SEQUENCE CHARACTERISTICS:
LENGTH: 129 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..129
OTHER INFORMATION: /note= "TRT motifs from human"
US-09-438-486-67

Query Match          95.4%   Score 145:   DB 11:   Length 129:
Best Local Similarity 93.3%   Pred. No. 7.7e-14:
Matches 28:   Conservative 2;   Mismatches 0;   Indels

Qy      1  LFFYRKSVWSKLSGIRQHKLKRVQLRDVS 30
        |||
Db      32  LFFYRKSVWSKLSGIRQHKLKRVQLRELS 61

RESULT 10
US-10-053-758-67
Sequence 67, Application US/10053758
Publication No US20030032075A1
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
           Lingner, Joachim
           Nakamura, Toru
           Chapman, Karen B.
           Morin, Gregg B.
           Harley, Calvin
           Andrews, William H.
TITLE OF INVENTION: No. US20030032075A1el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California

```

COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/053,758
FILING DATE: 18-Jan-2002
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 67:
SEQUENCE CHARACTERISTICS:
LENGTH: 129 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..129
OTHER INFORMATION: /note= "TRT motifs from human"
SEQUENCE DESCRIPTION: SEQ ID NO: 67:
US-10-053-758-67
Query Match 95.4%; Score 145; DB 15; Length 129;
Best Local Similarity 93.3%; Pred. No. 7.7e-14;
Matches 28; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
Qy 1 LFFYKSVWSKLSIGIRQHLKRVQLRDVS 30
Db 32 LFFYKSVWSKLSIGIRQHLKRVQLRELS 61
RESULT 11
US-10-054-295-67
Sequence 67, Application US/10054295
Publication No. US20030044953A1
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: No. US20030044953A1el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/054,295
FILING DATE: 18-Jan-2002
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/854,050
FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 67:
SEQUENCE CHARACTERISTICS:
LENGTH: 129 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..129
OTHER INFORMATION: /note= "TRT motifs from human"
SEQUENCE DESCRIPTION: SEQ ID NO: 67:
US-10-054-295-67
Query Match 95.4%; Score 145; DB 15; Length 129;
Best Local Similarity 93.3%; Pred. No. 7.7e-14;
Matches 28; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
Qy 1 LFFYKSVWSKLSIGIRQHLKRVQLRDVS 30
Db 32 LFFYKSVWSKLSIGIRQHLKRVQLRELS 61
RESULT 12
US-10-054-611-67
Sequence 67, Application US/10054611
Publication No. US20030059787A1
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: No. US20030059787A1el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/054,611
FILING DATE: 18-Jan-2002
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/854,050
FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 67:
SEQUENCE CHARACTERISTICS:
LENGTH: 129 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..129
OTHER INFORMATION: /note= "TRT motifs from human"
SEQUENCE DESCRIPTION: SEQ ID NO: 67:
US-10-054-611-67

Query Match 95.4%; Score 145; DB 15; Length 129;
Best Local Similarity 93.3%; Pred. No. 7.7e-14;
Matches 28; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LFFYRKSVWSKLSIGIRQHLKRVQLRDVS 30
Db 32 LFFYRKSVWSKLSIGIRQHLKRVQLRELS 61

RESULT 13
US-10-044-692-13
Sequence 13, Application US/10044692
Publication No. US20030096344A1
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND
THERAPEUTIC METHODS
NUMBER OF SEQUENCES: 335
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/044,692

FILING DATE: 11-Jan-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/912,951
FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002600US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 129 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..129
OTHER INFORMATION: /note= "TRT motifs from human"
SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-10-044-692-13

Query Match 95.4%; Score 145; DB 15; Length 129;
Best Local Similarity 93.3%; Pred. No. 7.7e-14;
Matches 28; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LFFYRKSVWSKLSIGIRQHLKRVQLRDVS 30
Db 32 LFFYRKSVWSKLSIGIRQHLKRVQLRELS 61

RESULT 14
US-10-044-539-13
Sequence 13, Application US/10044539
Publication No. US20030100093A1
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND
THERAPEUTIC METHODS
NUMBER OF SEQUENCES: 335
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/044,692

APPLICATION NUMBER: US/10/044,539
FILING DATE: 11-Jan-2002
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/912,951
FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002600US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 129 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1-129
OTHER INFORMATION: /note= "TRT motifs from human"
SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-10-044-539-13

Query Match 95.4%; Score 145; DB 15; Length 129;
Best Local Similarity 93.3%; Pred. No. 7.7e-14;
Matches 28; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
Qy 1 LFFYRKSVWSKLSQIGIRQHLKRVQLRDVS 30
Db 32 LFFYRKSVWSKLSQIGIRQHLKRVQLRELS 61

RESULT 15

US-10-044-692-10
Sequence 10, Application US/10044692
Publication No. US20030096344A1

GENERAL INFORMATION:

APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
Andrews, William H.

TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND THERAPEUTIC METHODS

NUMBER OF SEQUENCES: 335

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/044,692
FILING DATE: 11-Jan-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/912,951
FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002600US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 259 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1-259
OTHER INFORMATION: /note= "protein encoded by clone 712562"
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-10-044-692-10

Query Match 95.4%; Score 145; DB 15; Length 259;
Best Local Similarity 93.3%; Pred. No. 1.6e-13;
Matches 28; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LFFYRKSVWSKLSQIGIRQHLKRVQLRDVS 30
Db 25 LFFYRKSVWSKLSQIGIRQHLKRVQLRELS 54

Search completed: November 12, 2003, 19:55:47
Job time : 23.9623 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 12, 2003, 19:43:04 ; Search time 11.6981 Seconds
(without alignments)
246.626 Million cell updates/sec

Title: US-08-854-050-116
Perfect score: 152
Sequence: 1 LFFYRKSVMSKLSIGIRQHLKRVQLRDVS 30
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: PIR 76.*
2: pir1.*
3: pir2.*
4: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	145	95.4	1132	2 T03844	telomerase catalyt
2	65	42.8	1132	2 T31107	telomerase reverse
3	52	34.2	894	1 SYBYMX	leucine-tRNA ligas
4	52	34.2	2479	1 MNWRA	nonstructural poly
5	51.5	33.9	609	2 A64332	modulation factor
6	50.5	33.2	526	2 S48988	hypothetical prote
7	50.5	33.2	596	2 S32802	apolipoprotein B -
8	50.5	33.2	4563	1 LPHUB	apolipoprotein B-1
9	50	32.9	181	2 T45581	hypothetical prote
10	50	32.9	222	2 H64321	hypothetical prote
11	49	32.2	608	2 AD2061	hypothetical prote
12	49	32.2	660	2 F85069	hypothetical prote
13	49	32.2	958	2 S64249	hypothetical prote
14	48	31.6	1117	2 T14891	telomerase (EC 2.7
15	47.5	31.2	965	2 S58393	PER309 protein - y
16	47	30.9	72	2 B83345	conserved hypotet
17	47	30.9	234	2 A13168	transcription regu
18	47	30.9	281	2 H71227	hypothetical prote
19	47	30.9	448	2 AE2590	two component resp
20	47	30.9	456	2 F97372	probable two-compo
21	47	30.9	465	2 T40697	probable tata bind
22	47	30.9	878	2 T17245	hypothetical prote
23	47	30.9	905	2 T39572	probable proteinas
24	46.5	30.6	160	2 AC0835	SsrA (tmRNA)-bindi
25	46.5	30.6	167	2 G82735	hypothetical prote
26	46.5	30.6	170	2 E82735	hypothetical prote
27	46.5	30.6	439	2 D64510	hypothetical prote
28	46.5	30.6	1552	2 G86344	T22111.2 protein -
29	46	30.3	157	1 B70044	conserved hypotet

30 46 30.3 214 2 C65002 hypothetical prote
31 46 30.3 306 2 A71332 probable integrase
32 46 30.3 319 2 AC2421 iron(III) dicitrat
33 46 30.3 363 2 S55035 peroxidase (EC 1.1
34 46 30.3 380 2 T16883 hypothetical prote
35 46 30.3 410 2 D90175 NADH dehydrogenase
36 46 30.3 458 2 S68358 Delta8 sphingolipi
37 46 30.3 505 2 T15159 hypothetical prote
38 46 30.3 699 2 AG0371 probable acetyltra
39 46 30.3 747 2 T39744 conserved hypotet
40 46 30.3 783 2 T11904 NADH2 dehydrogenas
41 46 30.3 818 2 A59433 KIAA0672 protein l
42 46 30.3 2554 1 TVFF7L kinase-related pro
43 45.5 29.9 387 2 F75064 hypothetical prote
44 45.5 29.9 888 2 S23065 ufo protein - mous
45 45.5 29.9 894 1 A41527 protein-tyrosine k

ALIGNMENTS

RESULT 1

T03844

telomerase catalytic chain - human

N;Alternate names: telomerase reverse transcriptase

C;Species: Homo sapiens (man)

C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 08-Oct-1999

C;Accession: T03844

R;Nakamura, T.M.; Morin, G.B.; Chapman, K.B.; Weinrich, S.L.; Andrews, W.H.; Lingner, J.

Science 277, 955-959, 1997

A;Title: Telomerase catalytic subunit homologs from fission yeast and human.

A;Reference number: Z15111; MUID:97400623; PMID:9252327

A;Accession: T03844

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-1132 <NA>

A;Cross-references: EMBL:AF015950; NID:g2330016; PIDN:AAC51672.1; PID:g2330017

C;Experimental source: kidney

C;Genetics:

A;Gene: TPT

A;Map position: 5p

Query Match 95.4%; Score 145; DB 2; Length 1132;
Best Local Similarity 93.3%; Pred. No. 6.5e-13;
Matches 28; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LFFYRKSVMSKLSIGIRQHLKRVQLRDVS 30

Db 573 LFFYRKSVMSKLSIGIRQHLKRVQLRELS 602

RESULT 2

T31107

telomerase reverse transcriptase - Oxytricha trifallax

C;Species: Oxytricha trifallax

C;Date: 02-Sep-2000 #sequence_revision 02-Sep-2000 #text_change 02-Sep-2000

C;Accession: T31107

R;Bryan, T.M.; Sperger, J.M.; Chapman, K.B.; Cech, T.R.

Proc. Natl. Acad. Sci. U.S.A. 95, 8479-8484, 1998

A;Title: Telomerase reverse transcriptase genes in Tetrahymena thermophila and Oxytrich

A;Reference number: Z20985; MUID:98337940; PMID:9671703

A;Accession: T31107

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-1132 <BRY>

A;Cross-references: EMBL:AF060230; NID:g3342795; PID:g3342796; PIDN:AAC39163.1

C;Genetics:

A;Gene: TERT

Query Match 42.8%; Score 65; DB 2; Length 1132;
Best Local Similarity 30.3%; Pred. No. 0.32;
Matches 10; Conservative 14; Mismatches 5; Indels 4; Gaps 1;

A;Residues: 2165-2179 <CH1>
 A;Cross-references: GB:M18036; NID:G178799; PIDN:AAA51754.1; PID:G178900
 A;Note: this mRNA includes the stop codon of the organ-specific mRNA for apo48
 A;Accession: A40133
 A;Molecule type: protein
 A;Residues: 51-75;101-110;129-139;158-174;197-207;276-287;298-304;306-314;526-532;538-553
 36;1486-1498;1537-1556;1563-1572;1601-1610;1647-1661;1697-1724;1770-1781;1859-1897;1968-
 A;Note: these fragments were derived from apo48
 R;Hardman, D.A.; Protter, A.A.; Schilling, J.W.; Kane, J.P.
 Biochem. Biophys. Res. Commun. 149, 1214-1219, 1987
 A;Title: Carboxyl terminal analysis of human B-48 protein confirms the novel mechanism of
 A;Reference number: A28002; MUID:88106542; PMID:3426612
 A;Accession: A28002
 A;Molecule type: mRNA
 A;Residues: 2129-2179, 2181-2235 <HA2>
 A;Cross-references: GB:M18471
 A;Experimental source: intestine
 A;Note: this mRNA from intestine includes a stop codon created by RNA editing in place of
 R;Mehrabian, M.; Schumaker, V.N.; Fareed, G.C.; West, R.; Johnson, D.F.; Kirchgessner, T.
 Nucleic Acids Res. 13, 6937-6953, 1985
 A;Title: Human apolipoprotein B: identification of cDNA clones and characterization of m
 A;Reference number: A24269; MUID:86041888; PMID:3903660
 A;Accession: A24269
 A;Molecule type: mRNA
 A;Residues: 3056-3159 <MEH>
 A;Cross-references: GB:X03045; NID:G28783; PIDN:CAA26850.1; PID:G929609
 R;Hospatankar, A.V.; Higuchi, K.; Law, S.W.; Meglin, N.; Brewer Jr., H.B.
 Biochem. Biophys. Res. Commun. 148, 279-285, 1987
 A;Title: Identification of a novel in-frame translational stop codon in human intestine
 A;Reference number: A29659; MUID:88049670; PMID:2445342
 A;Accession: A29659
 A;Molecule type: mRNA
 A;Residues: 2169-2179 <HOS>
 A;Note: the sequence shown represents the carboxyl end of apolipoprotein B-48
 A;Note: two RNA species, 14.1kb and 7.5kb in length, were isolated from the human intest
 ch encodes the 250K apoB-48, CAA encoding 2180-Gln is substituted by the stop codon TAA,
 R;Yang, C.; Kim, T.W.; Weng, S.; Lee, B.; Yang, M.; Gotto Jr., A.M.
 Proc. Natl. Acad. Sci. U.S.A. 87, 5523-5527, 1990
 A;Title: Isolation and characterization of sulphhydryl and disulfide peptides of human ap
 A;Reference number: A35783; MUID:90319144; PMID:2115173
 A;Accession: A35783
 A;Contents: disulfide bonds
 A;Molecule type: protein
 A;Residues: 28-41;76-97, 'I', 99-100;175-193;206-215;239-249;259-266;357-399;455-490;512-5
 A;Note: cysteines at positions 1112, 1422, 1505, 1662, 3761, 3917, and 4217 have free su
 R;LeBoeuf, R.C.; Miller, C.; Shively, J.E.; Schumaker, V.N.; Balla, M.A.; Lusis, A.J.
 FEBS Lett. 170, 105-108, 1984
 A;Title: Human apolipoprotein B: partial amino acid sequence.
 A;Reference number: A22006; MUID:84208786; PMID:6373369
 A;Accession: A22006
 A;Molecule type: protein
 A;Residues: 873-892, 'K', 894-896 <LE1>
 A;Accession: B22006
 A;Molecule type: protein
 A;Residues: 3113, 'L', 3115-3130, 'R', 3135-3136, 'R' <LE2>
 R;Blackhart, B.D.; Ludwig, E.M.; Blerotti, V.R.; Caiati, L.; Onasch, M.A.; Wallis, S.C.;
 J. Biol. Chem. 261, 15364-15367, 1986
 A;Title: Structure of the human apolipoprotein B gene.
 A;Reference number: A92564; MUID:87057153; PMID:2946672
 A;Contents: annotation; Gene structure
 R;Wagener, R.; Pfizner, R.; Stoffel, W.
 Biol. Chem. Hoppe-Seyler 368, 419-425, 1987
 A;Title: Studies on the organization of the human apolipoprotein B 100 gene.
 A;Reference number: A90715; MUID:87271140; PMID:2886136
 A;Contents: annotation; Gene structure
 R;Weisgraber, K.H.; Rall Jr., S.C.
 J. Biol. Chem. 262, 11097-11103, 1987
 A;Title: Human apolipoprotein B-100 heparin-binding sites.
 A;Reference number: A92605; MUID:87280197; PMID:3301850
 A;Contents: annotation; Heparin binding and disulfide bond
 R;Dashti, N.; Lee, D.M.; Mok, T.
 Biochem. Biophys. Res. Commun. 137, 493-499, 1986

A;Title: Apolipoprotein B is a calcium binding protein.
 A;Reference number: A90125; MUID:86242245; PMID:3087360
 A;Contents: annotation; calcium binding
 R;Carlsson, P.; Olofsson, S.O.; Bondjers, G.; Darnfors, C.; Wiklund, O.; Bjursell, G.
 Nucleic Acids Res. 13, 8813-8826, 1985
 A;Title: Molecular cloning of human apolipoprotein B cDNA.
 A;Reference number: 137178; MUID:86093680; PMID:3841204
 A;Accession: I37180
 Query Match 33.2%; Score 50.5; DB 1; Length 4563;
 Best Local Similarity 50.0%; Pred. No. 1.8e+02;
 Matches 12; Conservative 3; Mismatches 4; Indels 5; Gaps 1;
 QY 4 YRKSVMKQLQ-----SIGIROHLK 22
 |||||: |||||:
 Db 3680 YDKSLWDFLKLDVTTSGIRQHLR 3703
 RESULT 9
 T45581
 hypothetical protein F11C1.190 - Arabidopsis thaliana
 C;Species: Arabidopsis thaliana (mouse-ear cress)
 C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 04-Feb-2000
 R;Bargues, M.; Collado, M.C.; Navarro, P.; Terol, J.; Perez-Alonso, M.; Mewes, H.W.; Ma
 submitted to the Protein Sequence Database, December 1999
 A;Reference number: Z23007
 A;Accession: T45581
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-181 <BAR>
 A;Cross-references: EMBL:AL132976
 A;Experimental source: cultivar Columbia; BAC clone F11C1
 C;Genetics:
 A;Map position: 3
 A;Introns: 9/1; 148/1
 A;Note: F11C1.190
 Query Match 32.9%; Score 50; DB 2; Length 181;
 Best Local Similarity 47.4%; Pred. No. 7.5;
 Matches 9; Conservative 3; Mismatches 7; Indels 0; Gaps 0;
 QY 5 RKSVMKQLSIGIROHLKR 23
 |||||: |||||:
 Db 51 REEAWSKRQDISGRHRLR 69
 RESULT 10
 H64321
 hypothetical protein MJ0175 - Methanococcus jannaschii
 C;Species: Methanococcus jannaschii
 C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
 C;Accession: H64321
 R;Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake,
 ; Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.
 rson, J.D.; Sadow, P.W.; Hama, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
 Science 273, 1058-1073, 1996
 A;Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese,
 A;Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii
 A;Reference number: A64300; MUID:96337999; PMID:8688087
 A;Accession: H64321
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-222 <BUL>
 A;Cross-references: GB:U67474; GB:L77117; NID:G1590921; PIDN:AAB98160.1; PID:G1590927;
 C;Genetics:
 A;Map position: REV178140-177472
 A;Start codon: GTG
 Query Match 32.9%; Score 50; DB 2; Length 222;
 Best Local Similarity 53.3%; Pred. No. 9.2;
 Matches 8; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

C;Accession: S64249
R;Fartmann, B.; Kramer, B.; Kramer, W.
submitted to the Protein Sequence Database, May 1996
A;Reference number: S64248

A: Accession: D01040
A: Molecule type: DNA

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 12, 2003, 19:41:59 ; Search time 6.22642 Seconds
(without alignments)
226.583 Million cell updates/sec

Title: US-08-854-050-116
Perfect score: 152
Sequence: 1 LPFYKSVMSKLSIGIRQLKRVQLRDVS 30

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	145	95.4	1132	1	TERT_HUMAN
2	136	89.5	1122	1	TERT_MOUSE
3	65	42.8	1132	1	TERT_OXYTR
4	55	36.2	1011	1	HDA9_HUMAN
5	52	34.2	633	1	PAN2_HUMAN
6	52	34.2	894	1	SYLM_SACDO
7	52	34.2	2479	1	POLN_RRVN
8	51.5	33.9	609	1	VA58_METJA
9	50.5	33.2	526	1	YH07_YEAST
10	50.5	33.2	4563	1	APB_HUMAN
11	50	32.9	222	1	Y175_METJA
12	50	32.9	1031	1	TERT_EUPAE
13	49	32.2	958	1	YGX7_YEAST
14	48	31.6	1117	1	TERT_TETH
15	48	31.6	1122	1	HDA5_HUMAN
16	47.5	31.2	160	1	SSRP_PASMU
17	47.5	31.2	965	1	PT09_YEAST
18	47	30.9	206	1	CU32_HUMAN
19	47	30.9	281	1	ALF1_PYRHO
20	47	30.9	938	1	HDA7_MOUSE
21	47	30.9	932	1	HDA7_HUMAN
22	46.5	30.6	159	1	SSRP_SALTJ
23	46.5	30.6	439	1	YZ04_METJA
24	46	30.3	214	1	YFCF_ECOLI
25	46	30.3	783	1	NOO3_TETH
26	46	30.3	1080	1	HDA4_CHICK
27	46	30.3	1084	1	HDA4_HUMAN
28	46	30.3	1113	1	HDA5_MOUSE
29	46	30.3	2554	1	7LES_DROME
30	45.5	29.9	887	1	UFO_HUMAN
31	45.5	29.9	888	1	UFO_MOUSE
32	45.5	29.9	1547	1	RRPO_PMW
33	45	29.6	488	1	SYP_BORBU

ALIGNMENTS

RESULT 1

TERT_HUMAN STANDARD; PRT; 1132 AA.
 ID TERT_HUMAN STANDARD; PRT; 1132 AA.
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Telomerase reverse transcriptase (EC 2.7.7.-) (Telomerase catalytic subunit) (HEST2).
 DE TERT OR TRT OR EST2 OR TCS1.
 GN Homo sapiens (Human).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OC NCBI_TaxID=9606;
 OX [1]
 RN SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RX MEDLINE=97400623; PubMed=9252327;
 RA Nakamura T.M., Morin G.B., Chapman K.B., Weinrich S.L., Andrews W.H., Lingner J., Harley C.B., Cech T.R.;
 RA "Telomerase catalytic subunit homologs from fission yeast and human."; Science 277:955-959(1997).
 RL [2]
 RN SEQUENCE FROM N.A.
 RX MEDLINE=97433088; PubMed=9288757;
 RA Meyerson M., Counter C.M., Eaton E.N., Ellison L.W., Steiner P., Caddle S.D., Ziaugra L., Beijersbergen R.L., Davidoff M.J., Liu Q., Bacchetti S., Haber D.A., Weinberg R.A.;
 RA "hEST2, the putative human telomerase catalytic subunit gene, is up-regulated in tumor cells and during immortalization."; Cell 90:785-795(1997).
 RL [3]
 RN SEQUENCE FROM N.A.
 RX MEDLINE=99267414; PubMed=10333526;
 RA Wick M., Zubov D., Hagen G.;
 RA "Genomic organization and promoter characterization of the gene encoding the human telomerase reverse transcriptase (hTERT)."; Gene 232:97-106(1999).
 RL [4]
 RN SEQUENCE FROM N.A.
 RX Londono-Vallejo J.A.;
 RA "Sequence of a BAC carrying the entire hTERT gene."; Submitted (Oct-2001) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: TELOMERASE IS A RIBONUCLEOPROTEIN ENZYME ESSENTIAL FOR THE REPLICATION OF CHROMOSOME TERMINI IN MOST EUKARYOTES. IT ELONGATES TELOMERES. IT IS A REVERSE TRANSCRIPTASE THAT ADDS SIMPLE SEQUENCE REPEATS TO CHROMOSOME ENDS BY COPYING A TEMPLATE SEQUENCE WITHIN THE RNA COMPONENT OF THE ENZYME.
 CC -!- SUBUNIT: Interacts with PINK1.
 CC -!- SUBCELLULAR LOCATION: Nuclear.
 CC -!- DISEASE: ACTIVATION OF TELOMERASE HAS BEEN IMPLICATED IN CELL IMMORTALIZATION AND CANCER CELL PATHOGENESIS.
 CC -!- SIMILARITY: BELONGS TO THE REVERSE TRANSCRIPTASE FAMILY.
 CC TELOMERASE SUBFAMILY.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration

34 45 29.6 620 1 SYT_FUSNN
 35 45 29.6 646 1 MU18_HUMAN
 36 44.5 29.3 159 1 SSRP_ECOLI
 37 44.5 29.3 161 1 SSRP_HAEIN
 38 44.5 29.3 625 1 HTPG_BUCAP
 39 44.5 29.3 626 1 HTPG_BUCBP
 40 44.5 29.3 636 1 PAPB_HUMAN
 41 44 28.9 317 1 NIR3_RHILP
 42 44 28.9 358 1 PE12_ARATH
 43 44 28.9 415 1 CSCB_ECOLI
 44 44 28.9 450 1 NH14_CAEEL
 45 44 28.9 492 1 NHR4_CAEEL

Q8rf66 fusobacteri
 P43121 homo sapien
 P32052 escherichia
 P44967 haemophilus
 O8k981 buchnera ap
 Q89a93 buchnera ap
 Q9nrj5 homo sapien
 P41504 rhizobium l
 Q96520 arabidopsis
 P30000 escherichia
 O02151 caenorhabdi
 O45436 caenorhabdi

CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).

CC -----
 CC EMBL; AF015950; AAC51672.1; -;
 CC EMBL; AF018167; AAC51724.1; -;
 CC EMBL; AF128894; AAD30037.1; -;
 CC EMBL; AF128893; AAD30037.1; JOINED.
 CC EMBL; AY007685; AAG32289.1; -;
 CC PIR; T03844; T03844.
 CC Genew; HGNC:11730; TERT.
 CC MIM; 187270; -;

CC GO; GO:000596; C:telomere; TAS.
 CC GO; GO:0003721; F:telomeric template RNA reverse transcriptase. .; TAS.
 CC GO; GO:0007003; P:telomeric binding; TAS.
 CC InterPro; IPR000477; RVTse.

CC InterPro; IPR000477; RVTse.
 CC Pfam; PF00078; RVT_1
 CC PRINTS; PR01365; TELOMERASERT.
 CC Transferase; RNA-directed DNA polymerase; Telomere; Nuclear protein;
 CC DNA-binding.
 CC FT CONFLICT 516 516 D -> G (IN REF. 2).
 CC SEQUENCE 1132 AA; 126996 MW; 94E35469C4CA33A0 CRC64;

Query Match 95.4%; Score 145; DB 1; Length 1132;
 Best Local Similarity 93.3%; Pred. No. 5.9e-14;
 Matches 28; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LFFYRKSVWSKLQSIGIRQHLKRVQLRDVS 30
 |||||
 DB 573 LFFYRKSVWSKLQSIGIRQHLKRVQLREL 602

RESULT 2

TERT_MOUSE
 ID TERT_MOUSE STANDARD; PRT; 1122 AA.
 AC 070372; G35432;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Telomerase reverse transcriptase (EC 2.7.7.-) (Telomerase catalytic
 DE subunit).
 GN TERT.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98241176; PubMed=9582020;
 RA Greenberg R.A., Allsopp R.C., Chin L., Morin G.B., Depinho R.A.;
 RT "Expression of mouse telomerase reverse transcriptase during
 RT development, differentiation and proliferation.";
 RL Oncogene 16:1723-1730(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98393668; PubMed=9724727;
 RA Martin-Rivera L., Herrera E., Albar J.P., Blasco M.A.;
 RT "Expression of mouse telomerase catalytic subunit in embryos and
 RT adult tissues.";
 RL Proc. Natl. Acad. Sci. U.S.A. 95:10471-10476(1998).
 RN [3]
 RP SEQUENCE OF 550-616 FROM N.A.
 RA Driesi R., Cleveland J.L.;
 RT "Partial sequence of Mus musculus telomerase catalytic subunit
 RT homolog.";
 RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: TELOMERASE IS A RIBONUCLEOPROTEIN ENZYME ESSENTIAL FOR
 CC THE REPLICATION OF CHROMOSOME TERMINI IN MOST EUKARYOTES. IT
 CC ELONGATES TELOMERES. IT IS A REVERSE TRANSCRIPTASE THAT ADDS

CC SIMPLE SEQUENCE REPEATS TO CHROMOSOME ENDS BY COPYING A TEMPLATE
 CC SEQUENCE WITHIN THE RNA COMPONENT OF THE ENZYME.
 CC -!- SUBUNIT: Interacts with PINK1 (By similarity).
 CC -!- SUBCELLULAR LOCATION: Nuclear.
 CC -!- SIMILARITY: BELONGS TO THE REVERSE TRANSCRIPTASE FAMILY.
 CC TELOMERASE SUBFAMILY.

CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).

CC EMBL; AF051911; AAC09323.1; -;
 CC EMBL; AF073311; AAC34821.1; -;
 CC EMBL; AF029235; AAB84200.1; -;
 CC MGD; MGI:1202709; TERT.
 CC InterPro; IPR000477; RVTse.
 CC InterPro; IPR003545; Telomerase_RT.
 CC Pfam; PF00078; RVT_1
 CC PRINTS; PR01365; TELOMERASERT.
 CC Transferase; RNA-directed DNA polymerase; Telomere; Nuclear protein;
 CC DNA-binding.
 CC KW CONFLICT 553 553 I -> V (IN REF. 3).
 CC FT CONFLICT 1122 AA; 127977 MW; P85266905DD6558C CRC64;
 CC SEQUENCE

Query Match 89.5%; Score 136; DB 1; Length 1122;
 Best Local Similarity 83.3%; Pred. No. 1.4e-12;
 Matches 25; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 LFFYRKSVWSKLQSIGIRQHLKRVQLRDVS 30
 |||||
 DB 563 LFFYRKSVWSKLQSIGIRQHLKRVQLREL 592

RESULT 3

TERT_OXYTR
 ID TERT_OXYTR STANDARD; PRT; 1132 AA.
 AC 076332;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Telomerase reverse transcriptase (EC 2.7.7.-) (Telomerase catalytic
 DE subunit) (Telomerase subunit P133).
 GN TERT.
 OS Oxytricha trifallax.
 OC Eukaryota; Alveolata; Ciliophora; Spirotrichea; Stichotrichia;
 OC Stichotrichida; Oxytrichidae; Oxytricha.
 OX NCBI_TaxID=5946;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98337940; PubMed=9671703;
 RA Bryan T.M., Sperger J.M., Chapman K.B., Cech T.R.;
 RT "Telomerase reverse transcriptase genes identified in Tetrahymena
 RT thermophila and Oxytricha trifallax.";
 RL Proc. Natl. Acad. Sci. U.S.A. 95:8479-8484(1998).
 CC -!- FUNCTION: TELOMERASE IS A RIBONUCLEOPROTEIN ENZYME ESSENTIAL FOR
 CC THE REPLICATION OF CHROMOSOME TERMINI IN MOST EUKARYOTES. IT
 CC ELONGATES TELOMERES. IT IS A REVERSE TRANSCRIPTASE THAT ADDS
 CC SIMPLE SEQUENCE REPEATS TO CHROMOSOME ENDS BY COPYING A TEMPLATE
 CC SEQUENCE WITHIN THE RNA COMPONENT OF THE ENZYME.
 CC -!- SUBCELLULAR LOCATION: Nuclear.
 CC -!- SIMILARITY: BELONGS TO THE REVERSE TRANSCRIPTASE FAMILY.
 CC TELOMERASE SUBFAMILY.

CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).

"Mammalian pannexin family homologous to invertebrate gap-junction proteins are differentially expressed in nervous tissue."; Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.

(2) SEQUENCE FROM N. A.

MEDLINE=20057165; PubMed=10591208; Dunham I., Hunt A.R., Collins J.E., Bruskiewich R., Beare D.M., Clamp M., Smink L.R., Ainscough R., Almeida J.P., Babage A.K., Baggett C., Bailey J., Barlow K.F., Bates K.N., Beagley O.P., Bird C.P., Blakey S.E., Bridgman A.M., Buck D., Burgess J., Burrill W.D., Burton J., Carder C., Carter N.P., Chen Y., Clark G., Clegg S.M., Cobley V.E., Cole C.G., Collier R.E., Connor R., Conroy D., Corby N.R., Coville G.J., Cox A.V., Davis J., Dawson E., Dhani P.D., Dockree C., Dodsworth S.J., Durbin R.M., Ellington A.G., Evans K.L., Fey J.M., Fleming K., French L., Garner A.A., Gilbert J.G.R., Goward M.E., Grahham D.W., Griffiths M.N.D., Hall C., Hall R.E., Hall-Tamlyn G., Heathcote R.V., Ho S., Holmes S., Hunt S.E., Jones M.C., Kershaw J., Kimberley A.M., King A., Laird G.K., Langford C.F., Leversha M.A., Lloyd C., Lloyd D.M., Martyn I.D., Mashreghi-Mohammadi M., Matthews L.H., McCann O.T., Mcclay J., McLaren S., McMurray A.A., Milne S.A., Mortimore B.J., Odell C.N., Pavitt R., Pearce A.V., Pearson D., Phillimore B.J.C.T., Phillips S.E., Plumb R.K., Ramsay H., Ramsey Y., Rogers L., Ross M.T., Scott C.E., Sehra H.K., Skuce C.D., Smalley S., Smith M.L., Soderlund C., Spragon I., Steward C.A., Sulton J.F., Swann R.M., Vaudin M., Wall M., Wallis J.W., Whiteley M.N., Willey D.L., Williams L., Williams S.A., Williamson H., Wilmer T.E., Wilming L., Wright C.L., Hubbard T., Bentley D.R., Beck S., Rogers J., Shimizu N., Minoshima S., Kawasaki K., Sasaki T., Asakawa S., Kudoh J., Shintani A., Shibuya K., Yoshizaki Y., Aoki N., Matsuyama S., Roe B.A., Chen F., Chu L., Crabtree J., Deschamps S., Do A., Do T., Dorman A., Fang F., Fu Y., Hu P., Hua A., Kenton S., Lai H., Lao H.I., Lewis J., Lewis S., Lin S.-P., Loh P., Malaj E., Nguyen T., Pan H., Phan S., Qi S., Qian Y., Ray L., Ren Q., Shaull S., Sloan D., Song L., Wang Q., Wang Y., Wang Z., White J., Willingham D., Wu H., Yao Z., Zhan M., Zhang G., Chlesoe S., Murray J., Miller N., Minx P., Fulton R., Johnson D., Bemis G., Bentley D., Bradehaw H., Bourne S., Cordes M., Du Z., Fulton L., Goela D., Graves T., Hawkins J., Hinds K., Kemp K., Latreille P., Layman D., Ozersky P., Rohlfing T., Scheet P., Walker C., Wamsley A., Wohlmann P., Pepin K., Nelson J., Korf I., Bedell J.A., Hillier L., Mardis E., Waterston R., Wilson R., Emanuel B.S., Shaikh T., Kurahashi H., Saitta S., Budarf M.L., Mcdermid H.E., Johnson A., Wong A.C.C., Morrow B.E., Edelmann L., Kim U.J., Shizuya H., Simon M.I., Dumanski J.P., Peyraud M., Kedra D., Seroussi E., Franssion I., Tapia I., Bruder C.E., O'Brien K.S., Wilkinson P., Bodentetch A., Hartman K., Hu X., Khan A.S., Lane L., Tiliahun Y., Wright H.; "The DNA sequence of human chromosome 22";

Nature 402:489-495 (1999).

-!- FUNCTION: STRUCTURAL COMPONENT OF THE GAP JUNCTIONS

-!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).

-!- ALTERNATIVE PRODUCTS:

Event=Alternative splicing; Named isoforms=2;

Name=1:

name=1)
IsoId=096RD6-1: Sequence=Displayed:

Name=2: 1001a-g-00100 1) 00400000-00000000

name=z,
IsoId=096RD6-2: Sequence=VSP 002677:

IS01d-Q36KD0-2, sequence=VSE_V02077,
-!- STMILABILITY: Belongs to the innixin family.

--- SIMPLER!!!: BELONGS TO THE IMLEXIN FAMILY. ---

This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation at the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See [http://www.isb-sib.ch/](http://www.isb-sib.ch/announce/) or send an email to license@sib-sib.ch).

[illegible]

EMBL; AF398510; AAK91715.1;

EMBL: AF398511; AAK91716.1;

EMBL: AL022328; CAB63042.1;

Genew: HGNC:8600: PAX2;

Gap junction: Transmembrane

cap junction, transmission		
TRANSMEM	38	60

MEMORANDUM

```

FT TRANSMEM      114      136      POTENTIAL.
FT TRANSMEM      217      239      POTENTIAL.
FT TRANSMEM      283      305      POTENTIAL.
FT VARSPLIC       1      124      Missing (in isoform 2) .
FT /FTId=VSP_002677.
SQ SEQUENCE      633 AA;   69478 MW;   C89CF833E0251D58 CRC64;

Query Match          34.2%; Score 52; DB 1; Length 633;
Best Local Similarity 38.2%; Pred.No. 4.2;
Matches 13; Conservative 9; Mismatches 4; Gaps 2;

QY 1 LFFYRKS--VWSKLSIGI--RHHLKRVQLRDVS 30
    ||:|||::||::|||::|||::|||::|||::
DB 302 LFIFRKSNFIDKLHKVGIKTRQWRRSQFC DIN 335

RESULT 6
SYLM SACDO
ID SYLM SACDO STANDARD; PRT; 894 AA.
AC P13503;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Leucyl-tRNA synthetase, mitochondrial precursor (EC 6.1.1.4)
DE (Leucine--tRNA ligase) (Leurs).
GN NAM2.
OS Saccharomyces douglasii (Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=46617;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HM300;
RX MEDLINE=89039717; PubMed=3054483;
RA Herbert C.J., Dujardin G., Labouesse M., Slonimski P.P.;
RT "Divergence of the mitochondrial leucyl tRNA synthetase genes in two
RT closely related yeasts Saccharomyces cerevisiae and Saccharomyces
RT douglasii: a paradigm of incipient evolution.";
RL Mol. Gen. Genet. 213:297-309(1988).
RN [2]
RP FUNCTION.
RX MEDLINE=88211560; PubMed=3284745;
RA Herbert C.J., Labouesse M., Dujardin G., Slonimski P.P.;
RT "The NAM2 proteins from S. cerevisiae and S. douglasii are
RT mitochondrial leucyl-tRNA synthetases, and are involved in mRNA
RT splicing.";
RL EMBO J. 7:473-483(1988).
CC -|- CATALYTIC ACTIVITY: ATP + L-leucine + tRNA(Leu) = AMP +
CC diphosphate + L-leucyl-tRNA(Leu).
CC -|- SUBCELLULAR LOCATION: Mitochondrial matrix.
CC -|- SIMILARITY: Belongs to class-I aminoacyl-tRNA synthetase family.
-----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
-----
CC EMBL; X12864; CAA31343.1; --
DR InterPro; IPR002302; Leu-tRNA-syntla.
DR InterPro; IPR002300; tRNA-synt_1a.
DR InterPro; IPR001412; tRNA-synt_1.
DR Pfam; PF00133; tRNA-synt_1; 1.
DR PRINTS; PR00985; TRNASYNTHLEU.
DR TIGRFAMs; TIGR00396; leus_bact; 1.
DR PROSITE; PS00178; AA_TRNA_LIGASE_I; 1.
KW Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
KW Mitochondrion; Transit peptide.
FT CHAIN           1 9 MITOCHONDRION (BY SIMILARITY) .
FT SITE            10 894 LEUCYL-TRNA SYNTHETASE.
FT SITE            56 66 "HIGH" REGION.

```

```

FT SITE          646   650      "KMSKS" REGION.
FT BINDING      649   649      ATP (BY SIMILARITY).
SQ SEQUENCE    894 AA; 102193 MW; AE42C20193DDF107 CRC64;

Query Match      34.2%; Score 52; DB 1; Length 894;
Best Local Similarity 41.7%; Pred. No. 6.1;
Matches 10; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

QY 5 RKSWSKLSQIGIRQLKRVQLRD 28
Db 421 RKSIMGLKSLKSLKNIIRVRD 444

RESULT 7
POLN_RRVN      STANDARD; PRT; 2479 AA.
ID POLN_RRVN
AC P13887;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Nonstructural polyprotein [Contains: Nonstructural protein NSP1;
DE Nonstructural protein NSP2; Nonstructural protein NSP3; Nonstructural
DE protein NSP4].
OS Ross river virus (strain NB5092) (RRV).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Togaviridae;
OC Alphavirus.
OX NCBI_TaxID=11031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88179556; PubMed=2833022;
RA Faragher S.G., Meek A.D.J., Rice C.M., Dalgarno L.;
RT "Genome sequences of a mouse-avirulent and a mouse-virulent strain of
RT Ross River virus.";
RL Virology 163:509-526(1988).
CC -!- FUNCTION: NSP2 MAY BE INVOLVED IN RNA BINDING DURING REPLICATION.
CC -!- PTM: SPECIFIC ENZYMAIC CLEAVAGES IN VIVO YIELD MATURE PROTEINS.
CC -!- MISCELLANEOUS: READTHROUGH OF THE TERMINATOR CODON UGA OCCURS
CC BETWEEN THE CODONS FOR 1862-PHE AND 1863-LEU.
-----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
-----
CC EMBL; M20162; AAA96329.1; ALT_SEQ.
CC PIR; A28605; MNWVRA.
CC MEROPS; C09.001; -.
CC InterPro; IPR002589; Alpp.
CC InterPro; IPR002620; Peptidase_C9.
CC InterPro; IPR001788; RNA_dep_RNAPol2.
CC InterPro; IPR007095; RNA_pol_DS_PS.
CC InterPro; IPR007094; RNA_pol_PSVir.
CC InterPro; IPR002588; V_methyltransf.
CC InterPro; IPR000606; Viral_helicase1.
CC Pfam; PF01661; Alpp; 1.
CC Pfam; PF01707; Peptidase_C9; 1.
CC Pfam; PF00978; RNA_dep_RNAPol2; 1.
CC Pfam; PF01443; Viral_helicase1; 1.
CC Pfam; PF01660; Vmethyltransf; 1.
CC SMART; SM00506; Alpp; 1.
CC Polyprotein; Nonstructural protein; RNA-binding; Helicase.
FT CHAIN 1 533 NONSTRUCTURAL PROTEIN NSP1.
FT CHAIN 534 1331 NONSTRUCTURAL PROTEIN NSP2.
FT CHAIN 1332 1868 NONSTRUCTURAL PROTEIN NSP3.
FT CHAIN 1869 2479 NONSTRUCTURAL PROTEIN NSP4.
SQ SEQUENCE 2479 AA; 276436 MW; E306EBAFDFF02CAB CRC64;

Query Match      34.2%; Score 52; DB 1; Length 2479;
Best Local Similarity 55.0%; Pred. No. 18;
Matches 11; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

```

```

QY 3 FYRKSVSKLSQIGIRQLK 22
Db 448 FVPSLWSSSLSIGIRQRIK 467

RESULT 8
YA58_METJA      STANDARD; PRT; 609 AA.
ID YA58_METJA
AC Q58458;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein MJ1058.
DE MJ1058.
OS Methanococcus jannaschii.
OC Archaea; Euryarchaeota; Methanococci; Methanococcales;
OC Methanocaldococcaceae; Methanocaldococcus.
OX NCBI_TaxID=2190;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
RX MEDLINE=96337999; PubMed=8688087;
RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
RA Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,
RA Kervlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
RA Scott J.L., Geoghegan N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
RA Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
RT "Complete genome sequence of the methanogenic archaeon, Methanococcus
RT jannaschii.";
RL Science 273:1058-1073(1996).
CC -!- SIMILARITY: BELONGS TO THE NODU / CMCH FAMILY.
-----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
-----
CC EMBL; U67549; AAB99062.1; -.
CC PIR; A64432; A64432.
CC TIGR; MJ1058; -.
CC InterPro; IPR003696; Carbtransf.
CC Pfam; PF02543; CMCH_Nodu; 1.
CC KW Hypothetical protein; Transferase; Complete proteome.
CC SEQUENCE 609 AA; 71733 MW; C91899CF01CB84EA CRC64;

Query Match      33.9%; Score 51.5; DB 1; Length 609;
Best Local Similarity 35.5%; Pred. No. 4.8;
Matches 11; Conservative 11; Mismatches 8; Indels 1; Gaps 1;

QY 1 LFFYR-KSVWSKLSQIGIRQLKRVQLRDVS 30
Db 129 LLFKRFRNNYNNKLNLAIKRELKIKPRKQVS 159

RESULT 9
YH07_YEAST      STANDARD; PRT; 526 AA.
ID YH07_YEAST
AC P38850;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Hypothetical 60.5 kDa protein in SKN7-TWT1 intergenic region.
DE YHR207C.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.

```

```

OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C / AB972;
RA MEDLINE=94378003; PubMed=8091229;
RA Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Dover J.,
RA Du Z., Favello A., Fulton L., Gattung S., Geisel C., Kirsten J.,
RA Kucaba T., Hillier L., Jier M., Johnston L., Langston Y.,
RA Latreille P., Louis E.J., Macri C., Mardis E., Menezes S., Mouser L.,
RA Nham M., Rifkin L., Riles L., St Peter H., Trevaakis E., Vaughan K.,
RA Vagnati D., Wilcox L., Wohlman P., Waterston R., Wilson R.,
RA "Complete nucleotide sequence of Saccharomyces cerevisiae chromosome
VIII.";
RT Science 265:2077-2082(1994).
RL Science 265:2077-2082(1994).
CC -1- SIMILARITY: Contains 1 SET domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U00029; AAB69736.1; --
DR PIR; S48988; S48988.
DR SGD; S0001250; YHR207C.
DR InterPro; IPR001214; SET.
DR Pfam; PF00856; SET; 2.
DR SMART; SM00317; SET; 1.
DR PROSITE; PS00280; SET; 1.
KW Hypothetical protein.
FT DOMAIN 111 407 SET.
SQ SEQUENCE 526 AA; 60547 MW; 1113CB9C5223DC7D CRC64;
Query Match 33.2%; Score 50.5; DB 1; Length 526;
Best Local Similarity 48.0%; Pred. No. 5.8;
Matches 12; Conservative 3; Mismatches 7; Indels 3; Gaps 1;
Qy 6 KSVMSKLSQIGIRHKLKRVLDVDS 30
Db 260 KEQWOKLASISQRE---RIKLKRDAS 281
RESULT 10
APB HUMAN
ID APB HUMAN STANDARD; PRT; 4563 AA.
AC P04114; Q00502; Q13787;
DT 01-NOV-1986 (Rel. 03, Created)
DT 01-NOV-1986 (Rel. 03, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Apolipoprotein B-100 precursor (Apo B-100) [Contains: Apolipoprotein
DE B-48 (Apo B-48)].
GN APOB.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=87016385; PubMed=3763409;
RA Knott T.C., Wallis S.C., Powell L.M., Pease R.J., Lusis A.J.,
RA Blackhart B., McCarthy B.J., Mahley R.W., Levy-Wilson B., Scott J.;
RT "Complete cDNA and derived protein sequence of human apolipoprotein
RT B-100.";
RT Nucleic Acids Res. 14:7501-7503(1986).
RN [2]
RP SEQUENCE FROM N.A.
RC MEDLINE=88003974; PubMed=3652907;
RA Ludwig E.H., Blackhart B.D., Pierotti V.R., Caiati L., Fortier C.,
RA Knott T., Scott J., Mahley R.W., Levy-Wilson B., McCarthy B.J.;
RT "DNA sequence of the human apolipoprotein B gene.";

```

```

RL DNA 6:363-372 (1987).
RN [3]
RP SEQUENCE FROM N.A.
RC MEDLINE=87008488; PubMed=3759943;
RA Chen S.-H., Yang C.-Y., Chen P.-F., Setzer D., Tanimura M., Li W.-H.,
RA Gotto A.M. Jr., Chan L.;
RT "The complete cDNA and amino acid sequence of human apolipoprotein
RT B-100.";
RL J. Biol. Chem. 261:12918-12921(1986).
RN [4]
RP SEQUENCE FROM N.A.
RC MEDLINE=87041416; PubMed=3464946;
RA Law S.W., Grant S.M., Higuchi K., Hospattankar A.V., Lackner K.J.,
RA Lee N., Brewer H.B. Jr.;
RT "Human liver apolipoprotein B-100 cDNA: complete nucleic acid and
RT derived amino acid sequence.";
RL Proc. Natl. Acad. Sci. U.S.A. 83:8142-8146(1986).
RN [5]
RP SEQUENCE FROM N.A.
RC MEDLINE=87161758; PubMed=3030729;
RA Cladaras C., Hadzopoulou-Cladaras M., Nolte R.T., Atkinson D.,
RA Zannis V.I.;
RT "The complete sequence and structural analysis of human
RT apolipoprotein B-100: relationship between apoB-100 and apoB-48
RT forms.";
RL EMBO J. 5:3495-3507(1986).
RN [6]
RP SEQUENCE OF 709-906 FROM N.A.
RC MEDLINE=85270450; PubMed=3860836;
RA Deeb S.S., Motulsky A.G., Albers J.J.;
RT "A partial cDNA clone for human apolipoprotein B.";
RL Proc. Natl. Acad. Sci. U.S.A. 82:4983-4986(1985).
RN [7]
RP SEQUENCE OF 3056-3159 FROM N.A.
RC MEDLINE=86041888; PubMed=3903660;
RA Mehrabian M., Schumaker V.N., Fareed G.C., West R., Johnson D.F.,
RA Kirchgessner T.G., Lin H.-C., Wang X., Ma Y., Mendiaz E., Lusis A.J.;
RT "Human apolipoprotein B: identification of cDNA clones and
RT characterization of mRNA.";
RL Nucleic Acids Res. 13:6937-6953(1985).
RN [8]
RP SEQUENCE OF 1937-2018 AND 3811-4334 FROM N.A.
RC MEDLINE=86093680; PubMed=3841204;
RA Carlsson P., Olofsson S.O., Bondjers G., Darnfors C., Wiklund O.,
RA Bjursell G.;
RT "Molecular cloning of human apolipoprotein B cDNA.";
RL Nucleic Acids Res. 13:8813-8826(1985).
RN [9]
RP SEQUENCE OF 3109-4563 FROM N.A.
RC MEDLINE=85300528; PubMed=2994225;
RA Knott T.J., Rall S.C. Jr., Innerarity T.L., Jacobson S.F.,
RA Urdea M.S., Levy-Wilson B., Powell L.M., Pease R.J., Eddy R.,
RA Nakai H., Byers M., Priestley L.M., Robertson E., Rall L.B.,
RA Batsholtz C., Shows T.B., Mahley R.W., Scott J.;
RT "Human apolipoprotein B: structure of carboxyl-terminal domains,
RT sites of gene expression, and chromosomal localization.";
RL Science 230:37-43(1985).
RN [10]
RP SEQUENCE OF 1-291 FROM N.A.
RC MEDLINE=86149325; PubMed=3513177;
RA Protter A.A., Hardman D.A., Schilling J.W., Miller J., Appleby V.,
RA Chen G.C., Kirsher S.W., McEnroe G., Kane J.P.;
RT "Isolation of a cDNA clone encoding the amino-terminal region of
RT human apolipoprotein B.";
RL Proc. Natl. Acad. Sci. U.S.A. 83:1467-1471(1986).
RN [11]
RP SEQUENCE OF 1-1670 FROM N.A.
RC MEDLINE=86287319; PubMed=3461454;
RA Protter A.A., Hardman D.A., Sato K.Y., Schilling J.W.,
RA Yamanaka M., Hori Y.J., Hjerild K.A., Chen G.C., Kane J.P.;
RT "Analysis of cDNA clones encoding the entire B-26 region of human
RT apolipoprotein B.";
RL Proc. Natl. Acad. Sci. U.S.A. 83:5678-5682(1986).

```

RN PARTIAL SEQUENCE, AND IDENTIFICATION OF APO-B48.
 RX MEDLINE=88018019; PubMed=3659919;
 RA Chen S.-H., Habib G., Yang C.-H., Gu Z.-W., Lee B.R., Weng S.-H.,
 RA Silberman S.R., Cai S.-J., Deslypere J.P., Rosseneu M.,
 RA Gotto A.M. Jr., Li W.-H., Chan L.,
 RT "Apolipoprotein B-48 is the product of a messenger RNA with an organ-
 RT specific in-frame stop codon."
 RL Science 238:363-366(1997).
 RN [12]
 RN DOMAINS.
 RP MEDLINE=87039351; PubMed=3773997;
 RA Knott T.C., Pease R.J., Fowell L.M., Wallis S.C., Rall S.C. Jr.,
 RA Innerarity F.L., Blackhart B., Taylor W.R., Marcel Y., Milne R.,
 RA Johnson D., Fuller M., Lusis A.J., McCarthy B.J., Mahley R.W.,
 RA Levy-Wilson B., Scott J.,
 RT "Complete protein sequence and identification of structural domains
 RT of human apolipoprotein B."
 RL Nature 323:734-738(1986).
 RN [14]
 RN DOMAINS.
 RA Yang C.-Y., Chen S.-H., Gianturco S.H., Bradley W.A., Sparrow J.T.,
 RA Tanimura M., Li W.-H., Sparrow D.A., Deloof H., Rosseneu M.,
 RA Lee F.-S., Gu Z.-W., Gotto A.M. Jr., Chan L.,
 RT "Sequence, structure, receptor-binding domains and internal repeats
 RT of human apolipoprotein B-100."
 RL Nature 323:738-742(1986).
 RN [15]
 RN CALCIUM-BINDING DATA.
 RP MEDLINE=86242245; PubMed=3087360;
 RA Dashi N., Lee D.M., Mok T.,
 RT "Apolipoprotein B is a calcium binding protein."
 RL Biochem. Biophys. Res. Commun. 137:493-499(1986).
 RN [16]
 RN PALMITOYLATION OF CYS-1112.
 RP MEDLINE=20143590; PubMed=10679026;
 RA Zhao Y., McCabe J.B., Vance J., Berthiaume L.G.,
 RT "Palmitoylation of apolipoprotein B is required for proper
 RT intracellular sorting and transport of cholesterol esters and
 RT triglycerides."
 RL Mol. Biol. Cell 11:721-734(2000).
 RN [17]
 RN VARIANT SER-4338.
 RP MEDLINE=91071750; PubMed=1979313;
 RA Navajas M., Laurent A.-M., Moreel J.-F., Ragab A., Cambou J.-P.,
 RA Cuny G., Cambien F., Roizes G.,
 RT "Detection by denaturing gradient gel electrophoresis of a new
 RT polymorphism in the apolipoprotein B gene."
 RL Hum. Genet. 86:91-93(1990).
 RN [18]
 RN VARIANT FDB GLN-3527.
 RP MEDLINE=89098975; PubMed=2563166;
 RA Soria L.F., Ludwig E.H., Clarke H.R.G., Vega G.L., Grundy S.M.,
 RA McCarthy B.J.,
 RT "Association between a specific apolipoprotein B mutation and
 RT familial defective apolipoprotein B-100."
 RL Proc. Natl. Acad. Sci. U.S.A. 86:587-591(1989).
 RN [19]
 RN VARIANT LEU-2739.
 RP MEDLINE=91016974; PubMed=2216805;
 RA Huang L.-S., Gavish D., Breslow J.L.,
 RT "Sequence polymorphism in the human apoB gene at position 8344."
 RL Nucleic Acids Res. 18:5922-5922(1990).
 RN [20]
 RN VARIANT FDB CYS-3558.
 RP MEDLINE=95190020; PubMed=7883971;
 RA Pullinger C.M., Hennessey L.K., Chatterton J.E., Liu W., Love J.A.,
 RA Mendel C.R., Frost P.H., Malloy M.J., Schumaker V.N., Kane J.P.,
 RT "Familial ligand-defective apolipoprotein B. Identification of a new
 RT mutation that decreases LDL receptor binding affinity."
 RL J. Clin. Invest. 95:1225-1234(1995).
 RN [21]
 RN VARIANTS LEU-1437; SER-1914; LYS-2566; THR-3121; ALA-3945; MET-4128

AND THR-4481.
 RP MEDLINE=97044521; PubMed=8889592;
 RA Poirier O., Ricard S., Behague I., Souriau C., Evans A.E.,
 RA Arveiler D., Marques-Vidal P., Luc G., Roizes G., Cambien F.,
 RT "Detection of new variants in the apolipoprotein B (Apo B) gene by
 RT PCR-SSCP."
 RL Hum. Mutat. 8:282-285(1996).
 RN [22]
 RN VARIANTS FDB GLN-3527 AND CYS-3558.
 RP MEDLINE=97403938; PubMed=9259199;
 RA Rabes J.P., Varret M., Saint-Jore B., Erlich D., Jondeau G.,
 RA Krepf M., Giraudet P., Junien C., Boileau C.,
 RT "Familial ligand-defective apolipoprotein B-100: simultaneous
 RT detection of the ARG3500-->GLN and ARG3531-->CYS mutations in a
 RT French population."
 RL Hum. Mutat. 10:160-163(1997).
 RN [23]
 RN VARIANTS SER-1914; ARG-1923; LEU-2739; ASP-3319; THR-3427; GLN-3432
 RP AND ILE-3921.
 RX MEDLINE=98141125; PubMed=9490296;
 RA Lerer T.P., Bakken K.S., Hoel V., Hjermann I., Berg K.,
 RT "Screening for mutations of the apolipoprotein B gene causing
 RT hypocholesterolemia."
 RL Hum. Genet. 102:44-49(1998).
 CC -!- FUNCTION: APOLOPROTEIN B IS A MAJOR PROTEIN CONSTITUENT OF
 CC CHYLOMICRONS, VLDL AND LDL. IT FUNCTIONS AS A RECOGNITION SIGNAL
 CC FOR THE CELLULAR BINDING AND INTERNALIZATION OF LDL PARTICLES BY
 CC THE APOB/E RECEPTOR.
 Query Match 33.2%; Score 50.5; DB 1; Length 4563;
 Best Local Similarity 50.0%; Pred. No. 60;
 Matches 12; Conservative 3; Mismatches 4; Indels 5; Gaps 1;
 QY 4 YRSVWSKIQ-----SIGIRHLK 22
 DB 3680 YDKSLWDFLKDVTTSIGRRQHLR 3703
 RESULT 11
 Y175 METJA
 ID Y175 METJA STANDARD; PRT; 222 AA.
 AC Q57639;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hypothetical protein MJ0175.
 GN MJ0175.
 OS Methanococcus jannaschii.
 OC Archaea; Euryarchaeota; Methanococci; Methanococcales;
 OC Methanocaldococcaceae; Methanocaldococcus.
 OX NCBI_TaxID=2190;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
 RX MEDLINE=96337999; PubMed=8688087;
 RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
 RA Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,
 RA Kerlavage A.R., Dougherty B.A., Tomb J.-P., Adams M.D., Reich C.I.,
 RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
 RA Scott J.L., Geoghegan N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
 RA Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
 RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
 RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.,
 RT "Complete genome sequence of the methanogenic archaeon, Methanococcus
 RT jannaschii."
 RL Science 273:1058-1073(1996).
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>)

or send an email to license@isb-sib.ch.

```
CC -----
CC EMBL; U67474; BAB98160.1; -.
CC PIR; H64321; H64321.
CC TIGR; MJ0175; -.
CC DR InterPro; IPR002848; Translin.
CC DR Pfam; PF01997; Translin; 1.
CC KW Hypothetical protein; Complete proteome.
CC SQ SEQUENCE 222 AA; 26425 MW; 9FBBB385C9FFD3D3 CRC64;

Query Match 32.9%; Score 50; DB 1; Length 222;
Best Local Similarity 53.3%; Pred. No. 2.7;
Matches 8; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 12 LQSIGIRHKLKRVOL 26
DB 203 IQNLKREHLKRVQI 217

RESULT 12
TERT_EUPAE STANDARD; PRT; 1031 AA.
AC O00939;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Telomerase reverse transcriptase (EC 2.7.7.-) (Telomerase catalytic
DE subunit) (Telomerase subunit P123).
OS Euplotides aediculatus.
OC Eukaryota; Alveolata; Ciliophora; Spirotriches; Hypotrichia;
OC Euplotida; Euplotidae; Euplotes.
OX NCBI_TaxID=5940;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97274210; PubMed=9110970;
RA Lingner J., Hughes T.R., Shevchenko A., Mann M., Lundblad V.,
RA Cech T.R.;
RT "Reverse transcriptase motifs in the catalytic subunit of
RT telomerase".
RL Science 276:561-567(1997).
CC -!- FUNCTION: TELOMERASE IS A RIBONUCLEOPROTEIN ENZYME ESSENTIAL FOR
CC THE REPLICATION OF CHROMOSOME TERMINI IN MOST EUKARYOTES. IT
CC ELONGATES TELOMERES. IT IS A REVERSE TRANSCRIPTASE THAT ADDS
CC SINGLE SEQUENCE REPEATS TO CHROMOSOME ENDS BY COPYING A TEMPLATE
CC SEQUENCE WITHIN THE RNA COMPONENT OF THE ENZYME.
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- SIMILARITY: BELONGS TO THE REVERSE TRANSCRIPTASE FAMILY.
CC TELOMERASE SUBFAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U95964; AAC47515.1; -.
CC InterPro; IPR000477; RVTse.
CC InterPro; IPR003545; Telomerase_RT.
CC Pfam; PF00078; rvt; 1.
CC PRINTS; PR01365; TELOMERASRT.
CC Transferrase; RNA-directed DNA polymerase; Telomere; Nuclear protein;
CC DNA-binding.
CC SQ SEQUENCE 1031 AA; 122562 MW; 57B87A63A1FED60F CRC64;

Query Match 32.9%; Score 50; DB 1; Length 1031;
Best Local Similarity 28.1%; Pred. No. 14;
Matches 9; Conservative 10; Mismatches 9; Indels 4; Gaps 1;

QY 2 FFYRKSVMSKLSQSTGI-----RQHLKRVQLRDV 29
DB 469 YYVRKNIWDVIMKMSIADLKKETLAEVQKEV 500
```

```
RESULT 13
YGX7_YEAST STANDARD; PRT; 958 AA.
AC P53076;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Hypothetical 108.2 kDa protein in SAP4-OST5 intergenic region.
DE YGL227W.
GN YGL227W.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RA Fartmann B., Kramer B., Kramer W.;
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Contains 1 Lish domain.
CC -!- SIMILARITY: Contains 1 CTLH domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; Z72749; CAA96943.1; -.
CC DR PIR; S64249; S64249.
CC DR SGD; S0003196; VID30.
CC DR GO; GO:0006808; P:regulation of nitrogen utilization; IMP.
CC InterPro; IPR006595; CTLH.
CC InterPro; IPR006594; Lish.
CC InterPro; IPR003877; SPRY_receptor.
CC Pfam; PF00622; SPRY; 1.
CC SMART; SM00668; CTLH; 1.
CC SMART; SM00667; Lish; 1.
CC SMART; SM00449; SPRY; 1.
CC PROSITE; PS00897; CTLH; 1.
CC PROSITE; PS00896; Lish; 1.
CC KW Hypothetical protein.
CC FT DOMAIN 710 742 Lish.
CC FT DOMAIN 769 826 CTLH.
CC FT DOMAIN 165 185 POLY-ASP.
CC FT DOMAIN 450 453 POLY-SER.
CC SQ SEQUENCE 958 AA; 108178 MW; 335ADD152949F8C8 CRC64;

Query Match 32.2%; Score 49; DB 1; Length 958;
Best Local Similarity 53.8%; Pred. No. 19;
Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 5 RKSVWSKLSQSIGI 17
DB 71 RKEIWSKLMNLGV 83

RESULT 14
TERT_TETTH STANDARD; PRT; 1117 AA.
AC O77418;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Telomerase reverse transcriptase (EC 2.7.7.-) (Telomerase catalytic
DE subunit) (Telomerase subunit P133).
GN TERT.
OS Tetrahymena thermophila.
OC Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Hymenostomatida;
OC Tetrahymenina; Tetrahymena.
OX NCBI_TaxID=5911;
```


[9]
 UNBIQUITINATION.
 PubMed=12354939;
 Hook S.S., Orian A., Cowley S.M., Eisenman R.N.;
 "Histone deacetylase 6 binds polyubiquitin through its zinc finger
 (PAZ domain) and copurifies with deubiquitinating enzymes.";
 Proc. Natl. Acad. Sci. U.S.A. 99:13425-13430(2002).
 -!- FUNCTION: Responsible for the deacetylation of lysine residues on
 the N-terminal part of the core histones (H2A, H2B, H3 and H4).
 Histone deacetylation gives a tag for epigenetic repression and
 plays an important role in transcriptional regulation, cell cycle
 progression and developmental events. Histone deacetylases act via
 the formation of large multiprotein complexes. Involved in muscle
 maturation by repressing transcription of myocyte enhancer MEPC2.
 During muscle differentiation, it shuttles into the cytoplasm,
 allowing the expression of myocyte enhancer factors.
 -!- SUBUNIT: Interacts with HDAC7 and NCOR2 (By similarity). Interacts
 with MEPC2. Interacts with a 14-3-3 chaperone protein.
 -!- SUBCELLULAR LOCATION: Nuclear and cytoplasmic. Shuttles between
 the nucleus and the cytoplasm. In muscle cells, it shuttles into
 the cytoplasm during myocyte differentiation. The export to
 cytoplasm depends on the interaction with a 14-3-3 chaperone
 protein and is due to its phosphorylation at Ser-259 and Ser-498
 by CamK.
 -!- ALTERNATIVE PRODUCTS:
 Event-Alternative splicing; Named isoforms=2;
 Name=1;
 IsoId=Q9UQL6-1; Sequence=Displayed;
 Name=2;
 IsoId=Q9UQL6-2; Sequence=VSP_002081;
 Note=No experimental confirmation available;
 TISSUE SPECIFICITY: Ubiquitous.
 -!- DOMAIN: The nuclear export sequence mediates the shuttling between
 the nucleus and the cytoplasm (By similarity).
 -!- PTM: Phosphorylated by CamK at Ser-259 and Ser-498. The
 phosphorylation is required for the export to the cytoplasm.
 -!- PTM: Ubiquitinated. Polyubiquitination however does not lead
 to its degradation.
 -!- SIMILARITY: BELONGS TO THE HISTONE DEACETYLASE / ACUC / APHA
 FAMILY. HD SUBFAMILY 2.
 -!- CAUTION: Ref.5 sequence differs from that shown due to a
 frameshift in position 1085.

 This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way
 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).

 EMBL; AF132608; AAD29047.1; -;
 EMBL; AB011172; BAA2526.2; ALT_INIT.
 EMBL; BC013140; AAH13140.1; ALT_TERM.
 EMBL; AF039691; AAC18040.1; ALT_FRAME.
 EMBL; HGNC:14068; HDACS.
 MIM; 605315; -;
 GO; GO:0005737; C:cytoplasm; TAS.
 GO; GO:0005634; C:nucleus; TAS.
 GO; GO:0004407; F:histone deacetylase activity; TAS.
 GO; GO:0006342; P:chromatin silencing; TAS.
 GO; GO:0006355; P:regulation of transcription, DNA-dependent; TAS.
 InterPro; IPR000286; His deacetylase.
 Pfam; PF00850; Hist_deacetyl; 1.
 PRINTS; PR01270; HDASUPER.
 Hydrolase; Nuclear protein; Chromatin regulator;
 Transcription regulation; Repressor; Phosphorylation; Ub1 conjugation;
 Alternative splicing.
 FT DOMAIN 684 1028 HISTONE DEACETYLASE.
 FT DOMAIN 1081 1122 NUCLEAR EXPORT.
 FT DOMAIN 47 52 POLY-GLY.
 FT DOMAIN 85 92 POLY-GLN.
 FT DOMAIN 596 599 POLY-GLU.

FT	DOMAIN	1099	1104	POLY-ALA.
FT	ACT_SITE	833	833	BY SIMILARITY.
FT	MOD_RES	259	259	PHOSPHORYLATION (BY CAMK).
FT	MOD_RES	498	498	PHOSPHORYLATION (BY CAMK).
FT	VARSPLIC	684	768	Missing (in isoform 2).
FT	MUTAGEN	1086	1086	/FTId=VSP_002081.
FT	MUTAGEN	1092	1092	V->A: REDUCES CAMK-DEPENDENT NUCLEAR EXPORT.
FT	MUTAGEN	1092	1092	L->A: REDUCES CAMK-DEPENDENT NUCLEAR EXPORT.
FT	MUTAGEN	259	259	S->A: REDUCES CAMK-DEPENDENT PHOSPHORYLATION AND THE SUBSEQUENT NUCLEAR EXPORT. ABOLISHES NUCLEAR EXPORT WHEN ASSOCIATED WITH A-498.
FT	MUTAGEN	279	279	S->A: NO EFFECT.
FT	MUTAGEN	498	498	S->A: REDUCES CAMK-DEPENDENT PHOSPHORYLATION AND THE SUBSEQUENT NUCLEAR EXPORT. ABOLISHES NUCLEAR EXPORT WHEN ASSOCIATED WITH A-259.
FT	MUTAGEN	661	661	S->A: NO EFFECT.
FT	MUTAGEN	713	713	S->A: NO EFFECT.
FT	CONFLICT	593	593	E -> D (IN REF. 2).
FT	CONFLICT	671	671	S -> N (IN REF. 5).
FT	CONFLICT	684	684	G -> S (IN REF. 5).
FT	CONFLICT	1026	1026	E -> K (IN REF. 5).
FT	CONFLICT	1074	1074	E -> G (IN REF. 5).
FT	CONFLICT	1093	1093	S -> L (IN REF. 5).
SQ	SEQUENCE	1122 AA;	121991 MW;	CF4BBB8B9A288FEC CRC64;

Query Match 31.6%; Score 48; DB 1; Length 1122;
 Best Local Similarity 36.4%; Pred. No. 32;
 Matches 8; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

Qy	6	KSVWSKLSQSIGIRQHKLKRVQLR	27
Db	712	QSIWSRLQETGLSKCERNGR	733

Search completed: November 12, 2003, 19:48:03
 Job time : 7.22642 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 12, 2003, 19:42:29 ; Search time 28.6792 Seconds
(without alignments)
269.937 Million cell updates/sec

Title: US-08-854-050-116
Perfect score: 152
Sequence: 1 LFFYKSVMSKLSQIGIRHKLKRVQLRDVS 30

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL 23:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phase:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rvirus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	145	95.4	795	4	Q8NG38
2	145	95.4	807	4	Q8N6C3
3	145	95.4	1069	4	Q8NG46
4	136	89.5	52	11	Q9R0B3
5	136	89.5	575	11	Q9JK99
6	116	76.3	1128	11	Q9QXZ4
7	113	74.3	1191	13	Q9DE32
8	65	42.8	1108	5	Q8I826
9	61	40.1	1135	5	Q8I827
10	55	36.2	768	4	Q8N879
11	53.5	35.2	896	5	Q8MUQ8
12	52	34.2	330	5	P90634
13	51.5	33.9	378	17	Q8TP60
14	51	33.6	729	10	Q8S6N4
15	50.5	33.2	536	6	Q28473
16	50.5	33.2	3262	4	Q13788

17	50	32.9	181	10	Q9SND2	Q9smd2 arabidopsis
18	49.5	32.6	302	10	Q9FHL1	Q9fhl1 arabidopsis
19	49	32.2	198	15	Q9EAB1	Q9eab1 chimpanzee
20	49	32.2	351	11	Q9ERH5	Q9erh5 mus musculus
21	49	32.2	351	11	Q9EQ16	Q9eq16 mus musculus
22	49	32.2	608	16	Q8YVD6	Q8yvd6 anabaena sp
23	49	32.2	660	10	Q9S9W3	Q9s9w3 arabidopsis
24	49	32.2	1361	10	Q8LNN4	Q8lnn4 oryza sativ
25	49	32.2	1849	12	Q9JGK9	Q9jgk9 sagiyama vi
26	49	32.2	2467	12	Q9JGL0	Q9jgl0 sagiyama vi
27	48.5	31.9	1024	5	Q8MRZ8	Q8mrz8 drosophila
28	48.5	31.9	1056	5	Q9W3H0	Q9w3h0 drosophila
29	48	31.6	104	9	Q8SDQ2	Q8sdd2 staphylococ
30	48	31.6	191	4	Q96K29	Q96k29 homo sapien
31	48	31.6	809	4	Q9NQW8	Q9nqw8 homo sapien
32	47	30.9	72	16	Q9I169	Q9i169 pseudomonas
33	47	30.9	90	16	Q8K7P2	Q8k7p2 streptococ
34	47	30.9	101	16	Q8P2G5	Q8p2g5 streptococ
35	47	30.9	234	16	Q8UKM5	Q8ukm5 agrobacteri
36	47	30.9	281	1	Q8UJ308	Q8uj308 pyrococcus
37	47	30.9	439	3	O13295	O13295 penicillium
38	47	30.9	456	16	O8UJ24	O8uj24 agrobacteri
39	47	30.9	465	3	Q94692	Q94692 schizosacch
40	47	30.9	484	4	Q9H7L0	Q9h7l0 homo sapien
41	47	30.9	614	4	Q8WU14	Q8wu14 homo sapien
42	47	30.9	855	4	Q9NYK9	Q9nyk9 homo sapien
43	47	30.9	878	4	Q9UFU7	Q9ufu7 homo sapien
44	47	30.9	892	11	Q8C2C9	Q8c2c9 mus musculu
45	47	30.9	905	3	O94641	O94641 schizosacch

ALIGNMENTS

RESULT 1
Q8NG38 PRELIMINARY; PRT; 795 AA.
AC Q8NG38;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE ABG-deleted variant of telomerase reverse transcriptase.
GN TERT.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Stomach;
RA Hisatomi H., Nagao K., Kanamaru T., Hirata H., Miyachi K., Hikiiji H.;
RT "Exon 11 deleted variant of human reverse transcriptase";
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB086950; BAC11015.1; -
DR InterPro; IPR003545; Telomerase_RT.
DR PRINTS; PR01365; TELOMERASERT.
KW RNA-directed DNA polymerase.

Query Match 95.4%; Score 145; DB 4; Length 795;
Best Local Similarity 93.3%; Pred. No. 1.9e-13;
Matches 28; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LFFYKSVMSKLSQIGIRHKLKRVQLRDVS 30
Db 573 LFFYKSVMSKLSQIGIRHKLKRVQLRELS 602

RESULT 2
Q8N6C3 PRELIMINARY; PRT; 807 AA.
ID Q8N6C3
AC Q8N6C3;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)

```

DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Beta and gamma deletion isoform of telomerase reverse
DE transcriptase.
GN HTERT.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Stomach cancer;
RA Hisatomi H., Nagao K., Kanamaru T., Sumida H., Hirata H., Yamamoto M.,
RA Kazunasa H.;
RT "Both beta and gamma deletion isoform of human telomerase reverse
RT transcriptase.";
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB086379; BAC11014.1; -.
DR InterPro; IPR003545; Telomerase_RT.
DR PRINTS; PR01365; TELOMERASERT.
SQ SEQUENCE 807 AA; 90225 MW; 199664460CB5D763 CRC64;

Query Match 95.4%; Score 145; DB 4; Length 807;
Best Local Similarity 93.3%; Pred. No. 2e-13;
Matches 28; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LFFYRKSVWSKLSIGIGIROHLKRVQLRDVS 30
|||
573 LFFYRKSVWSKLSIGIGIROHLKRVQLRDVS 602

RESULT 3
Q8NG46 PRELIMINARY; PRT; 1069 AA.
ID Q8NG46
AC Q8NG46;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DE 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Telomerase reverse transcriptase.
GN HTERT.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Hisatomi H., Nagao K., Hirata H., Hikiji K., Kanamaru T.;
RT "Exon 11 deleted variant of the human telomerase reverse
RT transcriptase.";
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB085628; BAC11010.1; -.
DR InterPro; IPR003545; Telomerase_RT.
DR PRINTS; PR01365; TELOMERASERT.
KW RNA-directed DNA polymerase.
SQ SEQUENCE 1069 AA; 120047 MW; BE1E77A653B1C666 CRC64;

Query Match 95.4%; Score 145; DB 4; Length 1069;
Best Local Similarity 93.3%; Pred. No. 2.6e-13;
Matches 28; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LFFYRKSVWSKLSIGIGIROHLKRVQLRDVS 30
|||
573 LFFYRKSVWSKLSIGIGIROHLKRVQLRDVS 602

RESULT 4
Q9R0B3 PRELIMINARY; PRT; 52 AA.
ID Q9R0B3
AC Q9R0B3;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE Telomerase catalytic subunit (Fragment).

```

```

OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Drissi R., Cleveland J.L.;
RT "Sequence of a Mus musculus telomerase catalytic subunit intron.";
RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF090439; RAD54013.1; -.
DR NON_TER 1
FT NON_TER 52
SQ SEQUENCE 52 AA; 6479 MW; 41473425E44BDA9C CRC64;

Query Match 89.5%; Score 136; DB 11; Length 52;
Best Local Similarity 83.3%; Pred. No. 2.6e-13;
Matches 25; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LFFYRKSVWSKLSIGIGIROHLKRVQLRDVS 30
|||
7 LFFYRKSVWSKLSIGIGIROHLKRVQLRDVS 36

RESULT 5
Q9JK99 PRELIMINARY; PRT; 575 AA.
ID Q9JK99
AC Q9JK99;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Telomerase catalytic subunit (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Wong S., Gao S., Xu X., Yu H.;
RT "Rat telomerase catalytic subunit, rTERT.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF247818; AAF62177.1; -.
DR InterPro; IPR000477; RVTse.
DR InterPro; IPR003545; Telomerase_RT.
DR Pfam; PF00078; rvt; 1.
DR PRINTS; PR01365; TELOMERASERT.
KW RNA-directed DNA polymerase; Transferase.
FT NON_TER 1
SQ SEQUENCE 575 AA; 65672 MW; F80C81BD7F6A91A3 CRC64;

Query Match 89.5%; Score 136; DB 11; Length 575;
Best Local Similarity 83.3%; Pred. No. 3.2e-12;
Matches 25; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LFFYRKSVWSKLSIGIGIROHLKRVQLRDVS 30
|||
16 LFFYRKSVWSKLSIGIGIROHLKRVQLRDVS 45

RESULT 6
Q9QXZ4 PRELIMINARY; PRT; 1128 AA.
ID Q9QXZ4
AC Q9QXZ4;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Telomerase catalytic subunit.
OS Mesocricetus auratus (Golden hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Mesocricetus.
OX NCBI_TaxID=10036;
RN [1]
RP SEQUENCE FROM N.A.

```

```
RX MEDLINE=21240330; PubMed=11342218;
RA Guo W., Okamoto M., Lee Y.M., Baluda M.A., Park N.H.;
RT "Enhanced activity of cloned hamster TERT gene promoter in transformed
RL cells.";
RL Biochim. Biophys. Acta 1517:398-409(2001).
DR EMBL; AF149012; AAF17334.1; -.
DR InterPro; IPR000477; RVTse.
DR InterPro; IPR003545; Telomerase_RT.
DR Pfam; PF00078; rvt; 1.
DR PRINTS; PR01365; TELOMERASERT.
KW RNA-directed DNA polymerase; Transferase.
SQ SEQUENCE 1128 AA; 128394 MW; 1D4F81249012174E CRC64;

Query Match 76.3%; Score 116; DB 11; Length 1128;
Best Local Similarity 66.7%; Pred. No. 7.5e-09;
Matches 20; Conservative 8; Mismatches 2; Indels 0; Gaps 0;

QY 1 LFFYKSVMSKLSIGIGIHOHLKRVQLRDVS 30
DB 567 LFFYKSVMSKLSIGIGIHOHLKRVQLRDVS 596

RESULT 7
Q9DE32 PRELIMINARY; PRT; 1191 AA.
AC Q9DE32
DT 01-MAR-2001 (TEMBLrel. 16, Created)
DT 01-MAR-2001 (TEMBLrel. 16, Last sequence update)
DT 01-MAR-2003 (TEMBLrel. 23, Last annotation update)
DE Telomerase reverse transcriptase.
GN TERT.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA Kuranoto M., Ishikawa F.;
RT "Telomerase reverse transcriptase of Xenopus laevis.";
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF212299; BAG43537.1; -.
DR InterPro; IPR000477; RVTse.
DR Pfam; PF00078; rvt; 2.
DR PRINTS; PR01365; TELOMERASERT.
KW RNA-directed DNA polymerase; Transferase.
SQ SEQUENCE 1191 AA; 138016 MW; 9BD9D776869A57D6 CRC64;

Query Match 74.3%; Score 113; DB 13; Length 1191;
Best Local Similarity 66.7%; Pred. No. 2.3e-08;
Matches 20; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

QY 1 LFFYKSVMSKLSIGIGIHOHLKRVQLRDVS 30
DB 628 LFFYKSVMSKLSIGIGIHOHLKRVQLRDVS 657

RESULT 8
Q81826 PRELIMINARY; PRT; 1108 AA.
AC Q81826
DT 01-MAR-2003 (TEMBLrel. 23, Created)
DT 01-MAR-2003 (TEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TEMBLrel. 23, Last annotation update)
DE Telomerase (Fragment).
OS Sterkiella sp. Aspen.
OC Eukaryota; Alveolata; Ciliophora; Spirotrichea; Stichotrichia;
OC Stichotrichida; Oxytrichidae; Sterkiella.
OX NCBI_TaxID=200599;
RN [1]
RP SEQUENCE FROM N.A.
RA Marandi S.S., Prescott D.M.;
```

```
RT "The macronuclear telomerase gene in two closely related
RT Stichotrichous ciliates.";
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY116502; RAN87867.1; -.
FT NON TER 1
SQ SEQUENCE 1108 AA; 131535 MW; EC8262E01B8E0PAD CRC64;

Query Match 42.8%; Score 65; DB 5; Length 1108;
Best Local Similarity 30.3%; Pred. No. 0.46;
Matches 10; Conservative 14; Mismatches 5; Indels 4; Gaps 1;

QY 1 LFFYKSVMSKLSIGIGI----RQHLKRVQLRDV 29
DB 548 IFYRKNINWMIMRLSIDLLKQNLKQVEKEM 590

RESULT 9
Q81827 PRELIMINARY; PRT; 1135 AA.
AC Q81827
DT 01-MAR-2003 (TEMBLrel. 23, Created)
DT 01-MAR-2003 (TEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TEMBLrel. 23, Last annotation update)
DE Telomerase.
OS Sterkiella sp. Aspen.
OC Eukaryota; Alveolata; Ciliophora; Spirotrichea; Stichotrichia;
OC Stichotrichida; Oxytrichidae; Sterkiella.
OX NCBI_TaxID=200599;
RN [1]
RP SEQUENCE FROM N.A.
RA Marandi S.S., Prescott D.M.;
RT "The macronuclear telomerase gene in two closely related
RT Stichotrichous ciliates.";
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY116501; RAN87866.1; -.
SQ SEQUENCE 1135 AA; 134341 MW; 3661E5D9300A4942 CRC64;

Query Match 40.1%; Score 61; DB 5; Length 1135;
Best Local Similarity 27.3%; Pred. No. 1.9;
Matches 9; Conservative 14; Mismatches 6; Indels 4; Gaps 1;

QY 1 LFFYKSVMSKLSIGIGI----RQHLKRVQLRDV 29
DB 575 IFYRKNINWMIMRLSIDLLKQNLKQVEKEM 607

RESULT 10
Q8N879 PRELIMINARY; PRT; 768 AA.
AC Q8N879
DT 01-OCT-2002 (TEMBLrel. 22, Created)
DT 01-OCT-2002 (TEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TEMBLrel. 23, Last annotation update)
DE Hypothetical protein FLJ39859.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Tanigami A., Fujiwara T., Shibahara T., Goto Y., Hirao M., Shimizu F.,
RA Wakebe H., Ono T., Hishigaki H., Watanabe T., Ozaki K., Sugiyama T.,
RA Irie R., Otsuki T., Sato H., Ota T., Wakamatsu A., Ishii S.,
RA Yamamoto J., Isono Y., Kawai-Hio Y., Saito K., Nishikawa T.,
RA Kimura K., Yamashita H., Matsuo K., Nakamura Y., Sekine M.,
RA Kikuchi H., Kanda K., Wagatsuma M., Murakawa K., Kanehori K.,
RA Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami B., Suzuki Y.,
RA Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.;
RT "NEDO human cDNA sequencing project.";
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK097178; BAC04971.1; -.
DR InterPro; IPR000286; His_deacetylase.
```

```
DR Pfam; PF00850; Hist deacetyl; 1.
KW Hypothetical protein.
SQ SEQUENCE 768 AA; 84836 MW; D47A16B47F4C25E2 CRC64;

Query Match 36.2%; Score 55; DB 4; Length 768;
Best Local Similarity 40.0%; Pred. No. 11;
Matches 10; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

QY 6 KSVWSKLSQSIGIRQHLKRVQLRDVS 30
DB 640 OSIWSRLQETGLLNKCIQGRKAS 664

RESULT 11
Q8MUQ8 PRELIMINARY; PRT; 896 AA.
AC Q8MUQ8;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Telomerase reverse transcriptase.
OS Paramesium tetraurelia.
OC Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Peniculida;
OC Paramesium.
OX NCBI_TaxID=5888;
RN [1]
RP SEQUENCE FROM N.A.
RA Romero D.P., Ye A.J.;
RT "A unique pause pattern during telomere addition by the error-prone
RT telomerase from the ciliate Paramesium tetraurelia.";
RL Gene 0:0-0(2002).
DR EMBL; AF515460; AAM03860.1; -.
DR InterPro; IPR000477; RVTS.
DR InterPro; IPR003545; Telomerase_RT.
DR Pfam; PF000078; rvt; 2.
DR PRINTS; PR01365; TELOMERASERT.
KW RNA-directed DNA polymerase; Transferase.
SQ SEQUENCE 896 AA; 107237 MW; 697031F9DD61A883 CRC64;

Query Match 35.2%; Score 53.5; DB 5; Length 896;
Best Local Similarity 33.3%; Pred. No. 21;
Matches 10; Conservative 8; Mismatches 11; Indels 1; Gaps 1;

QY 1 LFFYRKVSWSKLSQSIGIRQHLKRVQLRDVS 30
DB 404 LFFYRKETWLVLSLNQ-LSSNNLKQIS 432

RESULT 12
P90634 PRELIMINARY; PRT; 330 AA.
AC P90634;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DE G1m1.
DE 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
GN G1m1.
OS Leishmania donovani.
OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
OX NCBI_TaxID=5661;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Ld4;
RX MEDLINE=97184434; PubMed=9032236;
RA Flaspohler J.A., Rickoll W.L., Beverley S.M., Parsons M.;
RT "Functional identification of a Leishmania gene related to the peroxin
RT 2 gene reveals common ancestry of glycosomes and peroxisomes.";
RL Mol. Cell. Biol. 17,1093-1101(1997)
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR EMBL; U80074; AAB48828.1; -.
DR InterPro; IPR006845; Pex2_Pex12.
DR InterPro; IPR001841; Znf_Ring.
DR Pfam; PF04757; Pex2_Pex12; 1.

DR Pfam; PF00097; zf-C3HC4; 1.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS00518; ZF_RING_1; 1.
DR PROSITE; PS00089; ZF_RING_2; 1.
KW Metal-binding; Zinc; Zinc-finger.
FT VARIANT 239 239 Q -> *.
SQ SEQUENCE 330 AA; 38021 MW; A46F0DCE821A554A CRC64;

Query Match 34.2%; Score 52; DB 5; Length 330;
Best Local Similarity 56.0%; Pred. No. 13;
Matches 14; Conservative 2; Mismatches 7; Indels 2; Gaps 1;

QY 4 YKSVWSKLSQSIGIRQHLKRVQLRD 28
DB 90 YRLSVRMGQSIGDR-LQNLVLRD 112

RESULT 13
Q8TP60 PRELIMINARY; PRT; 378 AA.
AC Q8TP60;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Hypothetical protein MA2058.
GN MA2058.
OS Methanosarcina acetivorans.
OC Archaea; Euryarchaeota; Methanococci; Methanosarcinales;
OC Methanosarcinaceae; Methanosarcina.
OX NCBI_TaxID=2214;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C2A / ATCC 35395 / DSM 2834;
RX MEDLINE=21929760; PubMed=1932238;
RA Galagan J.E., Nusbaum C., Roy A., Endrizzi M.G., Macdonald P.,
RA Fitzhugh W., Calvo S., Engels R., Smirnov S., Ancoor D., Brown A.,
RA Allen N., Naylor J., Stange-Thomann N., DeArelano K., Johnson R.,
RA Linton L., McEwan P., McKernan K., Talamas J., Tirrell A., Ye W.,
RA Zimmer A., Barber P.D., Cann I., Graham D.E., Grahame D.A., Guss A.M.,
RA Hedderich R., Ingram-Smith C., Kuettnner H.C., Krzycki J.A.,
RA Leigh J.A., Li W., Liu J., Mukhopadhyay B., Reeve J.N., Smith K.,
RA Springer T.A., Umayar L.A., White O., White R.H., de Macario E.C.,
RA Ferry J.G., Jarrell K.F., Jing H., Macario A.J.L., Paulsen I.,
RA Pritchett M., Sowers K.R., Swanson R.V., Zinder S.H., Lander E.,
RA Metcalf W.W., Birren B.;
RT "The genome of Methanosarcina acetivorans reveals extensive metabolic
RT and physiological diversity.";
RL Genome Res. 12:532-542(2002).
DR EMBL; AB010892; AAM05460.1; -.
DR InterPro; IPR001450; 4Fe4S_ferredoxin.
DR InterPro; IPR001395; Aldo/Ket_red.
DR Pfam; PF00248; aldo_ket_red; 1.
DR Pfam; PF00037; fer4; 1.
DR ProDom; PD000288; Aldo/ket_red; 1.
DR PROSITE; PS00198; 4Fe4S_FERREDOXIN; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 378 AA; 42942 MW; 2F628946601E3121 CRC64;

Query Match 33.9%; Score 51.5; DB 17; Length 378;
Best Local Similarity 35.7%; Pred. No. 17;
Matches 10; Conservative 7; Mismatches 6; Indels 5; Gaps 1;

QY 3 FY-----RKSVWSKLSQSIGIRQHLKRVQ 25
DB 115 FYLLHAVKSYWEKMSFGVIEFLERAR 142

RESULT 14
Q8S6N4 PRELIMINARY; PRT; 729 AA.
AC Q8S6N4;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
```

```

SQ  SEQUENCE  596 AA;  66757 MW;  B13BBA74E25C3120 CRC64;
      Query Match      33.2%;  Score 50.5;  DB 6;  Length 596;
      Best Local Similarity 50.0%;  Pred.No. 40;
      Matches 12;  Conservative 3;  Mismatches 4;  Indels 5;  Gaps 1;

Qy      4  YRKSVMSKIQ-----SIGIRQHLK 22
      |||:| |: ||| |||:
Db      521 YGKSLWDFLKLVDVTTSIGRRQHLR 544

Search completed: November 12, 2003, 19:50:46
Job time : 29.8459 secs

```

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 12, 2003, 19:41:04 ; Search time 33.6226 Seconds
(without alignments)
127.462 Million cell updates/sec

Title: US-08-854-050-117

Perfect score: 139

Sequence: 1 PALLTSRLRFPKPGRLPIVNDYV 27

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.*
- 2: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
- 3: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*
- 4: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.*
- 5: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1984.DAT.*
- 6: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1985.DAT.*
- 7: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1986.DAT.*
- 8: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1987.DAT.*
- 9: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1988.DAT.*
- 10: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1989.DAT.*
- 11: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1990.DAT.*
- 12: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1991.DAT.*
- 13: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1992.DAT.*
- 14: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1993.DAT.*
- 15: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1994.DAT.*
- 16: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1995.DAT.*
- 17: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1996.DAT.*
- 18: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1997.DAT.*
- 19: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.*
- 20: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*
- 21: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
- 22: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
- 23: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*
- 24: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	139	100.0	27	AAW57390	Human telomerase r
2	139	100.0	27	AAW57396	Human telomerase r
3	139	100.0	131	AAW57385	Amino acid sequenc
4	139	100.0	259	AAW46998	Human telomerase r
5	139	100.0	283	AAW43128	Human telomerase r
6	139	100.0	437	AAW25461	Human CRT-1 protei
7	139	100.0	438	AAW25462	Human CRT-1 protei
8	139	100.0	514	AAW47003	Glutathione-S-tran
9	139	100.0	531	AAW47002	Glutathione-S-tran

10	139	100.0	564	19	AAW56109	Human telomerase r
11	139	100.0	591	20	AAW97384	A catalytic telome
12	139	100.0	617	20	AAW00636	N-terminal truncat
13	139	100.0	622	20	AAW25463	Human CRT-1 protei
14	139	100.0	807	19	AAW46997	Human telomerase r
15	139	100.0	807	20	AAW00637	N-terminal truncat
16	139	100.0	807	20	AAW00646	Truncated telomera
17	139	100.0	936	20	AAW00642	Truncated telomera
18	139	100.0	936	20	AAW00651	Truncated telomera
19	139	100.0	948	20	AAW00639	N-terminal truncat
20	139	100.0	948	20	AAW00648	Truncated telomera
21	139	100.0	949	19	AAW61149	Human telomerase p
22	139	100.0	1041	20	AAW00643	Altered C-terminus
23	139	100.0	1041	20	AAW00652	Altered C-terminus
24	139	100.0	1053	20	AAW00640	Altered C-terminus
25	139	100.0	1093	20	AAW00649	Altered C-terminus
26	139	100.0	1120	20	AAW00641	Telomerase protein
27	139	100.0	1120	20	AAW00650	Telomerase (ver. 2
28	139	100.0	1132	19	AAW71376	Human telomerase c
29	139	100.0	1132	19	AAW46957	Human telomerase r
30	139	100.0	1132	19	AAW56113	Human telomerase r
31	139	100.0	1132	20	AAW43621	A human telomerase
32	139	100.0	1132	20	AAW28881	Human telomerase r
33	139	100.0	1132	20	AAW32090	Human telomerase r
34	139	100.0	1132	20	AAW28401	Human EST2 protein
35	139	100.0	1132	20	AAW26580	Human telomerase r
36	139	100.0	1132	20	AAW00627	Human telomerase p
37	139	100.0	1132	20	AAW00638	Truncated telomera
38	139	100.0	1132	20	AAW90251	Human catalytic te
39	139	100.0	1132	21	AAW95666	hEST2, a human tel
40	139	100.0	1132	22	AAW82765	Human telomerase r
41	139	100.0	1132	22	AAW99930	Human telomerase p
42	139	100.0	1132	22	AAW64329	Human protein #2.
43	139	100.0	1132	22	AAW64859	Heart muscle cell
44	139	100.0	1132	23	AAE29226	Human telomerase r
45	139	100.0	1132	23	AAU72735	Human telomerase r

ALIGNMENTS

RESULT 1
AAW57390
ID AAW57390 standard; peptide; 27 AA.
XX AC AAW57390;
XX AC AAW57390;
DT 13-AUG-1998 (first entry)
XX
DE Human telomerase reverse transcriptase antigenic peptide.
XX
KW Human: telomerase reverse transcriptase; hTERT; TRT; diagnosis;
KW prognosis; cell proliferation; cancer; ageing; ribonucleoprotein;
KW antigenic.
XX
OS Synthetic.
OS Homo sapiens.
PN GB2317891-A.
PD 08-APR-1998.
XX
PF 01-OCT-1997; 97GB-0020890.
XX
PR 14-AUG-1997; 97US-0915503.
PR 01-OCT-1996; 96US-0724643.
PR 18-APR-1997; 97US-0844419.
PR 25-APR-1997; 97US-0846017.
PR 06-MAY-1997; 97US-0851843.
PR 09-MAY-1997; 97US-0854050.
PR 14-AUG-1997; 97US-0911312.
PR 14-AUG-1997; 97US-0912951.
XX

(GERO-) GERON CORP.
 (UYTE-) UNIV TECHNOLOGY CORP.
 Andrews WH, Cech TR, Chapman KB, Harley C, Lingner J;
 Morin GB, Nakamura T, Harley CB;
 WPI; 1998-171633/16.
 Pure and recombinant human Telomerase Reverse Transcriptase and its
 variants - are useful in the diagnosis, prognosis and treatment of
 cell proliferation conditions especially cancer and ageing
 Example 8; Page 259; 387pp; English.
 The present sequence represents an antigenic peptide from human
 telomerase reverse transcriptase (hTERT), from the present invention. The
 present invention also describes the following methods: (A) determining
 whether a test compound is a modulator of hTERT, by detecting the change
 in hTERT recombinant protein or polynucleotide, on administration of the
 compound; (B) preparation of recombinant telomerase by contacting a
 protein preparation of hTERT with a telomerase RNA component; (C)
 detection of the hTERT RNA or protein in a sample by binding a relevant
 probe to the sample and detecting the complex formed or in the case of
 RNA detection, amplifying the product and correlating the presence of
 complex or amplification product with presence of hTERT in the sample;
 and (D) increasing the proliferation of a vertebrate cell by increasing
 hTERT expression; and (E) the use of an agent that causes an increase in
 cell vertebrate cell proliferation to create a medicament that inhibits
 ageing. A protein preparation of hTERT and the polynucleotide encoding
 hTERT can be used in the manufacture of medicaments for inhibiting the
 effect of ageing or cancer. Inhibitors of telomerase activity can be
 used to treat conditions that are associated with high telomerase
 activity. A protein preparation of hTERT can also be used in the new
 methods.
 .XX
 SQ Sequence 27 AA;
 Query Match 100.0%; Score 139; DB 19; Length 27;
 Best Local Similarity 100.0%; Pred. No. 9e-16;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 PALLTSRLRFPKPDGLRPVNDYV 27
 DB 1 PALLTSRLRFPKPDGLRPVNDYV 27
 RESULT 2
 AAW57396
 ID AAW57396 standard; peptide; 27 AA.
 XX
 AC AAW57396;
 DT 13-AUG-1998 (first entry)
 DE Human telomerase reverse transcriptase antigenic peptide A-3.
 KW Human; telomerase reverse transcriptase; hTERT; TRT; diagnosis;
 KW prognosis; cell proliferation; cancer; ageing; ribonucleoprotein.
 XX Synthetic.
 OS Homo sapiens.
 XX GB2317891-A.
 XX
 PD 08-APR-1998.
 XX
 PF 01-OCT-1997; 97GB-0020890.
 XX
 PR 14-AUG-1997; 97US-0915503.
 PR 01-OCT-1996; 96US-0724643.
 PR 18-APR-1997; 97US-0844419.
 PR 25-APR-1997; 97US-0846017.
 PR 06-MAY-1997; 97US-0851843.
 PR
 (GERO-) GERON CORP.
 (UYTE-) UNIV TECHNOLOGY CORP.
 Andrews WH, Cech TR, Chapman KB, Harley C, Lingner J;
 Morin GB, Nakamura T, Harley CB;
 WPI; 1998-171633/16.
 Pure and recombinant human Telomerase Reverse Transcriptase and its
 variants - are useful in the diagnosis, prognosis and treatment of
 cell proliferation conditions especially cancer and ageing
 Example 8; Fig 54; 387pp; English.
 The present sequence represents an antigenic peptide from human
 telomerase reverse transcriptase (hTERT), from the present invention. The
 present invention also describes the following methods: (A) determining
 whether a test compound is a modulator of hTERT, by detecting the change
 in hTERT recombinant protein or polynucleotide, on administration of the
 compound; (B) preparation of recombinant telomerase by contacting a
 protein preparation of hTERT with a telomerase RNA component; (C)
 detection of the hTERT RNA or protein in a sample by binding a relevant
 probe to the sample and detecting the complex formed or in the case of
 RNA detection, amplifying the product and correlating the presence of
 complex or amplification product with presence of hTERT in the sample;
 and (D) increasing the proliferation of a vertebrate cell by increasing
 hTERT expression; and (E) the use of an agent that causes an increase in
 cell vertebrate cell proliferation to create a medicament that inhibits
 ageing. A protein preparation of hTERT and the polynucleotide encoding
 hTERT can be used in the manufacture of medicaments for inhibiting the
 effect of ageing or cancer. Inhibitors of telomerase activity can be
 used to treat conditions that are associated with high telomerase
 activity. A protein preparation of hTERT can also be used in the new
 methods.
 .XX
 SQ Sequence 27 AA;
 Query Match 100.0%; Score 139; DB 19; Length 27;
 Best Local Similarity 100.0%; Pred. No. 9e-16;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 PALLTSRLRFPKPDGLRPVNDYV 27
 DB 1 PALLTSRLRFPKPDGLRPVNDYV 27
 RESULT 3
 AAW97385
 ID AAW97385 standard; Protein; 131 AA.
 XX
 AC AAW97385;
 DT 14-MAY-1999 (first entry)
 DE Amino acid sequence of the specification.
 DE Catalytic telomerase; diagnosis; disease; telomerase activity.
 XX Homo sapiens.
 OS
 KW JP11046768-A.
 XX
 PN 23-FEB-1999.
 XX
 PD 01-AUG-1997; 97JP-0207708.
 XX
 PF 01-AUG-1997; 97JP-0207708.
 PR
 XX (MITU) MITSUBISHI CHEM CORP.
 PA

XX
DR WPI; 1999-208111/18.
DR N-PSDB; AAX15924.
XX
PT New catalytic protein of telomerase of a higher animal and a gene
PT coding it - useful for diagnosis of diseases caused by the change in
PT activity of a telomerase
XX
XX Example 1; Page 14; 18pp; Japanese.
XX
XX The specification describes a human catalytic telomerase protein.
CC The products are useful in drug compositions for the diagnosis
CC of diseases caused by the change in activity of telomerase. The
CC present sequence appears in the specification.
XX
SQ Sequence 131 AA;
Query Match 100.0%; Score 139; DB 20; Length 131;
Best Local Similarity 100.0%; Pred. No. 6.1e-15;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PALLTSRLRFIPKPDGLRPVNMVYV 27
Db 73 PALLTSRLRFIPKPDGLRPVNMVYV 99
|||||
|||||

RESULT 4
AAW46998
ID AAW46998 standard; Protein; 259 AA.
XX
AC AAW46998;
XX
XX 13-AUG-1998 (first entry)
XX Human telomerase reverse transcriptase protein from cDNA clone 712562.
XX
XX Human; telomerase reverse transcriptase; hTERT; TRT; diagnosis;
KW prognosis; cell proliferation; cancer; ageing; ribonucleoprotein.
XX
XX Homo sapiens.
XX GB2317891-A.
XX
XX 08-APR-1998.
XX
XX 01-OCT-1997; 97GB-0020890.
XX
XX 14-AUG-1997; 97US-0915503.
PR 01-OCT-1996; 96US-0724643.
PR 18-APR-1997; 97US-0844419.
PR 25-APR-1997; 97US-0846017.
PR 06-MAY-1997; 97US-0851843.
PR 09-MAY-1997; 97US-0854050.
PR 14-AUG-1997; 97US-0911312.
PR 14-AUG-1997; 97US-0912951.
XX
XX (GERO-) GERON CORP.
PA (UYTE-) UNIV TECHNOLOGY CORP.
XX
XX Andrews WH, Cech TR, Chapman KB, Harley C, Lingner J;
PI Morin GB, Nakamura T, Harley CB;
XX
XX WPI; 1998-171633/16.
DR N-PSDB; AAV22379.
XX
XX Pure and recombinant human Telomerase Reverse Transcriptase and its
PT variants - are useful in the diagnosis, prognosis and treatment of
PT cell proliferation conditions especially cancer and ageing
XX
XX Example 1; Fig 19; 387pp; English.
PS
XX The present sequence represents a human telomerase reverse transcriptase
CC (hTERT) protein from a cDNA clone from the present invention. The present

CC invention also describes the following methods: (A) determining whether
CC a test compound is a modulator of hTERT, by detecting the change in hTERT
CC recombinant protein or polynucleotide, on administration of the compound;
CC (B) preparation of recombinant telomerase by contacting a protein
CC preparation of hTERT with a telomerase RNA component; (C) detection of
CC the hTERT RNA or protein in a sample by binding a relevant probe to the
CC sample and detecting the complex formed or in the case of RNA detection,
CC amplifying the product and correlating the presence of hTERT in the sample; and (D)
CC amplification product with presence of hTERT in the sample; and (D)
CC increasing the proliferation of a vertebrate cell by increasing hTERT
CC expression; and (E) the use of an agent that causes an increase in cell
CC vertebrate cell proliferation to create a medicament that inhibits
CC ageing. A protein preparation of hTERT and the polynucleotide encoding
CC hTERT can be used in the manufacture of medicaments for inhibiting the
CC effect of ageing or cancer. Inhibitors of telomerase activity can be
CC used to treat conditions that are associated with high telomerase
CC activity. A protein preparation of hTERT can also be used in the new
CC methods.
XX
SQ Sequence 259 AA;
Query Match 100.0%; Score 139; DB 19; Length 259;
Best Local Similarity 100.0%; Pred. No. 1.4e-14;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PALLTSRLRFIPKPDGLRPVNMVYV 27
Db 66 PALLTSRLRFIPKPDGLRPVNMVYV 92
|||||
|||||

RESULT 5
AAY43128
ID AAY43128 standard; Protein; 283 AA.
XX
AC AAY43128;
XX
XX 20-DEC-1999 (first entry)
XX Human telomerase reverse transcriptase.
DE Human telomerase reverse transcriptase.
KW Human telomerase reverse transcriptase; hTERT; antibody; diagnosis;
KW telomerase-related disease; cancer.
XX
XX Homo sapiens.
XX WO9950407-A1.
PN 07-OCT-1999.
XX
XX 26-MAR-1999; 99WO-JP01557.
PF 26-MAR-1998; 98JP-0098486.
PR (KYOW) KYOWA HAKKO KOGYO KK.
XX
XX Hanai N, Yamasaki M, Shibata K, Furuya A, Mikuni O, Anazawa H;
PI WPI; 1999-591316/50.
DR
XX New monoclonal antibody recognizing human telomerase catalytic subunit
PT (hTERT) useful for treating and diagnosing cancer -
PT
XX Claim 2; Page 72-73; 78pp; Japanese.
PS
XX This sequence represents the human telomerase reverse transcriptase
CC (hTERT). The invention relates to a monoclonal antibody recognising the
CC hTERT. The antibody can be used for the investigation, diagnosis and
CC treatment of telomerase-related diseases, especially diseases in which
CC telomerase expression is up-regulated e.g. cancers.
XX
XX Sequence 283 AA;
SQ
Query Match 100.0%; Score 139; DB 20; Length 283;

Best Local Similarity 100.0%; Pred. No. 1.5e-14;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PALLTSRLRFPKPDGLRPVNDYV 27
DB 66 PALLTSRLRFPKPDGLRPVNDYV 92

RESULT 6

ID AAY25461 standard; Protein; 437 AA.

AC AAY25461;

DT 22-SEP-1999 (first entry)

DE Human CRT-1 protein #1.

KW CRT-1; reverse transcriptase; telomerase; inhibitor; detection;
telomerase activity; cancer cell; screening; human.

OS Homo sapiens.

FH Key Location/Qualifiers
FT Protein 1..437
FT /label= CRT-1
FT /note= "Partial sequence, no stop codon given"

XX (CHUS) CHUGAI SEIYAKU KK.

PN WO9935261-A1.

XX 15-JUL-1999.

XX 08-JAN-1999; 99WO-JP00039.

XX 06-MAY-1998; 98JP-0139177.

XX 08-JAN-1998; 98JP-0013232.

XX 30-JAN-1998; 98JP-0033584.

XX (CHUS) CHUGAI SEIYAKU KK.

XX Tauchiya M, Yoshida K;

XX WPI; 1999-430393/36.

XX N-PSDB; AAX88243.

XX Novel gene, useful in detection of telomerase activity and cancer
cells as well as screening telomerase inhibitors for treatment of
cancers

PS Claim 2; Page 31-32; 44pp; Japanese.

CC This invention describes novel human CRT-1 genes and their encoded
proteins containing a reverse transcriptase motif, which act as
telomerase inhibitors. The gene, its encoded protein and derived
antibodies can be used to provide base sequence information, detect
telomerase activity and cancer cells, and to screen telomerase
inhibitors. The detection method is simple and effective.

XX SQ Sequence 437 AA;

Query Match 100.0%; Score 139; DB 20; Length 437;
Best Local Similarity 100.0%; Pred. No. 2.6e-14;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PALLTSRLRFPKPDGLRPVNDYV 27
DB 104 PALLTSRLRFPKPDGLRPVNDYV 130

RESULT 7

AAY25462

ID AAY25462 standard; Protein; 438 AA.

XX

AC AAY25462;
XX 22-SEP-1999 (first entry)
XX Human CRT-1 protein #2.
DE CRT-1; reverse transcriptase; telomerase; inhibitor; detection;
telomerase activity; cancer cell; screening; human.
XX Homo sapiens.

XX Key Location/Qualifiers
FH Protein 1..438
FT /label= CRT-1
FT /note= "Partial sequence, no stop codon given"

XX WO9935261-A1.

XX 15-JUL-1999.

XX 08-JAN-1999; 99WO-JP00039.

XX 06-MAY-1998; 98JP-0139177.

XX 08-JAN-1998; 98JP-0013232.

XX 30-JAN-1998; 98JP-0033584.

XX (CHUS) CHUGAI SEIYAKU KK.

XX Tsuchiya M, Yoshida K;

XX WPI; 1999-430393/36.

XX N-PSDB; AAX88250.

XX Novel gene, useful in detection of telomerase activity and cancer
cells as well as screening telomerase inhibitors for treatment of
cancers

XX Example 1; Page 35-36; 44pp; Japanese.

XX This invention describes novel human CRT-1 genes and their encoded
proteins containing a reverse transcriptase motif, which act as
telomerase inhibitors. The gene, its encoded protein and derived
antibodies can be used to provide base sequence information, detect
telomerase activity and cancer cells, and to screen telomerase
inhibitors. The detection method is simple and effective.

XX SQ Sequence 438 AA;

Query Match 100.0%; Score 139; DB 20; Length 438;
Best Local Similarity 100.0%; Pred. No. 2.6e-14;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PALLTSRLRFPKPDGLRPVNDYV 27
DB 104 PALLTSRLRFPKPDGLRPVNDYV 130

RESULT 8

AAW47003

ID AAW47003 standard; Protein; 514 AA.

XX AAW47003;

XX 13-AUG-1998 (first entry)

XX Glutathione-S-transferase and hTERT fusion protein 3.

XX Human; telomerase reverse transcriptase; hTERT; diagnosis;
prognosis; cell proliferation; cancer; ageing; ribonucleoprotein.

XX Synthetic.

XX Homo sapiens.

XX

```

FH Key          Location/Qualifiers
FT Region      1..220
FT /note= "glutathione-S-transferase fragment"
FT Region      238..514
FT /note= "hTERT protein fragment"
XX
XX GB2317891-A.
XX
XX 08-APR-1998.
XX
XX 01-OCT-1997; 97GB-0020890.
XX
XX 14-AUG-1997; 97US-0915503.
XX 01-OCT-1996; 96US-0724643.
XX 18-APR-1997; 97US-0844419.
XX 25-APR-1997; 97US-0846017.
XX 06-MAY-1997; 97US-0851843.
XX 09-MAY-1997; 97US-0854050.
XX 14-AUG-1997; 97US-0911312.
XX 14-AUG-1997; 97US-0912951.
XX
XX (GERO-) GERON CORP.
XX (UYTE-) UNIV TECHNOLOGY CORP.
XX
XX Andrews WH, Cech TR, Chapman KB, Harley C, Lingner J;
XX Morin GB, Nakamura T, Harley CB;
XX WPI; 1998-171633/16.
XX
XX Pure and recombinant human Telomerase Reverse Transcriptase and its
XX variants - are useful in the diagnosis, prognosis and treatment of
XX cell proliferation conditions especially cancer and ageing
XX
XX Example 6; Page 226; 387pp; English.
XX
XX The present sequence represents a fusion protein from an example
XX of the present invention which describes human telomerase reverse
XX transcriptase (hTERT). The present invention also describes the
XX following methods: (A) determining whether a test compound is
XX a modulator of hTERT, by detecting the change in hTERT recombinant
XX protein or polynucleotide, on administration of the compound;
XX (B) preparation of recombinant telomerase by contacting a protein
XX preparation of hTERT with a telomerase RNA component; (C) detection
XX of the hTERT RNA or protein in a sample by binding a relevant
XX probe to the sample and detecting the complex formed or in the case of
XX RNA detection, amplifying the product and correlating the presence of
XX complex or amplification product with presence of hTERT in the sample;
XX and (D) increasing the proliferation of a vertebrate cell by increasing
XX hTERT expression; and (E) the use of an agent that causes an increase in
XX cell vertebrate cell proliferation to create a medicament that inhibits
XX ageing. A protein preparation of hTERT and the polynucleotide encoding
XX hTERT can be used in the manufacture of medicaments for inhibiting the
XX effect of ageing or cancer. Inhibitors of telomerase activity can be
XX used to treat conditions that are associated with high telomerase
XX activity. A protein preparation of hTERT can also be used in the new
XX methods.
XX
XX Sequence 514 AA;
XX
XX Query Match          100.0%; Score 139; DB 19; Length 514;
XX Best Local Similarity 100.0%; Pred. No. 3.2e-14;
XX Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 PALLTSRLRFPKPDGLRPLVNDYVV 27
XX |||||
XX Db 302 PALLTSRLRFPKPDGLRPLVNDYVV 328
XX
XX RESULT 9
XX AAW47002
XX ID AAW47002 standard; Protein; 531 AA.
XX
XX AC AAW47002;

```

```

XX 13-AUG-1998 (first entry)
XX
XX Glutathione-S-transferase and hTERT fusion protein 2.
XX
XX Human; telomerase reverse transcriptase; hTERT; TRT; diagnosis;
XX prognosis; cell proliferation; cancer; ageing; ribonucleoprotein.
XX
XX Synthetic.
XX OS Homo sapiens.
XX
XX Key          Location/Qualifiers
XX Region      1..221
XX /note= "glutathione-S-transferase fragment"
XX Region      249..531
XX /note= "hTERT protein fragment"
XX
XX GB2317891-A.
XX
XX 08-APR-1998.
XX
XX 01-OCT-1997; 97GB-0020890.
XX
XX 14-AUG-1997; 97US-0915503.
XX 01-OCT-1996; 96US-0724643.
XX 18-APR-1997; 97US-0844419.
XX 25-APR-1997; 97US-0846017.
XX 06-MAY-1997; 97US-0851843.
XX 09-MAY-1997; 97US-0854050.
XX 14-AUG-1997; 97US-0911312.
XX 14-AUG-1997; 97US-0912951.
XX
XX (GERO-) GERON CORP.
XX (UYTE-) UNIV TECHNOLOGY CORP.
XX
XX Andrews WH, Cech TR, Chapman KB, Harley C, Lingner J;
XX Morin GB, Nakamura T, Harley CB;
XX WPI; 1998-171633/16.
XX
XX Pure and recombinant human Telomerase Reverse Transcriptase and its
XX variants - are useful in the diagnosis, prognosis and treatment of
XX cell proliferation conditions especially cancer and ageing
XX
XX Example 6; Page 225; 387pp; English.
XX
XX The present sequence represents a fusion protein from an example
XX of the present invention which describes human telomerase reverse
XX transcriptase (hTERT). The present invention also describes the
XX following methods: (A) determining whether a test compound is
XX a modulator of hTERT, by detecting the change in hTERT recombinant
XX protein or polynucleotide, on administration of the compound;
XX (B) preparation of recombinant telomerase by contacting a protein
XX preparation of hTERT with a telomerase RNA component; (C) detection
XX of the hTERT RNA or protein in a sample by binding a relevant
XX probe to the sample and detecting the complex formed or in the case of
XX RNA detection, amplifying the product and correlating the presence of
XX complex or amplification product with presence of hTERT in the sample;
XX and (D) increasing the proliferation of a vertebrate cell by increasing
XX hTERT expression; and (E) the use of an agent that causes an increase in
XX cell vertebrate cell proliferation to create a medicament that inhibits
XX ageing. A protein preparation of hTERT and the polynucleotide encoding
XX hTERT can be used in the manufacture of medicaments for inhibiting the
XX effect of ageing or cancer. Inhibitors of telomerase activity can be
XX used to treat conditions that are associated with high telomerase
XX activity. A protein preparation of hTERT can also be used in the new
XX methods.
XX
XX Sequence 531 AA;
XX
XX Query Match          100.0%; Score 139; DB 19; Length 531;
XX Best Local Similarity 100.0%; Pred. No. 3.3e-14;
XX Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 PALLTSRLRFPKPDGLRPVNMNDYV 27
 DB 314 PALLTSRLRFPKPDGLRPVNMNDYV 340

RESULT 10
 AAW56109
 ID AAW56109 standard; Protein; 564 AA.

XX AAW56109;
 DT 13-AUG-1998 (first entry)

XX Human telomerase reverse transcriptase 63 kDa clone 712562 protein.
 XX Human; telomerase reverse transcriptase; hTERT; TRT; diagnosis;
 XX prognosis; cell proliferation; cancer; ageing; ribonucleoprotein.

XX Synthetic.
 XX Homo sapiens.

XX Key Location/Qualifiers
 FT Misc-difference 102
 FT /label= encoded by ARG

XX GB2317891-A.

XX 08-APR-1998.

XX 01-OCT-1997; 97GB-0020890.

XX 14-AUG-1997; 97US-0915503.

XX 01-OCT-1996; 96US-0724643.

XX 18-APR-1997; 97US-0844419.

XX 25-APR-1997; 97US-0846017.

XX 06-MAY-1997; 97US-0851843.

XX 09-MAY-1997; 97US-0854050.

XX 14-AUG-1997; 97US-0911312.

XX 14-AUG-1997; 97US-0912951.

XX (GERO-) GERON CORP.

XX (UYTE-) UNIV TECHNOLOGY CORP.

XX Andrews WH, Cech TR, Chapman KB, Harley C, Lingner J;

XX Morin GB, Nakamura T, Harley CB;

XX WPI; 1998-171633/16.

XX N-PSDB; AAV22426.

XX Pure and recombinant human Telomerase Reverse Transcriptase and its
 variants - are useful in the diagnosis, prognosis and treatment of
 cell proliferation conditions especially cancer and ageing

XX Example 1; Fig 68; 387pp; English.

XX The present sequence is a human telomerase reverse transcriptase (hTERT)
 clone protein from the present invention. The present invention also
 describes the following methods: (A) determining whether a test compound
 is a modulator of hTERT, by detecting the change in hTERT recombinant
 protein or polynucleotide, on administration of the compound; (B)
 preparation of recombinant telomerase by contacting a protein
 preparation of hTERT with a telomerase RNA component; (C) detection of
 the hTERT RNA or protein in a sample by binding a relevant probe to the
 sample and detecting the complex formed or in the case of RNA detection,
 amplifying the product and correlating the presence of complex or
 amplification product with presence of hTERT in the sample; and (D)
 increasing the proliferation of a vertebrate cell by increasing hTERT
 expression; and (E) the use of an agent that causes an increase in cell
 vertebrate cell proliferation to create a medicament that inhibits
 ageing. A protein preparation of hTERT and the polynucleotide encoding
 hTERT can be used in the manufacture of medicaments for inhibiting the
 effect of ageing or cancer. Inhibitors of telomerase activity can be

CC used to treat conditions that are associated with high telomerase
 CC activity..A protein preparation of hTERT can also be used in the new
 CC methods.

XX Sequence 564 AA;

Query Match 100.0%; Score 139; DB 19; Length 564;
 Best Local Similarity 100.0%; Pred. No. 3.5e-14;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PALLTSRLRFPKPDGLRPVNMNDYV 27
 DB 66 PALLTSRLRFPKPDGLRPVNMNDYV 92

RESULT 11

AAW97384
 ID AAW97384 standard; Protein; 591 AA.

XX AAW97384;

XX 14-MAY-1999 (first entry)

XX A catalytic telomerase protein.

XX Catalytic telomerase; diagnosis; disease; telomerase activity.

XX Homo sapiens.

XX JP11046768-A.

XX 23-FEB-1999.

XX 01-AUG-1997; 97JP-0207708.

XX 01-AUG-1997; 97JP-0207708.

XX (MITU) MITSUBISHI CHEM CORP.

XX WPI; 1999-208111/18.

XX N-PSDB; AAX15923.

XX New catalytic protein of telomerase of a higher animal and a gene
 coding it - useful for diagnosis of diseases caused by the change in
 activity of a telomerase

XX Claim 1; Page 11-14; 18pp; Japanese.

XX The present sequence represents a catalytic telomerase protein.
 CC The products are useful in drug compositions for the diagnosis
 CC of diseases caused by the change in activity of telomerase.

XX Sequence 591 AA;

Query Match 100.0%; Score 139; DB 20; Length 591;
 Best Local Similarity 100.0%; Pred. No. 3.7e-14;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PALLTSRLRFPKPDGLRPVNMNDYV 27
 DB 73 PALLTSRLRFPKPDGLRPVNMNDYV 99

RESULT 12

AAW00636
 ID AAW00636 standard; Protein; 617 AA.

XX AAW00636;

XX 26-JUL-1999 (first entry)

XX N-terminal truncated telomerase protein sequence.

XX

KW Telomerase; human; cancer; diagnosis; melanoma; skin cancer; leukaemia;
 KW neuroblastoma; breast carcinoma; colon carcinoma; lymphoma; osteosarcoma;
 KW smooth muscle cell hyperplasia; stem cell proliferation; Wilm's tumour;
 KW stem cell differentiation; organ regeneration; organ differentiation.

XX Homo sapiens.
 OS Synthetic.

XX WO9901560-A1.

XX 14-JAN-1999.

XX 01-JUL-1998; 98WO-US13835.

XX 09-SEP-1997; 97US-0058287.

XX 01-JUL-1997; 97US-0051410.

XX 21-JUL-1997; 97US-0053018.

XX 21-JUL-1997; 97US-0053329.

XX 04-AUG-1997; 97US-0054642.

XX (CMB-) CAMBIA BIOSYSTEMS LLC.

XX Bowtell D, Kilian A;
 PI WPI; 1999-106060/09.

XX N-PSDB; AAX18264.

XX New isolated vertebrate telomerase genes - used to develop products
 PT for treating cancers or for organ regeneration, nerve cell or brain
 PT cell growth following injury or bone marrow transplantation

XX Claim 4; Fig 11b-c; 134pp; English.

XX This sequence is a truncated human telomerase of the
 CC invention. Primers that amplify the telomerase coding sequence can be
 CC used in a method for diagnosing cancer in a patient. The telomerase can
 CC be used for detection, diagnosis and drug screening. Inhibitors of
 CC telomerase activity can be used to treat cancers such as melanomas,
 CC other skin cancers, neuroblastomas, breast carcinomas, colon carcinomas,
 CC leukaemias, lymphomas, osteosarcomas or smooth muscle cell hyperplasias
 CC or skin growths. Enhancers of telomerase may be used to stimulate stem
 CC cell proliferation and differentiation (expansion of haematopoietic stem
 CC cells could be administered in the bone marrow transplant context). As
 CC well, many tissues have stem cells. Proliferation of these cells may be
 CC useful in wound healing, hair growth, treatment of disease such as
 CC Wilm's tumour, organ regeneration or differentiation after injury or
 CC diseases, nerve cell or brain cell growth following injury.
 CC Note: The C-terminus of this sequence can be replaced by the sequence
 CC shown in AAY00653.

XX SQ Sequence 617 AA;

Query Match 100.0%; Score 139; DB 20; Length 617;
 Best Local Similarity 100.0%; Pred. No. 3.9e-14;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PALLTSRLRFIPKPDGLRPVNMDDYV 27
 |||||
 Db 574 PALLTSRLRFIPKPDGLRPVNMDDYV 600

RESULT 13

AAAY25463

ID AAY25463 standard; Protein; 622 AA.

XX AAY25463;

XX 22-SEP-1999 (first entry)

XX Human CRT-1 protein #3.

XX CRT-1; reverse transcriptase; telomerase; inhibitor; detection;
 KW telomerase activity; cancer cell; screening; human.

XX Homo sapiens.
 OS Key Location/Qualifiers
 FH Protein 1..622
 FT /label= CRT-1
 FT /note= "Partial sequence, no stop codon given"
 XX

XX WO9935261-A1.

XX 15-JUL-1999.

XX 08-JAN-1999; 99WO-JP00039.

XX 06-MAY-1998; 98JP-0139177.

XX 08-JAN-1998; 98JP-0013232.

XX 30-JAN-1998; 98JP-0033584.

XX (CHUS) CHUGAI SEIYAKU KK.

XX Tsuchiya M, Yoshida K;

XX WPI; 1999-430393/36.

XX N-PSDB; AAX88251.

XX Novel gene, useful in detection of telomerase activity and cancer
 PT cells as well as screening telomerase inhibitors for treatment of
 PT cancers

XX Example 1; Page 37-39; 44pp; Japanese.

XX This invention describes novel human CRT-1 genes and their encoded
 CC proteins containing a reverse transcriptase motif, which act as
 CC telomerase inhibitors. The gene, its encoded protein and derived
 CC antibodies can be used to provide base sequence information, detect
 CC telomerase activity and cancer cells, and to screen telomerase
 CC inhibitors. The detection method is simple and effective.

XX SQ Sequence 622 AA;

Query Match 100.0%; Score 139; DB 20; Length 622;
 Best Local Similarity 100.0%; Pred. No. 4e-14;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PALLTSRLRFIPKPDGLRPVNMDDYV 27
 |||||
 Db 104 PALLTSRLRFIPKPDGLRPVNMDDYV 130

RESULT 14

AAW46997

ID AAW46997 standard; Protein; 807 AA.

XX AAW46997;

XX 13-AUG-1998 (first entry)

XX Human telomerase reverse transcriptase Delta182 variant.

XX Human; telomerase reverse transcriptase; hTERT; TRF; diagnosis;
 KW prognosis; cell proliferation; cancer; ageing; ribonucleoprotein.

XX Synthetic.

XX OS Homo sapiens.

XX GB2317891-A.

XX 08-APR-1998.

XX 01-OCT-1997; 97GB-0020890.

XX 14-AUG-1997; 97US-0915503.

XX 01-OCT-1996; 96US-0724643.

PR 18-APR-1997; 97US-0844419.
PR 25-APR-1997; 97US-0846017.
PR 06-MAY-1997; 97US-0851843.
PR 09-MAY-1997; 97US-0854050.
PR 14-AUG-1997; 97US-0911312.
PR 14-AUG-1997; 97US-0912951.
XX (GERO-) GERON CORP.
PA (UYTE-) UNIV TECHNOLOGY CORP.

XX Andrews WH, Cech TR, Chapman KB, Harley C, Lingner J;
PI Morin GB, Nakamura T, Harley CB;
PI WPI: 1998-171633/16.
DR N-PSDB; AAV22382.

XX Pure and recombinant human Telomerase Reverse Transcriptase and its
PT variants - are useful in the diagnosis, prognosis and treatment of
PT cell proliferation conditions especially cancer and ageing
XX
XX Disclosure; Fig 20; 387pp; English.

XX The present sequence represents a human telomerase reverse transcriptase
CC (hTERT) variant from the present invention. The present invention also
CC describes the following methods: (A) determining whether a test compound
CC is a modulator of hTERT, by detecting the change in hTERT recombinant
CC protein or polynucleotide, on administration of the compound; (B)
CC preparation of recombinant telomerase by contacting a protein
CC preparation of hTERT with a telomerase RNA component; (C) detection of
CC the hTERT RNA or protein in a sample by binding a relevant probe to the
CC sample and detecting the complex formed or in the case of RNA detection,
CC amplifying the product and correlating the presence of complex or
CC amplification product with presence of hTERT in the sample; and (D)
CC increasing the proliferation of a vertebrate cell by increasing hTERT
CC expression; and (E) the use of an agent that causes an increase in cell
CC vertebrate cell proliferation to create a medicament that inhibits
CC ageing. A protein preparation of hTERT and the polynucleotide encoding
CC hTERT can be used in the manufacture of medicaments for inhibiting the
CC effect of ageing or cancer. Inhibitors of telomerase activity can be
CC used to treat conditions that are associated with high telomerase
CC activity. A protein preparation of hTERT can also be used in the new
CC methods.

XX Sequence 807 AA;

Query Match 100.0%; Score 139; DB 19; Length 807;
Best Local Similarity 100.0%; Pred. No. 5.5e-14;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PALLTSRLRFIPKPDGLRPIVNDYV 27
DB 614 PALLTSRLRFIPKPDGLRPIVNDYV 640

RESULT 15

AA00637
ID AA00637 standard; Protein; 807 AA.

XX
AC AA00637;

XX 26-JUL-1999 (first entry)

XX N-terminal truncated telomerase protein sequence.

XX Telomerase; human; cancer; diagnosis; melanoma; skin cancer; leukaemia;
KW neuroblastoma; breast carcinoma; colon carcinoma; lymphoma; osteosarcoma;
KW smooth muscle cell hyperplasia; stem cell proliferation; Wilm's tumour;
KW stem cell differentiation; organ regeneration; organ differentiation.

OS Homo sapiens.

OS Synthetic.

XX WO9901560-A1.

XX 14-JAN-1999.
XX 01-JUL-1998; 98WO-US13835.
XX 09-SEP-1997; 97US-0058287.
PR 01-JUL-1997; 97US-0051410.
PR 21-JUL-1997; 97US-0053018.
PR 21-JUL-1997; 97US-0053329.
PR 04-AUG-1997; 97US-0054642.
XX (CAME-) CAMBIA BIOSYSTEMS LLC.

XX Bowtell D, Kilian A;

XX WPI: 1999-106060/09.
DR N-PSDB; AAX18265.

XX New isolated vertebrate telomerase genes - used to develop products
PT for treating cancers or for organ regeneration, nerve cell or brain
PT cell growth following injury or bone marrow transplantation
XX

XX Claim 4; Fig 11d-e; 134pp; English.

XX This sequence is a truncated human telomerase of the
CC invention. Primers that amplify the telomerase coding sequence can be
CC used in a method for diagnosing cancer in a patient. The telomerase can
CC be used for detection, diagnosis and drug screening. Inhibitors of
CC telomerase activity can be used to treat cancers such as melanomas, other
CC skin cancers, neuroblastomas, breast carcinomas, colon carcinomas,
CC leukaemias, lymphomas, osteosarcomas or smooth muscle cell hyperplasias
CC or skin growths. Enhancers of telomerase may be used to stimulate stem
CC cell proliferation and differentiation (expansion of haematopoietic stem
CC cells could be administered in the bone marrow transplant context). As
CC well, many tissues have stem cells. Proliferation of these cells may be
CC useful in wound healing, hair growth, treatment of disease such as Wilm's
CC tumour, organ regeneration or differentiation after injury or diseases,
CC nerve cell or brain cell growth following injury.

XX Sequence 807 AA;

Query Match 100.0%; Score 139; DB 20; Length 807;
Best Local Similarity 100.0%; Pred. No. 5.5e-14;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PALLTSRLRFIPKPDGLRPIVNDYV 27
DB 614 PALLTSRLRFIPKPDGLRPIVNDYV 640

Search completed: November 12, 2003, 19:47:14
Job time : 33.6226 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 12, 2003, 19:43:50 ; Search time 12.566 Seconds
(without alignments)
90.911 Million cell updates/sec

Title: US-08-854-050-117

Perfect score: 139

Sequence: 1 PALLSRLRFLPKDGLRFLVMDYV 27

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*

1: /cgn2_6/prodata/1/iaa/5A COMB.pcp.*

2: /cgn2_6/prodata/1/iaa/5B COMB.pcp.*

3: /cgn2_6/prodata/1/iaa/6A COMB.pcp.*

4: /cgn2_6/prodata/1/iaa/6B COMB.pcp.*

5: /cgn2_6/prodata/1/iaa/PCTUS COMB.pcp.*

6: /cgn2_6/prodata/1/iaa/backfiles1.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	ID	Description
1	139	100.0	27	3	US-08-851-843A-117
2	139	100.0	27	3	US-08-851-843A-117
3	139	100.0	27	3	US-08-851-843A-117
4	139	100.0	27	4	US-08-854-050-117
5	139	100.0	27	4	US-08-854-050-117
6	139	100.0	27	4	US-08-854-050-117
7	139	100.0	30	3	US-08-851-843A-167
8	139	100.0	30	3	US-08-851-843A-167
9	139	100.0	30	3	US-08-854-050-167
10	139	100.0	30	4	US-08-854-050-167
11	139	100.0	54	3	US-08-854-050-167
12	139	100.0	129	3	US-08-851-843A-31
13	139	100.0	129	3	US-08-851-843A-67
14	139	100.0	129	3	US-08-851-843A-13
15	139	100.0	129	3	US-08-854-050-67
16	139	100.0	129	4	US-08-854-050-67
17	139	100.0	129	3	US-08-854-050-13
18	139	100.0	129	3	US-08-854-050-13
19	139	100.0	129	3	US-08-854-050-13
20	139	100.0	129	3	US-08-854-050-13
21	139	100.0	129	3	US-08-854-050-13
22	139	100.0	129	3	US-08-854-050-13
23	139	100.0	129	3	US-08-854-050-13
24	139	100.0	129	3	US-08-854-050-13
25	139	100.0	129	3	US-08-854-050-13
26	139	100.0	129	3	US-08-854-050-13
27	139	100.0	807	3	US-08-854-050-13

28 139 100.0 807 4 US-08-912-951-5
29 139 100.0 1003 3 US-08-851-843A-217
30 139 100.0 1003 3 US-08-974-549A-336
31 139 100.0 1003 3 US-08-854-050-217
32 139 100.0 1003 4 US-09-430-323-217
33 139 100.0 1132 3 US-08-851-843A-225
34 139 100.0 1132 3 US-08-974-549A-2
35 139 100.0 1132 3 US-08-974-549A-344
36 139 100.0 1132 3 US-08-854-050-225
37 139 100.0 1132 4 US-09-430-323-225
38 139 100.0 1132 4 US-09-128-354-2
39 139 100.0 1132 4 US-09-675-321-2
40 139 100.0 1132 4 US-09-052-919-2
41 139 100.0 1132 4 US-08-912-951-2
42 139 100.0 1154 3 US-08-974-549A-611
43 139 100.0 1154 4 US-08-912-951-323
44 139 100.0 1189 3 US-08-974-549A-613
45 139 100.0 1189 4 US-08-912-951-325

ALIGNMENTS

RESULT 1
US-08-851-843A-117
; Sequence 117, Application US/08851843A
; Patent No. 6093809
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin
; APPLICANT: Andrews, William H.
; NUMBER OF INVENTIONS: No. 6093809el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/851,843A
; FILING DATE: 06-MAY-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002930US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 117:

Sequence 5, Appli
Sequence 217, App
Sequence 336, App
Sequence 217, App
Sequence 217, App
Sequence 225, App
Sequence 2, Appli
Sequence 344, App
Sequence 225, App
Sequence 225, App
Sequence 2, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 611, App
Sequence 323, App
Sequence 613, App
Sequence 325, App

SEQUENCE CHARACTERISTICS:
LENGTH: 27 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-851-843A-117

Query Match 100.0%; Score 139, DB 3; Length 27;
Best Local Similarity 100.0%; Pred. No. 3.1e-15; Indels 0; Gaps 0;
Matches 27; Conservative 0; Mismatches 0;

QY 1 PALLTSRLRFIPKPDGLRPVNMVYV 27
|||||
Db 1 PALLTSRLRFIPKPDGLRPVNMVYV 27
|||||

RESULT 2

US-08-974-549A-237
; Sequence 237, Application US/08974549A
; Patent No. 6166178
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin B.
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 727
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,549A
; FILING DATE: 19-NOV-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/911,312
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/912,951
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/915,503
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/17618

; FILING DATE: 01-OCT-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/17885
; FILING DATE: 01-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph Ted
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002610US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 237:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-974-549A-237

Query Match 100.0%; Score 139, DB 3; Length 27;
Best Local Similarity 100.0%; Pred. No. 3.1e-15; Indels 0; Gaps 0;
Matches 27; Conservative 0; Mismatches 0;

QY 1 PALLTSRLRFIPKPDGLRPVNMVYV 27
|||||
Db 1 PALLTSRLRFIPKPDGLRPVNMVYV 27
|||||

RESULT 3

US-08-854-050-117
; Sequence 117, Application US/08854050
; Patent No. 6261836
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: No. 6261836el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/854,050
; FILING DATE: 09-MAY-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643

ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0300
TELEFAX: (415) 576-0300

FILED DATE: 14 AUG 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/912,951

```

; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA: US 08/915,503
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/17618
; FILING DATE: 01-OCT-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/17885
; FILING DATE: 01-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph Ted
; REGISTRATION NUMBER: 36,429
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 287:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..30
; OTHER INFORMATION: /note= "motif 0 peptide from human
; OTHER INFORMATION: telomerase core protein 1 (TCP1)"
US-08-974-549A-287

Query Match 100.0%; Score 139; DB 3; Length 30;
Best Local Similarity 100.0%; Pred. No. 3.5e-15;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PALLTSRLRFIPKPDGLRPVNMNDYV 27
Db 3 PALLTSRLRFIPKPDGLRPVNMNDYV 29

RESULT 8
US-08-854-050-167
; Sequence 167, Application US/08854050
; Patent No. 6261836
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: No. 6261836el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/854,050
; FILING DATE: 09-MAY-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997

```

```

; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 167:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..30
; OTHER INFORMATION: /note= "motif 0 peptide from human
; OTHER INFORMATION: telomerase core protein 1 (TCP1)"
US-08-854-050-167

Query Match 100.0%; Score 139; DB 3; Length 30;
Best Local Similarity 100.0%; Pred. No. 3.5e-15;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PALLTSRLRFIPKPDGLRPVNMNDYV 27
Db 3 PALLTSRLRFIPKPDGLRPVNMNDYV 29

RESULT 9
US-09-430-323-167
; Sequence 167, Application US/09430323
; Patent No. 6309867
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: No. 6309867el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/430,323
; FILING DATE: 29-Oct-1999
; CLASSIFICATION: <Unknown>

```

;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/854,050
;; FILING DATE: 09-MAY-1997
;; APPLICATION NUMBER: US 08/851,843
;; FILING DATE: 06-MAY-1997
;; APPLICATION NUMBER: US 08/846,017
;; FILING DATE: 25-APR-1997
;; APPLICATION NUMBER: US 08/844,419
;; FILING DATE: 18-APR-1997
;; APPLICATION NUMBER: US 08/724,643
;; FILING DATE: 01-OCT-1996
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Apple, Randolph T.
;; REGISTRATION NUMBER: 36,429
;; REFERENCE/DOCKET NUMBER: 015389-002930US
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (415) 576-0200
;; TELEFAX: (415) 576-0300
;; INFORMATION FOR SEQ ID NO: 167:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 30 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: <Unknown>
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; FEATURE:
;; NAME/KEY: Peptide
;; LOCATION: 1..30
;; OTHER INFORMATION: /note= "motif 0 peptide from human
;; telomerase core protein 1 (TCPI)"
;; SEQUENCE DESCRIPTION: SEQ ID NO: 167:
US-09-430-323-167

Query Match 100.0%; Score 139; DB 4; Length 30;
Best Local Similarity 100.0%; Pred. No. 3.5e-15;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PALLTSRLRFIPKPDGLRPVNMDDYV 27
Db 3 PALLTSRLRFIPKPDGLRPVNMDDYV 29

RESULT 10
US-08-974-549A-31
; Sequence 31, Application US/08974549A
; Patent No. 6166178
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin B.
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 727
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,549A
; FILING DATE: 19-NOV-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:

;; APPLICATION NUMBER: US 08/724,643
;; FILING DATE: 01-OCT-1996
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/844,419
;; FILING DATE: 18-APR-1997
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/846,017
;; FILING DATE: 25-APR-1997
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/851,843
;; FILING DATE: 06-MAY-1997
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/854,050
;; FILING DATE: 09-MAY-1997
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/911,312
;; FILING DATE: 14-AUG-1997
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/912,951
;; FILING DATE: 14-AUG-1997
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/915,503
;; FILING DATE: 14-AUG-1997
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: WO PCT/US97/17618
;; FILING DATE: 01-OCT-1997
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: WO PCT/US97/17885
;; FILING DATE: 01-OCT-1997
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Apple, Randolph Ted
;; REGISTRATION NUMBER: 36,429
;; REFERENCE/DOCKET NUMBER: 015389-002610US
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (415) 576-0200
;; TELEFAX: (415) 576-0300
;; INFORMATION FOR SEQ ID NO: 31:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 54 amino acids
;; TYPE: amino acid
;; STRANDEDNESS:
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; FEATURE:
;; NAME/KEY: Peptide
;; LOCATION: 1..54
;; OTHER INFORMATION: /note= "motif 1 and 2 peptide from
;; human TRT"
US-08-974-549A-31

Query Match 100.0%; Score 139; DB 3; Length 54;
Best Local Similarity 100.0%; Pred. No. 6.7e-15;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PALLTSRLRFIPKPDGLRPVNMDDYV 27
Db 10 PALLTSRLRFIPKPDGLRPVNMDDYV 36

RESULT 11
US-08-912-951-31
; Sequence 31, Application US/08912951
; Patent No. 6475789
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND
; THERAPEUTIC METHODS

NUMBER OF SEQUENCES: 335
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/912,951
FILING DATE: 14-AUG-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002600US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 54 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..54
OTHER INFORMATION: /note= "motif 1 and 2 peptide from human TRT"
US-08-912-951-31
Query Match 100.0%; Score 139; DB 4; Length 54;
Best Local Similarity 100.0%; Pred. No. 6.7e-15;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 PALLTSRLRFIPKPDGLRPVNMVYV 27
Db 10 PALLTSRLRFIPKPDGLRPVNMVYV 36
RESULT 12
US-08-851-843A-67
; Sequence 67, Application US/08851843A
; Patent No. 6091809
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.

APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin
APPLICANT: Andrews, William H.
TITLE OF INVENTION: No. 6093809el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/851,843A
FILING DATE: 06-MAY-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 67:
SEQUENCE CHARACTERISTICS:
LENGTH: 129 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..129
OTHER INFORMATION: /note= "TRT motifs from human"
US-08-851-843A-67
Query Match 100.0%; Score 139; DB 3; Length 129;
Best Local Similarity 100.0%; Pred. No. 1.8e-14;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 PALLTSRLRFIPKPDGLRPVNMVYV 27
Db 73 PALLTSRLRFIPKPDGLRPVNMVYV 99
RESULT 13
US-08-974-549A-13
; Sequence 13, Application US/08974549A
; Patent No. 6166178
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru

APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin B.
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,549A
FILING DATE: 19-NOV-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 129 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1-129
OTHER INFORMATION: /note= "TRT motifs from human"

US-08-974-549A-13

Query Match 100.0%; Score 139; DB 3; Length 129;

Best Local Similarity 100.0%; Pred. No. 1.8e-14;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 PALLTSRLRFIPKPDGLRPVNMVYV 27
DB 73 PALLTSRLRFIPKPDGLRPVNMVYV 99
RESULT 14
US-08-854-050-67
Sequence 67, Application US/08854050
Patent No. 6261836
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin
APPLICANT: Andrews, William H.
TITLE OF INVENTION: No. 6261836el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/854,050
FILING DATE: 09-MAY-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 67:
SEQUENCE CHARACTERISTICS:
LENGTH: 129 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1-129
OTHER INFORMATION: /note= "TRT motifs from human"

US-08-854-050-67

Query Match 100.0%; Score 139; DB 3; Length 129;
Best Local Similarity 100.0%; Pred. No. 1.8e-14;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PALLTSRLRFIPKPDGLRPVNMDDYV 27
Db 73 PALLTSRLRFIPKPDGLRPVNMDDYV 99

Best Local Similarity 100.0%; Pred. No. 1.8e-14;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PALLTSRLRFIPKPDGLRPVNMDDYV 27
Db 73 PALLTSRLRFIPKPDGLRPVNMDDYV 99

Search completed: November 12, 2003, 19:53:28
Job time : 13.566 secs

RESULT 15
US-09-430-323-67
; Sequence 67, Application US/09430323
; Patent No. 6309867
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin
; Andrews, William H.
; TITLE OF INVENTION: No. 6309867el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/430,323
; FILING DATE: 29-Oct-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002930US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 67:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 129 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURES:
; NAME/KEY: Peptide
; LOCATION: 1..129
; OTHER INFORMATION: /note= "TRT motifs from human"
; SEQUENCE DESCRIPTION: SEQ ID NO: 67:
US-09-430-323-67

Query Match 100.0%; Score 139; DB 4; Length 129;

THIS PAGE BLANK (ISPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

QM protein - protein search, using sw model

Run on: November 12, 2003, 19:47:20 ; Search time 21.566 Seconds
(without alignments)
215.025 Million cell updates/sec

Title: US-08-854-050-117
Perfect score: 139
Sequence: 1 PALLTSRLRIFPKDGLRIVNMDYV 27

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 644079 seqs, 171749292 residues

Total number of hits satisfying chosen parameters: 644079

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA.*

1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pcp.*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pcp.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pcp.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pcp.*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pcp.*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pcp.*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pcp.*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pcp.*
9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pcp.*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pcp.*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pcp.*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pcp.*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pcp.*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pcp.*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pcp.*
16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pcp.*
17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pcp.*
18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	139	100.0	27	10	US-09-843-676-117
2	139	100.0	27	10	US-09-843-676-117
3	139	100.0	27	11	US-09-843-676-117
4	139	100.0	27	15	US-09-843-676-117
5	139	100.0	27	15	US-09-843-676-117
6	139	100.0	27	15	US-09-843-676-117
7	139	100.0	27	15	US-09-843-676-117
8	139	100.0	27	15	US-09-843-676-117
9	139	100.0	30	10	US-09-843-676-117
10	139	100.0	30	10	US-09-843-676-117
11	139	100.0	30	11	US-09-843-676-117
12	139	100.0	30	15	US-09-843-676-117
13	139	100.0	30	15	US-09-843-676-117
14	139	100.0	30	15	US-09-843-676-117
15	139	100.0	54	15	US-10-044-692-31

16	139	100.0	54	15	US-10-044-692-31	Sequence 31, Appl
17	139	100.0	129	10	US-09-843-676-67	Sequence 67, Appl
18	139	100.0	129	10	US-09-843-676-67	Sequence 67, Appl
19	139	100.0	129	11	US-09-438-486-67	Sequence 67, Appl
20	139	100.0	129	15	US-10-053-758-67	Sequence 67, Appl
21	139	100.0	129	15	US-10-054-295-67	Sequence 67, Appl
22	139	100.0	129	15	US-10-054-295-67	Sequence 67, Appl
23	139	100.0	129	15	US-10-054-611-67	Sequence 67, Appl
24	139	100.0	129	15	US-10-044-692-13	Sequence 13, Appl
25	139	100.0	259	15	US-10-044-692-10	Sequence 10, Appl
26	139	100.0	259	15	US-10-044-692-10	Sequence 10, Appl
27	139	100.0	291	12	US-10-282-960-3	Sequence 3, Appl
28	139	100.0	437	15	US-10-294-778-2	Sequence 2, Appl
29	139	100.0	438	15	US-10-294-778-10	Sequence 10, Appl
30	139	100.0	500	12	US-10-282-960-81	Sequence 81, Appl
31	139	100.0	515	15	US-10-044-692-318	Sequence 318, Appl
32	139	100.0	515	15	US-10-044-692-318	Sequence 318, Appl
33	139	100.0	530	15	US-10-044-692-317	Sequence 317, Appl
34	139	100.0	530	15	US-10-044-692-317	Sequence 317, Appl
35	139	100.0	564	10	US-09-843-676-101	Sequence 101, Appl
36	139	100.0	564	10	US-09-766-253-101	Sequence 101, Appl
37	139	100.0	564	11	US-09-438-486-101	Sequence 101, Appl
38	139	100.0	564	15	US-10-053-758-101	Sequence 101, Appl
39	139	100.0	564	15	US-10-054-295-101	Sequence 101, Appl
40	139	100.0	564	15	US-10-054-295-101	Sequence 101, Appl
41	139	100.0	622	15	US-10-294-778-12	Sequence 12, Appl
42	139	100.0	807	15	US-10-044-692-5	Sequence 5, Appl
43	139	100.0	807	15	US-10-044-692-5	Sequence 5, Appl
44	139	100.0	1003	10	US-09-843-676-217	Sequence 217, Appl
45	139	100.0	1003	11	US-09-438-486-217	Sequence 217, Appl

ALIGNMENTS

RESULT 1

US-09-843-676-117
; Sequence 117, Application US/09843676
; Patent No. US20020164786A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lirgner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin
; Andrews, William H.
; TITLE OF INVENTION: No. US20020164786A1el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; Zip: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/843,676
; FILING DATE: 26-APR-2001
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/724,643

```
;
; FILING DATE: 01-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002930US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 117:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; MOLECULE TYPE: linear
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 117:
US-09-843-676-117

Query Match 100.0%; Score 139; DB 10; Length 27;
Best Local Similarity 100.0%; Pred. No. 2.7e-14;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PALLTSRLRFIPKPDGLRPVNMDDYV 27
Db 1 PALLTSRLRFIPKPDGLRPVNMDDYV 27

RESULT 2
US-09-766-253-117
; Sequence 117, Application US/09766253
; Publication No. US20020187471A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Linger, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin
; Andrews, William H.
; TITLE OF INVENTION: No. US20020187471A1 Telomerase
; NUMBER OF SEQUENCES: 171
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 19-Jan-2001
; APPLICATION NUMBER: US/09/766,253
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/846,017
; FILING DATE: 1997-04-25
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002920US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 117:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
```

```
;
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 117:
US-09-766-253-117

Query Match 100.0%; Score 139; DB 10; Length 27;
Best Local Similarity 100.0%; Pred. No. 2.7e-14;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PALLTSRLRFIPKPDGLRPVNMDDYV 27
Db 1 PALLTSRLRFIPKPDGLRPVNMDDYV 27

RESULT 3
US-09-438-486-117
; Sequence 117, Application US/09438486
; Publication No. US20030009019A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Linger, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: No. US20030009019A1 Telomerase
; NUMBER OF SEQUENCES: 223
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 12-NOV-1999
; APPLICATION NUMBER: US/09/438,486
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002931US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 117:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
```

```

; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-438-486-117
Query Match 100.0%; Score 139; DB 11; Length 27;
Best Local Similarity 100.0%; Pred. No. 2.7e-14;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PALLTSRLRFIPKPDGLRPIVNMDDYV 27
Db 1 PALLTSRLRFIPKPDGLRPIVNMDDYV 27

RESULT 4
US-10-053-758-117
; Sequence 117, Application US/10053758
; Publication No. US20030032075A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin
; Andrews, William H.
; TITLE OF INVENTION: No. US20030032075A1el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; STREET: Townsend and Townsend and Crew LLP
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/053,758
; FILING DATE: 18-Jan-2002
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002930US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0300
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 117:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 117:
US-10-053-758-117
Query Match 100.0%; Score 139; DB 15; Length 27;
Best Local Similarity 100.0%; Pred. No. 2.7e-14;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PALLTSRLRFIPKPDGLRPIVNMDDYV 27
Db 1 PALLTSRLRFIPKPDGLRPIVNMDDYV 27

RESULT 5
US-10-054-295-117
; Sequence 117, Application US/10054295
; Publication No. US20030044953A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin
; Andrews, William H.
; TITLE OF INVENTION: No. US20030044953A1el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; STREET: Townsend and Townsend and Crew LLP
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/054,295
; FILING DATE: 18-Jan-2002
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/854,050
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002930US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 117:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 117:
US-10-054-295-117
Query Match 100.0%; Score 139; DB 15; Length 27;
Best Local Similarity 100.0%; Pred. No. 2.7e-14;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PALLTSRLRFIPKPDGLRPIVNMDDYV 27
Db 1 PALLTSRLRFIPKPDGLRPIVNMDDYV 27

RESULT 6
Query Match 100.0%; Score 139; DB 15; Length 27;
Best Local Similarity 100.0%; Pred. No. 2.7e-14;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PALLTSRLRFIPKPDGLRPIVNMDDYV 27
Db 1 PALLTSRLRFIPKPDGLRPIVNMDDYV 27
```

US-10-054-611-117
; Sequence 117, Application US/10054611
; Publication No. US20030059787A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin
; Andrews, William H.
; TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND
; THERAPEUTIC METHODS
; NUMBER OF SEQUENCES: 335
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/054,611
; FILING DATE: 18-Jan-2002
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/854,050
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002930US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 117:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 117:
US-10-054-611-117
Query Match 100.0%; Score 139; DB 15; Length 27;
Best Local Similarity 100.0%; Pred. No. 2.7e-14;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 PALLTSRLRFPKPDGLRPIVNDYV 27
Db 1 PALLTSRLRFPKPDGLRPIVNDYV 27
RESULT 7
US-10-044-692-116
; Sequence 116, Application US/10044692
; Publication No. US20030096344A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin
; Andrews, William H.
; TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND
; THERAPEUTIC METHODS
; NUMBER OF SEQUENCES: 335
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/044,692
; FILING DATE: 11-Jan-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/912,951
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002600US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 116:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 116:
US-10-044-692-116
Query Match 100.0%; Score 139; DB 15; Length 27;
Best Local Similarity 100.0%; Pred. No. 2.7e-14;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 PALLTSRLRFPKPDGLRPIVNDYV 27
Db 1 PALLTSRLRFPKPDGLRPIVNDYV 27
RESULT 8
US-10-044-539-116
; Sequence 116, Application US/10044539
; Publication No. US20030100093A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin
; Andrews, William H.

```
;/ TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND THERAPEUTIC METHODS
;/ NUMBER OF SEQUENCES: 335
;/ CORRESPONDENCE ADDRESS:
;/ ADDRESSEE: Townsend and Townsend and Crew LLP
;/ STREET: Two Embarcadero Center, 8th Floor
;/ CITY: San Francisco
;/ STATE: California
;/ COUNTRY: United States of America
;/ ZIP: 94111
;/ COMPUTER READABLE FORM:
;/ MEDIUM TYPE: Floppy disk
;/ COMPUTER: IBM PC compatible
;/ OPERATING SYSTEM: PC-DOS/MS-DOS
;/ SOFTWARE: PatentIn Release #1.0, Version #1.30
;/ CURRENT APPLICATION NUMBER: US/10/044,539
;/ FILING DATE: 11-Jan-2002
;/ CLASSIFICATION: 435
;/ PRIOR APPLICATION DATA:
;/ APPLICATION NUMBER: 08/912,951
;/ FILING DATE: <Unknown>
;/ APPLICATION NUMBER: US 08/854,050
;/ FILING DATE: 09-MAY-1997
;/ APPLICATION NUMBER: US 08/851,843
;/ FILING DATE: 06-MAY-1997
;/ APPLICATION NUMBER: US 08/846,017
;/ FILING DATE: 25-APR-1997
;/ APPLICATION NUMBER: US 08/844,419
;/ FILING DATE: 18-APR-1997
;/ APPLICATION NUMBER: US 08/724,643
;/ FILING DATE: 01-OCT-1996
;/ ATTORNEY/AGENT INFORMATION:
;/ NAME: Apple, Randolph T.
;/ REGISTRATION NUMBER: 36,429
;/ REFERENCE/DOCKET NUMBER: 015389-002600US
;/ TELECOMMUNICATION INFORMATION:
;/ TELEPHONE: (415) 576-0200
;/ TELEFAX: (415) 576-0300
;/ INFORMATION FOR SEQ ID NO: 116:
;/ SEQUENCE CHARACTERISTICS:
;/ LENGTH: 27 amino acids
;/ TYPE: amino acid
;/ STRANDEDNESS: <Unknown>
;/ TOPOLOGY: linear
;/ MOLECULE TYPE: peptide
;/ SEQUENCE DESCRIPTION: SEQ ID NO: 116:
US-10-044-539-116
Query Match 100.0%; Score 139; DB 15; Length 27;
Best Local Similarity 100.0%; Pred. No. 2.7e-14;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 PALLTSRLRFIPKPDGLRPIVNDYV 27
DB 1 PALLTSRLRFIPKPDGLRPIVNDYV 27
RESULT 9
US-09-843-676-167
; Sequence 167, Application US/09843676
; Patent No. US20020164786A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin
; Andrews, William H.
; TITLE OF INVENTION: No. US20020164786A1el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
;/
```

```
;/ ADDRESSEE: Townsend and Townsend and Crew LLP
;/ STREET: Two Embarcadero Center, 8th Floor
;/ CITY: San Francisco
;/ STATE: California
;/ COUNTRY: United States of America
;/ ZIP: 94111
;/ COMPUTER READABLE FORM:
;/ MEDIUM TYPE: Floppy disk
;/ COMPUTER: IBM PC compatible
;/ OPERATING SYSTEM: PC-DOS/MS-DOS
;/ SOFTWARE: PatentIn Release #1.0, Version #1.30
;/ CURRENT APPLICATION NUMBER: US/09/843,676
;/ FILING DATE: 26-Apr-2001
;/ CLASSIFICATION: 536
;/ PRIOR APPLICATION DATA:
;/ APPLICATION NUMBER: US/08/854,050
;/ FILING DATE: 09-MAY-1997
;/ APPLICATION NUMBER: US 08/846,017
;/ FILING DATE: 25-APR-1997
;/ APPLICATION NUMBER: US 08/844,419
;/ FILING DATE: 18-APR-1997
;/ APPLICATION NUMBER: US 08/724,643
;/ FILING DATE: 01-OCT-1996
;/ ATTORNEY/AGENT INFORMATION:
;/ NAME: Apple, Randolph T.
;/ REGISTRATION NUMBER: 36,429
;/ REFERENCE/DOCKET NUMBER: 015389-002930US
;/ TELECOMMUNICATION INFORMATION:
;/ TELEPHONE: (415) 576-0200
;/ TELEFAX: (415) 576-0300
;/ INFORMATION FOR SEQ ID NO: 167:
;/ SEQUENCE CHARACTERISTICS:
;/ LENGTH: 30 amino acids
;/ TYPE: amino acid
;/ STRANDEDNESS: <Unknown>
;/ TOPOLOGY: linear
;/ MOLECULE TYPE: peptide
;/ FEATURE:
;/ NAME/KEY: Peptide
;/ LOCATION: 1..30
;/ OTHER INFORMATION: /note= "motif 0 peptide from human telomerase core protein 1 (TCPI)"
;/ SEQUENCE DESCRIPTION: SEQ ID NO: 167:
US-09-843-676-167
Query Match 100.0%; Score 139; DB 10; Length 30;
Best Local Similarity 100.0%; Pred. No. 3.1e-14;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 PALLTSRLRFIPKPDGLRPIVNDYV 27
DB 3 PALLTSRLRFIPKPDGLRPIVNDYV 29
RESULT 10
US-09-766-253-167
; Sequence 167, Application US/09766253
; Publication No. US20020187471A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin
; Andrews, William H.
; TITLE OF INVENTION: No. US20020187471A1el Telomerase
; NUMBER OF SEQUENCES: 171
; CORRESPONDENCE ADDRESS:
;/ ADDRESSEE: Townsend and Townsend and Crew LLP
;/ STREET: Two Embarcadero Center, 8th Floor
;/ CITY: San Francisco
;/
```

STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/766,253
FILING DATE: 19-Jan-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/846,017
FILING DATE: 1997-04-25
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002920US
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 167:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 amino acids
TYPE: amino acid
STRADEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..30
OTHER INFORMATION: /note= "motif 0 peptide from human telomerase core protein 1 (TCPl)"
SEQUENCE DESCRIPTION: SEQ ID NO: 167:
US-09-766-253-167

Query Match 100.0%; Score 139; DB 10; Length 30;
Best Local Similarity 100.0%; Pred. No. 3.1e-14;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PALLTSRLRFPKPDGLRPVNMDDYV 27
Db 3 PALLTSRLRFPKPDGLRPVNMDDYV 29

RESULT 11

US-09-438-486-167
Sequence 167, Application US/09438486
Publication No. US20030009019A1
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin
APPLICANT: Andrews, William H.
TITLE OF INVENTION: No. US20030009019A1 Telomerase
NUMBER OF SEQUENCES: 223
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/438,486
FILING DATE: 12-NOV-1999
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002931US
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 167:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 amino acids
TYPE: amino acid
STRADEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..30
OTHER INFORMATION: /note= "motif 0 peptide from human telomerase core protein 1 (TCPl)"
US-09-438-486-167
Query Match 100.0%; Score 139; DB 11; Length 30;
Best Local Similarity 100.0%; Pred. No. 3.1e-14;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 PALLTSRLRFPKPDGLRPVNMDDYV 27
Db 3 PALLTSRLRFPKPDGLRPVNMDDYV 29
RESULT 12
US-10-053-758-167
Sequence 167, Application US/10053758
Publication No. US20030032075A1
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin
APPLICANT: Andrews, William H.
TITLE OF INVENTION: No. US20030032075A1 Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:

;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/10/053,758
;; FILING DATE: 18-Jan-2002
;; CLASSIFICATION: 536
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US/08/854,050
;; FILING DATE: 09-MAY-1997
;; APPLICATION NUMBER: US 08/851,843
;; FILING DATE: 06-MAY-1997
;; APPLICATION NUMBER: US 08/846,017
;; FILING DATE: 25-APR-1997
;; APPLICATION NUMBER: US 08/844,419
;; FILING DATE: 18-APR-1997
;; APPLICATION NUMBER: US 08/724,643
;; FILING DATE: 01-OCT-1996
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Apple, Randolph T.
;; REGISTRATION NUMBER: 36,429
;; REFERENCE/DOCKET NUMBER: 015389-002930US
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (415) 576-0300
;; TELEFAX: (415) 576-0300
;; INFORMATION FOR SEQ ID NO: 167:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 30 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: <Unknown>
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; FEATURE:
;; NAME/KEY: Peptide
;; LOCATION: 1..30
;; OTHER INFORMATION: /note= "motif 0 peptide from human
;; telomerase core protein 1 (TCP1)"
;; SEQUENCE DESCRIPTION: SEQ ID NO: 167:
US-10-053-758-167

Query Match 100.0%; Score 139; DB 15; Length 30;
Best Local Similarity 100.0%; Pred. No. 3.1e-14;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PALLTSRLRFPKPDGLRPVNMVYV 27
|||||
Db 3 PALLTSRLRFPKPDGLRPVNMVYV 29
|||||

RESULT 13
US-10-054-295-167
; Sequence 167, Application US/10054295
; Publication No. US20030044953A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin
; Andrews, William H.
; TITLE OF INVENTION: No. US20030044953A1el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/10/054,295
;; FILING DATE: 18-Jan-2002
;; CLASSIFICATION: 536
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/854,050
;; FILING DATE: <Unknown>
;; APPLICATION NUMBER: US 08/846,017
;; FILING DATE: 25-APR-1997
;; APPLICATION NUMBER: US 08/844,419
;; FILING DATE: 18-APR-1997
;; APPLICATION NUMBER: US 08/724,643
;; FILING DATE: 01-OCT-1996
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Apple, Randolph T.
;; REGISTRATION NUMBER: 36,429
;; REFERENCE/DOCKET NUMBER: 015389-002930US
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (415) 576-0200
;; TELEFAX: (415) 576-0300
;; INFORMATION FOR SEQ ID NO: 167:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 30 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: <Unknown>
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; FEATURE:
;; NAME/KEY: Peptide
;; LOCATION: 1..30
;; OTHER INFORMATION: /note= "motif 0 peptide from human
;; telomerase core protein 1 (TCP1)"
;; SEQUENCE DESCRIPTION: SEQ ID NO: 167:
US-10-054-295-167

Query Match 100.0%; Score 139; DB 15; Length 30;
Best Local Similarity 100.0%; Pred. No. 3.1e-14;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PALLTSRLRFPKPDGLRPVNMVYV 27
|||||
Db 3 PALLTSRLRFPKPDGLRPVNMVYV 29
|||||

RESULT 14
US-10-054-611-167
; Sequence 167, Application US/10054611
; Publication No. US20030059787A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin
; Andrews, William H.
; TITLE OF INVENTION: No. US20030059787A1el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/054,611
FILING DATE: 18-Jan-2002
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/854,050
FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 167:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..30
OTHER INFORMATION: /note= "motif 0 peptide from human telomerase core protein 1 (TCEP)"
SEQUENCE DESCRIPTION: SEQ ID NO: 167:
US-10-054-611-167
Query Match 100.0%; Score 139; DB 15; Length 30;
Best Local Similarity 100.0%; Pred. No. 3,1e-14;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 PALLTSRLRFIPKPDGLRPVNMDDYV 27
Db 3 PALLTSRLRFIPKPDGLRPVNMDDYV 29
RESULT 15
US-10-044-692-31
Sequence 31, Application US/10044692
Publication No. US20030096344A1
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
Andrews, William H.
TITLE-OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND THERAPEUTIC METHODS
NUMBER OF SEQUENCES: 335
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/044,692

FILING DATE: 11-Jan-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/912,951
FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002600US
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 54 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..54
OTHER INFORMATION: /note= "motif 1 and 2 peptide from human TET"
SEQUENCE DESCRIPTION: SEQ ID NO: 31:
US-10-044-692-31
Query Match 100.0%; Score 139; DB 15; Length 54;
Best Local Similarity 100.0%; Pred. No. 5,8e-14;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 PALLTSRLRFIPKPDGLRPVNMDDYV 27
Db 10 PALLTSRLRFIPKPDGLRPVNMDDYV 36
Search completed: November 12, 2003, 19:55:47
Job time : 21.566 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 12, 2003, 19:43:04 ; Search time 10.5283 Seconds
(without alignments)
246.626 Million cell updates/sec

Title: US-08-854-050-117

Perfect score: 139

Sequence: 1 PALLTSRLRFIPKPGRLPIVNMVYV 27

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR:*

2: PIR:*

3: PIR:*

4: PIR:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	139	100.0	1132	2 T03844	telomerase catalyt
2	52.5	37.8	214	2 C82255	adenylate kinase v
3	51	36.7	948	2 S51605	receptor-like tyro
4	51	36.7	2133	2 T42763	coagulation factor
5	49	35.3	282	2 T06600	acetyl-CoA carboxy
6	49	35.3	327	2 AF2859	conserved hypother
7	49	35.3	327	2 D97636	probable secreted
8	49	35.3	409	2 I48607	inositol 1,4,5-tri
9	49	35.3	2701	2 S17796	inositol-trisphosp
10	48	34.5	232	2 G86369	hypothetical prote
11	48	34.5	461	1 G64337	2-oxoglutarate/mal
12	48	34.5	803	2 T246803	hypothetical prote
13	47.5	34.2	164	2 H64803	ybfp protein - Esc
14	47	33.8	1132	2 T31107	telomerase reverse
15	46.5	33.5	203	2 D81934	probable periplasm
16	46.5	33.5	203	2 F81171	cryptic protein NM
17	46.5	33.5	203	2 A43857	cryptic protein cn
18	46.5	33.5	442	2 S58738	nitrate-binding pr
19	46.5	33.5	6420	2 T30283	polyketide synthas
20	46	33.1	428	2 T01489	hypothetical prote
21	46	33.1	449	1 Q4ADA5	maturaton (pIva2)
22	46	33.1	449	1 Q4ADA2	maturaton (pIva2)
23	46	33.1	1133	2 T51517	telomerase reverse
24	46	33.1	1239	2 G71266	probable ATP-depen
25	45.5	32.7	121	2 D69230	hypothetical prote
26	45.5	32.7	342	2 T27976	hypothetical prote
27	45.5	32.7	698	2 D82538	polysphosphate kina
28	45.5	32.7	939	2 C70876	hypothetical prote
29	45.5	32.7	1067	2 T18196	pol protein - silk

30 45 32.4 129 2 T44898 hypothetical prote
31 45 32.4 263 2 T00397 hypothetical prote
32 45 32.4 474 2 T47699 hypothetical prote
33 45 32.4 577 2 T12536 hypothetical prote
34 45 32.4 707 2 D86565 oligopeptide bindi
35 45 32.4 707 2 E72059 peptide ABC transp
36 45 32.4 737 2 T15615 hypothetical prote
37 45 32.4 797 2 H86865 hypothetical prote
38 44.5 32.0 291 2 AB1384 conserved hypother
39 44.5 32.0 291 2 AD1759 conserved hypother
40 44.5 32.0 319 2 H97386 lysosome [imported
41 44.5 32.0 337 2 A12604 phosphatase specific
42 44.5 32.0 374 1 F70584 probable glutamyl-
43 44.5 32.0 544 2 A72459 triacylglycerol li
44 44.5 32.0 549 2 JN0552 26S proteasome reg
45 44.5 32.0 893 2 A84591

ALIGNMENTS

RESULT 1

T03844

N;Alternate names: telomerase chain - human

C;Species: Homo sapiens (man)

C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 08-Oct-1999

C;Accession: T03844

R;Nakamura, T.M.; Morin, G.B.; Chapman, K.B.; Weinrich, S.L.; Andrews, W.H.; Lingner, J.

Science 277, 955-959, 1997

A;Title: telomerase catalytic subunit homologs from fission yeast and human.

A;Reference number: Z15111; MUID:97400623; PMID:9252327

A;Accession: T03844

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-1132 <NAK>

A;Cross-references: EMBL:AF015950; NID:g23330016; PIDN:AAC51672.1; PID:g23330017

A;Experimental source: kidney

C;Genetics:

A;Gene: TRT

A;Map position: 5p

Query Match 100.0%; Score 139; DB 2; Length 1132;
Best Local Similarity 100.0%; Pred. No. 2.5e-13;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PALLTSRLRFIPKPGRLPIVNMVYV 27

Db 614 PALLTSRLRFIPKPGRLPIVNMVYV 640

RESULT 2

C82255

adenylate kinase VC0986 [imported] - Vibrio cholerae (strain N16961 serogroup O1)

C;Species: Vibrio cholerae

C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001

C;Accession: C82255

R;Heidelberger, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.

Chardon, D.; Emolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers,

l, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.

Nature 406, 477-483, 2000

A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.

A;Reference number: A82035; MUID:20406833; PMID:10952301

A;Accession: C82255

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-214 <HEI>

A;Cross-references: GB:AE004180; GB:AE003852; NID:g9655445; PIDN:AAF94147.1; GSPDB:GN00

A;Experimental source: serogroup O1; strain N16961; biotype El Tor

C;Genetics:

A;Gene: VC0986

A;Map position: 1

C;Superfamily: adenylate kinase

Query Match 37.8%; Score 52.5; DB 2; Length 214;
 Best Local Similarity 46.2%; Pred. No. 1.4;
 Matches 12; Conservative 6; Mismatches 7; Indels 1; Gaps 1;

QY 3 LLSRLRFIPKPDGLRPI-VNMDYV 27
 |||: |||: |||: |||: |||:
 Db 82 LLDGFPRTIQADGLKEMGINVDYVI 107

RESULT 3
 S51605
 receptor-like tyrosine kinase Ehk-2 - rat
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 29-May-1998
 C:Accession: S51605
 R;Maisonnier, P.C.; Barrezuela, N.X.; Yancopoulos, G.D.
 Oncogene 8, 3277-3288, 1993
 A;Title: Ehk-1 and Ehk-2: two novel members of the Eph receptor-like tyrosine kinase fam
 A;Reference number: S49015; MUID:9406777; PMID:7504232
 A;Accession: S51605
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-948 <MAI>
 A;Cross-references: EMBL:S68030
 C;Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeat h
 C;Keywords: ATP; transmembrane protein
 F;628-336/Domain: protein kinase homology <KIN>
 F;636-644/Region: protein kinase ATP-binding motif

Query Match 36.7%; Score 51; DB 2; Length 948;
 Best Local Similarity 52.4%; Pred. No. 14;
 Matches 11; Conservative 4; Mismatches 4; Indels 2; Gaps 1;

QY 8 LRFPKPDGL--RPVNMVYV 26
 |||||: |||: |||: |||: |||:
 Db 385 LRFPRTPTGLINNSVVVLDV 405

RESULT 4
 T42763
 coagulation factor VIII precursor - pig
 C:Species: Sus scrofa domestica (domestic pig)
 C:Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jun-2000
 C:Accession: T42763
 R;Lollar, P.
 submitted to the EMBL Data Library, August 1996
 A;Reference number: Z22269
 A;Accession: T42763
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: mRNA
 A;Residues: 1-2133 <LOL>
 A;Cross-references: EMBL:U49517; NID:gl511633; PID:gl511634; PIDN:AAB06705.1
 C;Superfamily: coagulation factor VIII; discoidin I amino-terminal homology; ferroxidase
 C;Keywords: acute phase; blood coagulation; duplication; glycoprotein; hemophilia A; pla
 F;1-19/Domain: signal sequence #status predicted <SIG>
 F;20-2133/Product: coagulation factor VIII #status predicted <MAT>
 F;23-349/Domain: ferroxidase repeat homology <FOX1>
 F;402-730/Domain: ferroxidase repeat homology <FOX2>
 F;1498-1820/Domain: ferroxidase repeat homology <FOX3>

Query Match 36.7%; Score 51; DB 2; Length 2133;
 Best Local Similarity 72.7%; Pred. No. 38;
 Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 9 RFIPKPDGLRP 19
 |||: |||: |||: |||: |||:
 Db 612 RFLNPDGLQP 622

RESULT 5
 T06600
 acetyl-CoA carboxylase (EC 6.4.1.2), biotin carboxyl carrier chain precursor - soybean

N;Contains: biotin carboxyl carrier chain
 C;Species: Glycine max (soybean)
 C:Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 11-Jan-2002
 C:Accession: T06600
 R;Nielsen, N.C.; Reverdatto, S.V.; Beilinson, V.A.
 submitted to the EMBL Data Library, November 1995
 A;Reference number: Z15788
 A;Accession: T06600
 A;Status: translated from GB/EMBL/DBJ
 A;Molecule type: mRNA
 A;Residues: 1-262 <NIE>
 A;Cross-references: EMBL:U40666; NID:gl143318; PIDN:AAB67836.1; PID:gl143319
 A;Experimental source: strain Resnik
 C;Genetics:
 A;Gene: accB-1
 A;Genome: nuclear
 A;Complex: acetyl-CoA carboxylase is composed of biotin carboxylase (EC 6.3.4.14), carb
 C;Function: <ACC>
 A;Description: entire acetyl-CoA carboxylase complex catalyzes synthesis of malonyl-CoA
 carboxylation of biotin bound to biotin-carboxyl-carrier protein with bicarbonate; car
 A;Pathway: fatty acid biosynthesis
 C;Function: <BCC>
 A;Description: biotin carboxyl carrier chain is responsible for binding of biotin
 A;Pathway: fatty acid biosynthesis
 C;Superfamily: biotin carboxyl carrier protein; lipoyl/biotin-binding homology
 C;Keywords: biotin metabolism; chloroplast; fatty acid biosynthesis; ligase
 F;1-47/Domain: transit peptide (chloroplast) #status predicted <TNP>
 F;48-262/Product: acetyl-CoA carboxylase, biotin carboxyl carrier chain #status predict

Query Match 35.3%; Score 49; DB 2; Length 262;
 Best Local Similarity 66.7%; Pred. No. 6.2;
 Matches 10; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 4 LRSRLRFIPKPDGLR 18
 |||: |||: |||: |||: |||:
 Db 17 LTHSLRFSPKPNLR 31

RESULT 6
 AF2859
 conserved hypothetical protein Atu2303 [imported] - Agrobacterium tumefaciens (strain C
 C:Species: Agrobacterium tumefaciens
 C:Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
 C:Accession: AF2859
 R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo,
 erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutayavin, T.; Levy, R.; Li, M.; McClel
 ; Karp, P.; Romero, P.; Zhang, S.
 Science 294, 2317-2323, 2001
 A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
 ster, E.W.
 A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
 A;Reference number: AB2577; MUID:21608550; PMID:11743193
 A;Accession: AF2859
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-327 <KUR>
 A;Cross-references: GB:AE008688; PIDN:AAL43292.1; PID:gl17740782; GSPDB:GN00186
 A;Experimental source: strain C58 (Dupont)
 C;Genetics:
 A;Gene: Atu2303
 A;Map position: circular chromosome

Query Match 35.3%; Score 49; DB 2; Length 327;
 Best Local Similarity 55.8%; Pred. No. 8.1;
 Matches 10; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 8 LRFPKPDGLRPVNMVY 25
 |||: |||: |||: |||: |||:
 Db 215 LPLIPSGNRPPIAMVY 232

RESULT 7

D97636
Probable secreted protein AGR_C_4189 [imported] - Agrobacterium tumefaciens (strain CS8,
C:Species: Agrobacterium tumefaciens
C:Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 18-Nov-2002
C:Accession: D97636
R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,
A.; Liu, F.; Wollam, C.; Allinger, M.; Dougherty, D.; Scott, C.; Lappas, C.; Markelz, B.;
Science 294, 2323-2328, 2001
A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
A:Reference number: A97359; MUID:21608551; PMID:11743194
A:Accession: D97636
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-327 <KUR>
A:Cross-references: GB:AE007869; PIDN:AAK88045.1; PID:g15157467; GSPDB:GN00169
C:Genetics:
A:Gene: AGR_C_4189
A:Map position: circular chromosome

```
Query Match      35.3%; Score 49; DB 2; Length 327;
Best Local Similarity 55.6%; Pred. No. 8.1;
Matches 10; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
```

Qy 8 LRFPKPDGLRPVNM DY 25
| | | | |
| | | | |
Db 215 LPIUPEGGRNP IAMD Y 232

```

RESULT 8
I48607
inositol 1,4,5-trisphosphate receptor type 5 - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 15-Mar-1996 #sequence_revision 15-Mar-1996 #text_change 20-Aug-1999
C/Accession: I48607
R/De Smedt, H.; Missiaen, L.; Parys, J.B.; Bootman, M.D.; Mertens, L.; Van Den Bosch, L.
J. Biol. Chem. 269, 21691-21698, 1994
A/Title: Determination of relative amounts of inositol trisphosphate receptor mRNA isofo
A/Reference number: A53854; MUID:94342363; PMID:8063813
A/Accession: I48607
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-409 <RES>
A/Cross-references: EMBL:Z33908; NID:g512565; PIDN:CAA83957.1; PID:g512566
C/Superfamily: inositol-trisphosphate receptor

```

```

Query Match          35.3%; Score 49; DB 2; Length 409;
Best Local Similarity 50.0%; Pred. No. 11;
Matches 10; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY      2 ALATSLRLRFIPKPDGLRPV 21
      | : | | | | | | | | | | : | | |
Db      35 AICTSMLFFFSKPVGIRPFL 54

RESULT 9
S17796
inositol-trisphosphate receptor type 2 - rat
N:Alternate names: inositol-1,4,5-trisphosphate receptor type 2
C:Species: Rattus norvegicus (Norway rat)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Aug-1999
C:Accession: S17796
R:Suedhof, T.C.; Newton, C.L.; Archer III, B.T.; Ushkaryov, Y.A.; Mignery, G.A.

```

EMBL J. ID: J159-3206, 1991
A:Title: Structure of a novel Insp(3) receptor.
A:Reference number: S17796; MUID:92007769; PMID:1655411
A:Accession: S17796
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-2701 <SUE>
A:Cross-references: EMBL:X61677; NID:G56507; PIDN:CAA43852.1; PID:G56508
C:Superfamily: inositol-trisphosphate receptor
C:Keywords: transmembrane protein

Query Match 35.3% Score 49; DB 2; Length 2701;
Best Local Similarity 50.0%; Pred.No. 1e+02;
Matches 10; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QV 2 ALLTSRLRFPKPDGLRPV 11
| : | | | | | | | | | |
DB 2272 AICTSMLFFFSKPVGIRPFL 2291

RESULT 10
G86369
hypothetical protein F508.i5 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Dec-2001
C:Accession: G86369
R/Theologus, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso-
Chan, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marziali,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A>Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: AB6141; MUID:21016719; PMID:11130712
A:Accession: G86369
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-232 <STO>
A:Cross-references: GB:AE005172; NID:g4056442; PIDN:AAC98015.1; GSPDB:GN00141
C:Genetics:
A:Map position: 1

```

Query Match      34.5%; Score 48; DB 2; Length 232;
Best Local Similarity 48.0%; Pred. No. 7.7;
Matches 12; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

Qy 3 LLTSRLRFIPKDLRPIVMNMYV 27
    || : | | | | | | | |
Db 100 LLVKKRKVLKRDGPRQIVEDVKV 124

```

RESULT 11

G64537

2-oxoglutarate/malate translocator - *Helicobacter pylori* (strain 26695)

C:Species: *Helicobacter pylori*

C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999

C:Accession: G64537

R:Tomb, J.F.; White, O.; Karlavags, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.; Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalaf, H.G.; Glodek, A.; McKenn, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L. Nature 388, 539-547, 1997

A:Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C. A:Title: The complete genome sequence of the gastric pathogen *Helicobacter pylori*. A:Reference number: A64520; MUID:97394467; PMID:9252185

A:Accession: G64537

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-461 <TOM>

A:Cross-references: GB:AE000511; TIGR:HP0143

C:Superfamily: 2-oxoglutarate/malate translocator

```

Query Match      34.5%; Score 48; DB 1; Length 461;
Best Local Similarity 47.4%; Pred. No. 18;
Matches 9; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

Qy      1 PALLTSLRFLPKPDGLRP 19
      | | : : | : | | | |
Db      11 PFFIATLLYFLGAPDGLRP 29

RESULT 12

```

T24685
hypothetical protein T08D10.2 - *Caenorhabditis elegans*
C;Species: *Caenorhabditis elegans*
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Sep-2000
C;Accession: T24685
R;Lloyd, C.
submitted to the EMBL Data Library, August 1995
A;Reference number: Z19923
A;Accession: T24685
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-803 <WIL>
A;Cross-references: EMBL:Z50756; PIDN:CAA90637.1; GSPDB:GN00028; CESP:T08D10.2
A;Experimental source: clone T08D10
C;Genetics:
A;Gene: CESP:T08D10.2
A;Map position: X
A;Introns: 43/2; 64/1; 135/1; 272/3; 301/1; 345/2; 379/2; 520/1; 586/2; 643/2
C;Superfamily: *Caenorhabditis elegans* hypothetical protein Y40B1B.6
Query Match 34.5%; Score 48; DB 2; Length 803;
Best Local Similarity 66.7%; Pred. No. 34;
Matches 10; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
QY 13 KPDGLRPVNMDDYV 27
||||| :|||
Db 562 KPDGSVGLNADYV 576
RESULT 13
H64803
ybfP protein - *Escherichia coli* (strain K-12)
N;Alternate names: protein b0689
C;Species: *Escherichia coli*
C;Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 01-Mar-2002
C;Accession: H64803
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co
.A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of *Escherichia coli* K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Accession: H64803
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-164 <BLAT>
A;Cross-references: GB:AE000172; GB:U00096; NID:gl786896; PIDN:AAC73783.1; PID:gl786905;
A;Experimental source: strain K-12, substrain MG1655
C;Genetics:
A;Gene: ybfP
C;Keywords: transmembrane protein
F;7-23/Domain: transmembrane #status predicted <TMM>
Query Match 34.2%; Score 47.5; DB 2; Length 164;
Best Local Similarity 78.6%; Pred. No. 6.1;
Matches 11; Conservative 0; Mismatches 2; Indels 1; Gaps 1;
QY 13 KPDGLRPVNMDDYV 26
||| :|||
Db 117 KP-GTRPIVNDYV 129
RESULT 14
T31107
telomerase reverse transcriptase - *Oxytricha trifallax*
C;Species: *Oxytricha trifallax*
C;Date: 02-Sep-2000 #sequence_revision 02-Sep-2000 #text_change 02-Sep-2000
C;Accession: T31107
R;Bryan, T.M.; Sperger, J.M.; Chapman, K.B.; Cech, T.R.
Proc. Natl. Acad. Sci. U.S.A. 95, 8479-8484, 1998
A;Title: Telomerase reverse transcriptase genes in *Tetrahymena thermophila* and *Oxytricha*
A;Reference number: Z20985; MUID:98337940; PMID:9671703
A;Accession: T31107
A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA
A;Residues: 1-1132 <BRY>
A;Cross-references: EMBL:AF060230; NID:g3342795; PID:g3342796; PIDN:AAC39163.1
C;Genetics:
A;Gene: TERT
Query Match 33.8%; Score 47; DB 2; Length 1132;
Best Local Similarity 50.0%; Pred. No. 75;
Matches 9; Conservative 3; Mismatches 6; Indels 0; Gaps 0;
QY 7 RLRFIPKPDGLRPVNMDD 24
:||||| :|||
Db 617 KLRLIPKGTFRPIMTFN 634
RESULT 15
DB1934
probable periplasmic protein NMA0881 [imported] - *Neisseria meningitidis* (strain Z2491
C;Species: *Neisseria meningitidis*
C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001
C;Accession: DB1934
R;Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; More
; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream
Nature 404, 502-506, 2000
A;Title: Complete DNA sequence of a serogroup A strain of *Neisseria meningitidis* Z2491.
A;Reference number: A81775; MUID:20222556; PMID:10761919
A;Accession: DB1934
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-203 <PAR>
A;Cross-references: GB:AL162754; GB:AL157959; NID:g7379424; PIDN:CAB84161.1; PID:g73795
A;Experimental source: serogroup A, strain Z2491
C;Genetics:
A;Gene: cnp1; NMA0881
Query Match 33.5%; Score 46.5; DB 2; Length 203;
Best Local Similarity 41.7%; Pred. No. 11;
Matches 10; Conservative 6; Mismatches 7; Indels 1; Gaps 1;
QY 1 PALLTSRLRFIPKPDG-LRPVNM 23
||| :||| :||| :|||
Db 75 PKILLDSLQIMPAPDGSIRYILNI 98
Search completed: November 12, 2003, 19:52:01
Job time : 10.5283 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 12, 2003, 19:41:59 ; Search time 5.60377 Seconds
(without alignments)
226.583 Million cell updates/sec

Title: US-08-854-050-117

Perfect score: 139

Sequence: 1 PALLTSRLRPIPKDGLRPIVNMVYV 27

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %	Length	ID	Description
1	139	100.0	1132	1 TERT HUMAN	O14746 homo sapien
2	93	66.9	1122	1 TERT MOUSE	O70372 mus musculus
3	52.5	37.8	214	1 KAD_VIBCH	O9Ktb7 vibrio chol
4	51	36.7	948	1 EPA6 RAT	P54758 rattus norv
5	51	36.7	2133	1 FAF_PIG	P12263 sus scrofa
6	49	35.3	262	1 BCCP SOYBN	O42783 glycine max
7	49	35.3	1281	1 IP3S MOUSE	O92329 mus musculus
8	49	35.3	2701	1 IP3S HUMAN	O14571 homo sapien
9	49	35.3	2701	1 IP3S RAT	P29995 rattus norv
10	48.5	34.9	110	1 YHBV ACTAC	P96769 actinobacil
11	47.5	34.2	164	1 YBFP ECOLI	P75737 escherichia
12	47.5	34.2	214	1 KAD_VIBPA	O87th4 vibrio para
13	47	33.8	437	1 CTBQ XENLA	O9w758 xenopus lae
14	47	33.8	596	1 SDP_EIMBO	P42789 eimeria bov
15	47	33.8	1132	1 TERT_OXYTR	O76332 oxytricha t
16	46	33.1	449	1 PIV2 ADE02	P03272 human adeno
17	46	33.1	449	1 PIV2 ADE05	P03271 human adeno
18	45.5	32.7	214	1 KAD_VIBVU	O8dfm1 vibrio vuln
19	45.5	32.7	698	1 PPK_XYLPA	O9pac7 xylolla fas
20	45	32.4	797	1 SYPE_LACLA	O9c8b5 lactococcus
21	44.5	32.0	291	1 Y074_LISMO	O8y499 listeria mo
22	44.5	32.0	291	1 YQ17_LISIN	O928b9 listeria in
23	44.5	32.0	374	1 PST1 MYCTU	P15712 mycobacteri
24	44.5	32.0	549	1 LIP4 CANRU	P32948 candida rug
25	44.5	32.0	574	1 SYE_AERPE	O9y9h1 aeropyrum p
26	44	31.7	117	1 AMC2_PIG	P22352 sus scrofa
27	44	31.7	301	1 YE21 MYCTU	P71690 mycobacteri
28	44	31.7	410	1 YMM3 CAEEL	P34491 caenorhabdi
29	44	31.7	452	1 PIV2 ADE12	P12540 human adeno
30	44	31.7	923	1 TOR_DROME	P18475 drosophila
31	43.5	31.3	369	1 PROE CORGL	P46546 corynebacte
32	43.5	31.3	1203	1 ATB4_RAT	O64542 rattus norv
33	43	30.9	133	1 Y044_BORBU	O51073 borrelia bu

RESULT 1

TERT_HUMAN
ID TERT_HUMAN STANDARD; PRT; 1132 AA.
AC O14746; O14783;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Telomerase reverse transcriptase (EC 2.7.7.-) (Telomerase catalytic subunit) (HEST2).
GN TERT OR TRT OR EST2 OR TCS1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=97400623; PubMed=9252327;
RA Nakamura T.M., Morin G.B., Chapman K.B., Weinrich S.L., Andrews W.H., Lingner J., Harley C.B., Cech T.R.;
RT "Telomerase catalytic subunit homologs from fission yeast and human."; Science 277:955-959(1997).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=97433088; PubMed=9288757;
RA Meyerson M., Counter C.M., Eaton E.N., Ellison L.W., Steiner P., Caddle S.D., Ziaugra L., Beijersbergen R.L., Davidoff M.J., Liu Q., Bacchetti S., Haber D.A., Weinberg R.A.;
RT "hEST2, the putative human telomerase catalytic subunit gene, is up-regulated in tumor cells and during immortalization."; Cell 90:783-795(1997).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=99267414; PubMed=10333526;
RA Wick M., Zubov D., Hagen G.;
RT "Genomic organization and promoter characterization of the gene encoding the human telomerase reverse transcriptase (hTERT)."; Gene 232:97-106(1999).
RN [4]
RP SEQUENCE FROM N.A.
RA Londono-Vallejo J.A.;
RT "Sequence of a BAC carrying the entire hTERT gene."; Submitted (Oct-2001) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: TELOMERASE IS A RIBONUCLEOPROTEIN ENZYME ESSENTIAL FOR THE REPLICATION OF CHROMOSOME TERMINI IN MOST EUKARYOTES. IT ELONGATES TELOMERES. IT IS A REVERSE TRANSCRIPTASE THAT ADDS SIMPLE SEQUENCE REPEATS TO CHROMOSOME ENDS BY COPYING A TEMPLATE SEQUENCE WITHIN THE RNA COMPONENT OF THE ENZYME.
CC -!- SUBUNIT: Interacts with PINX1.
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- DISEASE: ACTIVATION OF TELOMERASE HAS BEEN IMPLICATED IN CELL IMMORTALIZATION AND CANCER CELL PATHOGENESIS.
CC -!- SIMILARITY: BELONGS TO THE REVERSE TRANSCRIPTASE FAMILY.
CC TELOMERASE SUBFAMILY.

This SWISS-PROT entry is copyright. It is produced through a collaboration

ALIGNMENTS

34 43 30.9 249 1 TRPC_PYRAE
35 43 30.9 269 1 T2S1_STRFI
36 43 30.9 369 1 DAPE_CORGL
37 43 30.9 389 1 TRP1_MAIZE
38 43 30.9 415 1 RL3_DROME
39 43 30.9 448 1 PIV2_ADE07
40 43 30.9 455 1 UFOG_HORVU
41 43 30.9 490 1 SYE_BORBU
42 43 30.9 577 1 POF3_SCHPO
43 43 30.9 831 1 NAPA_RHOSH
44 42.5 30.6 284 1 YI34_THETN
45 42.5 30.6 420 1 CLPX_BACSU

Q8zyx2 pyrobaculum
O52512 streptomyce
Q59284 corynebacte
P43283 zea mays (m
O16797 drosophila
P03273 human adeno
P14726 hordeum vul
O51345 borrelia bu
O74991 schizosacch
Q53176 rhodobacter
Q8r828 thermoanaer
P50866 bacillus su

CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
 CC or send an email to license@isb-sib.ch).
 CC -----

CC EMBL; AF015950; AAC51672.1; -;
 CC EMBL; AF018167; AAC51724.1; -;
 CC EMBL; AF128894; AAD30037.1; -;
 CC EMBL; AF128893; AAD30037.1; JOINED.
 CC EMBL; AY007685; AAG23289.1; -;
 CC PIR; T03844; T03844.
 CC Genew; HGNC:11730; TERT.
 CC MTM; 187270; -;
 CC GO; 0005696; C:telomeres; TAS.
 CC GO; 0003721; F:telomeric template RNA reverse transcriptas. .; TAS.
 CC GO; 0007003; P:telomere binding; TAS.
 CC InterPro; IPR00477; RVTse.
 CC InterPro; IPR003545; Telomerase_RT.
 CC Pfam; PF00078; rvt; 1.
 CC PRINTS; PR01365; TLOMERASERT.
 CC Transferase; RNA-directed DNA polymerase; Telomere; Nuclear protein;
 CC DNA-binding.
 CC KW TRANSFERASE; RNA-DIRECTED DNA POLYMERASE; TELOMERE; NUCLEAR PROTEIN;
 CC FT CONFLICT 516 516 D -> G (IN REF. 2).
 CC SEQUENCE 1132 AA; 126956 MW; 94E35469C4CA33A0 CRC64;

Query Match 100.0%; Score 139; DB 1; Length 1132;
 Best Local Similarity 100.0%; Pred. No. 8e-14;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PALLTSRLRFPKPDGLRPVNMDDYV 27
 |||||
 DB 614 PALLTSRLRFPKPDGLRPVNMDDYV 640

RESULT 2

TERT MOUSE
 ID TERT_MOUSE STANDARD; PRT; 1122 AA.
 AC O70372; G35432;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Telomerase reverse transcriptase (EC 2.7.7.-) (Telomerase catalytic
 DE subunit).
 GN TERT.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98241176; PubMed=9582020;
 RA Greenberg R.A., Allsopp R.C., Chin L., Morin G.B., Depinho R.A.;
 RT "Expression of mouse telomerase reverse transcriptase during
 RT development, differentiation and proliferation.";
 RL Oncogene 16:1723-1730(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=9833668; PubMed=9724727;
 RA Martin-Rivera L., Herrera E., Albar J.P., Blasco M.A.;
 RA "Expression of mouse telomerase catalytic subunit in embryos and
 RT adult tissues.";
 RL Proc. Natl. Acad. Sci. U.S.A. 95:10471-10476(1998).
 RN [3]
 RP SEQUENCE OF 550-616 FROM N.A.
 RX Drissi R., Cleveland J.L.;
 RA "Partial sequence of Mus musculus telomerase catalytic subunit
 RT homolog.";
 RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: TELOMERASE IS A RIBONUCLEOPROTEIN ENZYME ESSENTIAL FOR
 CC THE REPLICATION OF CHROMOSOME TERMINI IN MOST EUKARYOTES. IT
 CC ELONGATES TELOMERES. IT IS A REVERSE TRANSCRIPTASE THAT ADDS

CC SIMPLE SEQUENCE REPEATS TO CHROMOSOME ENDS BY COPYING A TEMPLATE
 CC SEQUENCE WITHIN THE RNA COMPONENT OF THE ENZYME.
 CC -!- SUBUNIT: Interacts with PINK1 (By similarity).
 CC -!- SUBCELLULAR LOCATION: Nuclear.
 CC -!- SIMILARITY: BELONGS TO THE REVERSE TRANSCRIPTASE FAMILY.
 CC TELOMERASE SUBFAMILY.
 CC -----

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
 CC or send an email to license@isb-sib.ch).
 CC -----

CC EMBL; AF051911; AAC09323.1; -;
 CC EMBL; AF073311; AAC34821.1; -;
 CC EMBL; AF029235; AAB84200.1; -;
 CC MGD; MGI:1202709; TERT.
 CC InterPro; IPR000477; RVTse.
 CC InterPro; IPR003545; Telomerase_RT.
 CC Pfam; PF00078; rvt; 1.
 CC PRINTS; PR01365; TLOMERASERT.
 CC Transferase; RNA-directed DNA polymerase; Telomere; Nuclear protein;
 CC DNA-binding.
 CC KW TRANSFERASE; RNA-DIRECTED DNA POLYMERASE; TELOMERE; NUCLEAR PROTEIN;
 CC FT CONFLICT 553 553 I -> V (IN REF. 3).
 CC SEQUENCE 1122 AA; 127977 MW; F85266905DD6558C CRC64;

Query Match 66.9%; Score 93; DB 1; Length 1122;
 Best Local Similarity 75.0%; Pred. No. 1.5e-06;
 Matches 18; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 ALLTSRLRFPKPDGLRPVNMDDY 25
 |:::|||||:|||||
 DB 605 AMPICLRFPKPDGLRPVNMDDY 628

RESULT 3

KAD VIBCH
 ID KAD_VIBCH STANDARD; PRT; 214 AA.
 AC Q9TBT7;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Adenylate kinase (EC 2.7.4.3) (ATP-AMP transphosphorylase).
 DE ADK OR VC0396.
 GN Vibrio cholerae.
 OS Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
 OC Vibrionaceae; Vibrio.
 OX NCBI_TaxID=666;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=E1 for N16961 / Serotype O1;
 RX MEDLINE=20406833; PubMed=10952301;
 RA Heideberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwin M.L.,
 RA Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
 RA Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
 RA Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
 RA McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
 RA Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
 RA Fraser C.M.;
 RT "DNA sequence of both chromosomes of the cholera pathogen Vibrio
 RT cholerae";
 RL Nature 406:477-483(2000).
 CC -!- FUNCTION: THIS SMALL UBQUITOUS ENZYME IS ESSENTIAL FOR
 CC MAINTENANCE AND CELL GROWTH.
 CC -!- CATALYTIC ACTIVITY: ATP + AMP = ADP + ADP.
 CC -!- SUBUNIT: Monomer (By similarity).
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -!- SIMILARITY: Belongs to the adenylate kinase family.
 CC -----

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

RX MEDLINE=94179260; PubMed=7510693;
 RA Lubin I.M., Healey J.F., Scandella D., Runge M.S., Lollar P.;
 RT "Elimination of a major inhibitor epitope in factor VIII.";
 RL J. Biol. Chem. 269:8639-8641(1994).
 CC -1- FUNCTION: FACTOR VIII, ALONG WITH CALCIUM AND PHOSPHOLIPID, ACTS
 CC AS A COFACTOR FOR FACTOR IXA WHEN IT CONVERTS FACTOR X TO THE
 CC ACTIVATED FORM, FACTOR XA.
 CC -1- SUBCELLULAR LOCATION: Extracellular.
 CC -1- SIMILARITY: Contains 3 F5/8 type A domains.
 CC -1- SIMILARITY: Contains 2 F5/8 type C domains.
 CC -1- SIMILARITY: STRONG, TO COAGULATION FACTOR V.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL; U49517; AB06705.1; --
 CC PIR; A25945; A25945.
 CC PIR; T42763; T42763.
 CC HSP; P00451; ICFG.
 CC InterPro; IPR001117; Cu-oxidase.
 CC InterPro; IPR000421; FA58 C.
 CC Pfam; PF00394; Cu-oxidase_3.
 CC Pfam; PF00754; F5_F8_type_C_2.
 CC SMART; SM00231; FA58C_2.
 CC PROSITE; PS01285; FA58C_1; 2.
 CC PROSITE; PS01286; FA58C_2; 2.
 CC PROSITE; PS50022; FA58C_3; 2.
 CC PROSITE; PS00079; MULTICOPPER OXIDASE1; 3.
 CC Blood coagulation; Repeat; Plasma; Acute phase; Calcium;
 KW Signal; Glycoprotein; Sulfation.
 FT SIGNAL 1 19 POTENTIAL.
 FT CHAIN 20 2133 COAGULATION FACTOR VIII.
 FT DOMAIN 20 357 F5/8 TYPE A 1.
 FT DOMAIN 20 357 PLASTOCYANIN-LIKE 1.
 FT DOMAIN 207 357 PLASTOCYANIN-LIKE 2.
 FT DOMAIN 399 730 F5/8 TYPE A 2.
 FT DOMAIN 583 730 PLASTOCYANIN-LIKE 3.
 FT DOMAIN 760 1599 PLASTOCYANIN-LIKE 4.
 FT DOMAIN 1495 1822 F5/8 TYPE A 3.
 FT DOMAIN 1495 1659 PLASTOCYANIN-LIKE 5.
 FT DOMAIN 1669 1822 PLASTOCYANIN-LIKE 6.
 FT DOMAIN 1822 1970 F5/8 TYPE C 1.
 FT DOMAIN 1975 2127 F5/8 TYPE C 2.
 FT SITE 391 392 CLEAVAGE (BY THROMBIN) (BY SIMILARITY).
 FT SITE 759 760 CLEAVAGE (BY THROMBIN) (BY SIMILARITY).
 FT SITE 1449 1450 CLEAVAGE (ACTIVATION) (BY SIMILARITY).
 FT SITE 1490 1491 CLEAVAGE (BY THROMBIN) (BY SIMILARITY).
 FT MOD RES 737 737 SULFATION (BY SIMILARITY).
 FT MOD RES 738 738 SULFATION (BY SIMILARITY).
 FT MOD RES 742 742 SULFATION (BY SIMILARITY).
 FT DISULFID 173 199 PROBABLE.
 FT DISULFID 547 573 PROBABLE.
 FT DISULFID 1633 1659 PROBABLE.
 FT DISULFID 1822 1970 BY SIMILARITY.
 FT DISULFID 1975 2127 BY SIMILARITY.
 FT CARBOHYD 233 233 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 259 259 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 601 601 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 929 929 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 985 985 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1025 1025 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1111 1111 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1181 1181 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1208 1208 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1245 1245 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1265 1265 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1335 1335 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 1408 1408 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1611 1611 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1919 1919 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CONFLICT 713 713 N -> M (IN REF. 2).
 FT CONFLICT 734 734 I -> T (IN REF. 2).
 FT CONFLICT 792 792 G -> Q (IN REF. 2).
 FT CONFLICT 1133 1133 E -> F (IN REF. 2).
 FT CONFLICT 1191 1191 I -> L (IN REF. 2).
 FT CONFLICT 1209 1209 R -> F (IN REF. 2).
 FT CONFLICT 1437 1437 C -> G (IN REF. 2).
 FT CONFLICT 1456 1456 F -> R (IN REF. 2).
 FT CONFLICT 1539 1539 F -> R (IN REF. 2).
 FT CONFLICT 1546 1546 Q -> N (IN REF. 2).
 SQ SEQUENCE 2133 AA; 239304 MW; 152BBA8997F570DA CRC64;
 Query Match 36.7%; Score 51; DB 1; Length 2133;
 Best Local Similarity 72.7%; Pred. No. 14;
 Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 9 REIPKPDGLRP 19
 DB 612 RELPNPDGLQP 622
 ||:|:||||:
 RESULT 6
 BCCP_SOYBN STANDARD; PRT; 262 AA.
 ID_BCCP_SOYBN
 AC Q42783;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Biotin carboxyl carrier protein of acetyl-CoA carboxylase, chloroplast
 DE precursor (BCCP).
 GN ACCB-1.
 OS Glycine max (Soybean).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eudicots I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
 OX NCBI_TaxID=3847;
 RN [1]_TaxID=3847;
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RC STRAIN=cv. Resnik;
 RA Reverdatto S.V., Beilinson V., Neilsen N.C.;
 RT "Characterization of a cDNA clone encoding a BCCP subunit of acetyl-
 RT CoA carboxylase from soybean."
 RL (In) Plant Gene Register PGR96-040.
 CC -1- FUNCTION: THIS PROTEIN IS A COMPONENT OF THE ACETYL COENZYME A
 CC CARBOXYLASE COMPLEX; FIRST, BIOTIN CARBOXYLASE CATALYZES THE
 CC CARBOXYLATION OF THE CARRIER PROTEIN AND THEN THE TRANSCARBOXYLASE
 CC TRANSFERS THE CARBOXYL GROUP TO FORM MALONYL-COA.
 CC -1- PATHWAY: Long-chain fatty acid biosynthesis; first step.
 CC -1- SUBCELLULAR LOCATION: Chloroplast.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL; U40666; AB67836.1; --
 CC PIR; T06600; T06600.
 CC HSP; P29905; 3BD0.
 CC InterPro; IPR001249; AccCoA biotinCC.
 CC InterPro; IPR001882; Biotin_attach.
 CC InterPro; IPR000089; Biotin_lipoyl.
 CC Pfam; PF00364; biotin_lipoyl; 1.
 CC PRINTS; PR01071; ACOABIOTINCC.
 CC TIGRFAfam; TIGR00531; BCCP; 1.
 CC PROSITE; PS00188; BIOTIN; 1.
 KW Fatty acid biosynthesis; Biotin; Chloroplast; Transit peptide.
 FT TRANSIT 1 47 CHLOROPLAST.


```

FT CHAIN 48 262 BIOTIN CARBOXYL CARRIER PROTEIN OF
FT BINDING 227 ACTYL-COA CARBOXYLASE.
FT BIOTIN (BY SIMILARITY).
SQ SEQUENCE 262 AA; 27657 MW; 79B273BD8B97DF48 CRC64;

Query Match 35.3%; Score 49; DB 1; Length 262;
Best Local Similarity 66.7%; Pred. No. 2.7; Indels 0; Gaps 0;
Matches 10; Conservative 1; Mismatches 4;

QY 4 LTSRLRFIPKPDGLR 18
Db 17 LTHSLRFSPKPNLR 31

RESULT 7
IP3S_MOUSE
ID IP3S_MOUSE STANDARD; PRT; 1281 AA.
AC Q92329; P70226; Q61744;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE Inositol 1,4,5-trisphosphate receptor type 2 (Type 2 inositol 1,4,5-
DE trisphosphate receptor) (Type 2 InsP3 receptor) (IP3 receptor isoform
DE 2) (InsP3R2) (inositol 1,4,5-trisphosphate type V receptor)
DE (Fragments).
GN IP3R2 OR IP3R5.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE OF 1-272 FROM N.A., AND ALTERNATIVE SPLICING.
RP TISSUE=Heart;
RC MEDLINE=98399819; PubMed=9729462;
RA Futatsugi A., Kuwahima G., Mikoshiba K.;
RT "Muscle-specific mRNA isoform encodes a protein composed mainly of the
RT N-terminal 175 residues of type 2 Ins(1,4,5)P3 receptor.";
RL Biochem. J. 334:559-563 (1998).
RN [2]
SEQUENCE OF 273-1281 FROM N.A.
RP STRAIN=C3H; TISSUE=Embryo;
RC MEDLINE=97218118; PubMed=9065779;
RA De Smedt H., Missiaen L., Parys J.B., Henning R.H., Sienaert I.,
RA Vanlinden S., Gijssels A., Hampens B., Casteels R.;
RT "Isoform diversity of the inositol trisphosphate receptor in cell
RT types of mouse origin.";
RL Biochem. J. 322:575-583 (1997).
RN [3]
SEQUENCE OF 818-1226 FROM N.A.
RP STRAIN=C3H; TISSUE=Embryo;
RC MEDLINE=94342363; PubMed=8063813;
RA De Smedt H., Missiaen L., Parys J.B., Bootman M.D., Mertens L.,
RA Van den Bosch L., Casteels R.;
RT "Determination of relative amounts of inositol trisphosphate receptor
RT mRNA isoforms by ratio polymerase chain reaction.";
RL J. Biol. Chem. 269:21691-21698 (1994).
CC -1- FUNCTION: RECEPTOR FOR INOSITOL 1,4,5-TRISPHOSPHATE. A SECOND
CC MESSENGER THAT MEDIATES THE RELEASE OF INTRACELLULAR CALCIUM.
CC -1- SUBUNIT: Homotetramer (By similarity).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Endoplasmic
CC reticulum (By similarity).
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=Long;
CC IsoId=Q92329-1; Sequence=Displayed;
CC Name=Short; Synonyms=IP3R;
CC IsoId=Q92329-2; Sequence=VSP_002701, VSP_002702;
CC -1- TISSUE SPECIFICITY: THE SHORT ISOFORM IS FOUND IN SKELETAL MUSCLE
CC AND HEART.
CC -1- DOMAIN: THE RECEPTOR CONTAINS A CALCIUM CHANNEL IN ITS C-TERMINAL
CC EXTREMITY. ITS LARGE N-TERMINAL CYTOPLASMIC REGION HAS THE LIGAND-
CC BINDING SITE IN THE N-TERMINUS AND MODULATORY SITES IN THE MIDDLE
CC PORTION IMMEDIATELY UPSTREAM OF THE CHANNEL REGION.

```

```

CC -1- PTM: PHOSPHORYLATED ON TYROSINE RESIDUES (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE INSP3 RECEPTOR FAMILY.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC -----
CC EMBL; AB012393; BAA33960.1; -.
CC EMBL; Z71173; CA94861.1; -.
CC EMBL; Z33908; CA983957.1; -.
CC FIR; I48607; I48607.
CC MGD; MGI:99418; Itpr2.
CC InterPro; IPR001682; Ca/Na_pore.
CC InterPro; IPR005821; Ion_trans.
CC InterPro; IPR003608; MIR.
CC Pfam; PF00520; Ion_trans; 2.
CC Pfam; PF02815; MIR; 1.
CC SMART; SM00472; MIR; 3.
CC Receptor; Transmembrane; Glycoprotein; Phosphorylation;
CC Endoplasmic reticulum; Ionic channel; Ion transport; Calcium channel;
CC Alternative splicing.
CC NON_CONS 272 273
CC FT DOMAIN 1 807 CYTOPLASMIC (POTENTIAL).
CC FT TRANSMEM 808 828 POTENTIAL.
CC FT DOMAIN 829 840 EXTRACELLULAR (POTENTIAL).
CC FT TRANSMEM 841 861 POTENTIAL.
CC FT DOMAIN 862 887 CYTOPLASMIC (POTENTIAL).
CC FT TRANSMEM 888 908 POTENTIAL.
CC FT DOMAIN 909 931 EXTRACELLULAR (POTENTIAL).
CC FT TRANSMEM 932 952 POTENTIAL.
CC FT DOMAIN 953 974 CYTOPLASMIC (POTENTIAL).
CC FT TRANSMEM 975 995 POTENTIAL.
CC FT DOMAIN 996 1101 EXTRACELLULAR (POTENTIAL).
CC FT TRANSMEM 1102 1122 POTENTIAL.
CC FT DOMAIN 1123 1281 CYTOPLASMIC (POTENTIAL).
CC FT MOD_RES 1187 1187 PHOSPHORYLATION (POTENTIAL).
CC FT VARSPPLIC 175 175 N -> NDMGAVI (in isoform Short).
CC FT VARSPPLIC 176 1281 /FTId=VSP_002701.
CC FT VARSPPLIC 176 1281 Missing (in isoform Short).
CC FT VARSPPLIC 176 1281 /FTId=VSP_002702.
SQ SEQUENCE 1281 AA; 145073 MW; FAE7899B8E9A5598 CRC64;

Query Match 35.3%; Score 49; DB 1; Length 1281;
Best Local Similarity 50.0%; Pred. No. 16; Indels 0; Gaps 0;
Matches 10; Conservative 3; Mismatches 7;

QY 2 ALLTSRLRFIPKPDGLRPV 21
Db 852 AICTSMLFFFSKPVGIRPFL 871

RESULT 8
IP3S_HUMAN
ID IP3S_HUMAN STANDARD; PRT; 2701 AA.
AC Q14571; O94773;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Inositol 1,4,5-trisphosphate receptor type 2 (Type 2 inositol 1,4,5-
DE trisphosphate receptor) (Type 2 InsP3 receptor) (IP3 receptor isoform
DE 2) (InsP3R2).
DE ITPR2.
GN Homo sapiens (Human).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A. (ISOFORM LONG).
RP MEDLINE=94363219; PubMed=8081734;

```



```

DR BUR; S17796; S17796.
DR InterPro; IPR000699; Ca-rel_channel.
DR InterPro; IPR001682; Ca/Na_pore.
DR InterPro; IPR005821; Ion_trans.
DR InterPro; IPR003608; MIR.
DR Pfam; PF00520; ion_trans; 1.
DR Pfam; PF02815; MIR; 4.
DR Pfam; PF01365; RYDR_ITPR; 2.
DR SMART; SMO0472; MIR; 4.
KW Receptor; Transmembrane; Phosphorylation; Endoplasmic reticulum;
KW Ionic channel; Ion transport; Calcium channel; Polymorphism.
FT DOMAIN 1 2227 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 2228 2248 POTENTIAL..
FT DOMAIN 2249 2260 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 2261 2281 POTENTIAL..
FT DOMAIN 2282 2284 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 2285 2305 POTENTIAL..
FT DOMAIN 2306 2307 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 2308 2328 POTENTIAL..
FT DOMAIN 2329 2351 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 2352 2372 POTENTIAL..
FT DOMAIN 2373 2394 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 2395 2415 POTENTIAL..
FT DOMAIN 2416 2521 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 2522 2542 POTENTIAL..
FT DOMAIN 2543 2601 EXTRACELLULAR (POTENTIAL).
FT MOD_RES 2607 2607 PHOSPHORYLATION (POTENTIAL).
FT VARIANT 689 689 D -> H.
FT VARIANT 1013 1013 G -> C.
FT VARIANT 1256 1256 L -> P.
FT VARIANT 2384 2384 V -> I.
FT VARIANT 2694 2694 E -> V.
FT CONFLICT 119 119 K -> N (IN REF. 2).
FT CONFLICT 344 344 H -> R (IN REF. 2).
FT CONFLICT 943 943 W -> V (IN REF. 2).
FT CONFLICT 1692 1692 S -> G (IN REF. 2).
FT CONFLICT 2556 2556 K -> E (IN REF. 2).
SQ SEQUENCE 2701 AA; 307054 MW; 42BF7F1024335984 CRC64;

Query Match 35.3%; Score 49; DB 1; Length 2701;
Best Local Similarity 50.0%; Pred. No. 38;
Matches 10; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 2 ALLTSRLRFLPKPGDGRPIV 21
: ||| ||| ||| ||| :
Db 2272 AICTMLFFSKPGVGRPFL 2291

RESULT 10
YHBJ_ACTAC STANDARD; PRT; 110 AA.
AC P96769;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Hypothetical UPF0042 protein H1146 homolog (Fragment).
OS Actinobacillus actinomycetemcomitans (Haemophilus
actinomycetemcomitans).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Actinobacillus.
OX NCBI_TaxID=714;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CUL1000;
RX MEDLINE=98295003; PubMed=9631542;
RA Kaplan J.B., Fine D.H.;
RT "Codon usage in Actinobacillus actinomycetemcomitans.";
RL FEMS Microbiol. Lett. 163:31-36(1998).
CC -/- SIMILARITY: Belongs to the UPF0042 family.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; A5000172; AAC73783.1; -.
CC FIR; H64803; H64803.
CC Ecogene; EGI4158; YBFP.
CC PROSITE; PS00013; PROKAR LIPOPROTEIN; 1.
KW Hypothetical protein; Membrane; Lipoprotein; Signal;
KW Complete proteome.
FT SIGNAL 1 22 POTENTIAL.
FT CHAIN 23 164 HYPOTHETICAL LIPOPROTEIN YBFP.
FT LIPID 23 23 N-ACYL DIGLYCERIDE (POTENTIAL).
SQ SEQUENCE 164 AA; 18282 MW; CCSA0AB1CBACC0EE CRC64;

Query Match 34.2%; Score 47.5; DB 1; Length 164;
Best Local Similarity 78.6%; Pred. No. 2.7;
Matches 11; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 13 KPDGLRPVNMVYV 26

```

use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).

EMBL; U89523; AAC46410.1; -.
 HAMAP; MF_00636; -. 1.
 InterPro; IPR005337; UPF0042.
 Pfam; PF03668; ATP_bind2; 1.
 KW Hypothetical protein.
 FT NON_TER 1 1
 FT NON_TER 110 110
 SQ SEQUENCE 110 AA; 12481 MW; EAESDF10D7547DB8 CRC64;

Query Match 34.9%; Score 48.5; DB 1; Length 110;
 Best Local Similarity 45.0%; Pred. No. 1.2;
 Matches 9; Conservative 4; Mismatches 4; Indels 3; Gaps 1;

QY 8 LRPIPKP---DGLRPVNMV 24
 :|||: |||: :
 Db 85 VRFLPNPHWNGQLRPLTGLD 104

RESULT 11
 YBFP_ECOLI STANDARD; PRT; 164 AA.
 AC P75737;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hypothetical lipoprotein ybfp precursor.
 GN YBFP OR B0689.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.
 OX NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K12 / MG1655;
 RX MEDLINE=97426617; PubMed=9278503;
 RA Blattner P.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
 Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
 Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
 Mau B., Shao Y.;
 RT "The complete genome sequence of Escherichia coli K-12.";
 RL Science 277:1453-1474(1997).
 CC -/- SUBCELLULAR LOCATION: Attached to the membrane by a lipid anchor (Probable).

This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).

EMBL; A5000172; AAC73783.1; -.
 FIR; H64803; H64803.
 Ecogene; EGI4158; YBFP.
 PROSITE; PS00013; PROKAR LIPOPROTEIN; 1.
 KW Hypothetical protein; Membrane; Lipoprotein; Signal;
 KW Complete proteome.
 FT SIGNAL 1 22 POTENTIAL.
 FT CHAIN 23 164 HYPOTHETICAL LIPOPROTEIN YBFP.
 FT LIPID 23 23 N-ACYL DIGLYCERIDE (POTENTIAL).
 SQ SEQUENCE 164 AA; 18282 MW; CCSA0AB1CBACC0EE CRC64;

Query Match 34.2%; Score 47.5; DB 1; Length 164;
 Best Local Similarity 78.6%; Pred. No. 2.7;
 Matches 11; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 13 KPDGLRPVNMVYV 26

BUR; S17796; S17796.
 InterPro; IPR000699; Ca-rel_channel.
 InterPro; IPR001682; Ca/Na_pore.
 InterPro; IPR005821; Ion_trans.
 InterPro; IPR003608; MIR.
 Pfam; PF00520; ion_trans; 1.
 Pfam; PF02815; MIR; 4.
 Pfam; PF01365; RYDR_ITPR; 2.
 SMART; SMO0472; MIR; 4.
 KW Receptor; Transmembrane; Phosphorylation; Endoplasmic reticulum;
 KW Ionic channel; Ion transport; Calcium channel; Polymorphism.
 FT DOMAIN 1 2227 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 2228 2248 POTENTIAL..
 FT DOMAIN 2249 2260 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 2261 2281 POTENTIAL..
 FT DOMAIN 2282 2284 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 2285 2305 POTENTIAL..
 FT DOMAIN 2306 2307 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 2308 2328 POTENTIAL..
 FT DOMAIN 2329 2351 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 2352 2372 POTENTIAL..
 FT DOMAIN 2373 2394 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 2395 2415 POTENTIAL..
 FT DOMAIN 2416 2521 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 2522 2542 POTENTIAL..
 FT DOMAIN 2543 2601 EXTRACELLULAR (POTENTIAL).
 FT MOD_RES 2607 2607 PHOSPHORYLATION (POTENTIAL).
 FT VARIANT 689 689 D -> H.
 FT VARIANT 1013 1013 G -> C.
 FT VARIANT 1256 1256 L -> P.
 FT VARIANT 2384 2384 V -> I.
 FT VARIANT 2694 2694 E -> V.
 FT CONFLICT 119 119 K -> N (IN REF. 2).
 FT CONFLICT 344 344 H -> R (IN REF. 2).
 FT CONFLICT 943 943 W -> V (IN REF. 2).
 FT CONFLICT 1692 1692 S -> G (IN REF. 2).
 FT CONFLICT 2556 2556 K -> E (IN REF. 2).
 SQ SEQUENCE 2701 AA; 307054 MW; 42BF7F1024335984 CRC64;

Query Match 35.3%; Score 49; DB 1; Length 2701;
 Best Local Similarity 50.0%; Pred. No. 38;
 Matches 10; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 2 ALLTSRLRFLPKPGDGRPIV 21
 : ||| ||| ||| ||| :
 Db 2272 AICTMLFFSKPGVGRPFL 2291

RESULT 10
 YHBJ_ACTAC STANDARD; PRT; 110 AA.
 AC P96769;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Hypothetical UPF0042 protein H1146 homolog (Fragment).
 OS Actinobacillus actinomycetemcomitans (Haemophilus
 actinomycetemcomitans).
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
 OC Pasteurellaceae; Actinobacillus.
 OX NCBI_TaxID=714;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CUL1000;
 RX MEDLINE=98295003; PubMed=9631542;
 RA Kaplan J.B., Fine D.H.;
 RT "Codon usage in Actinobacillus actinomycetemcomitans.";
 RL FEMS Microbiol. Lett. 163:31-36(1998).
 CC -/- SIMILARITY: Belongs to the UPF0042 family.

This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its

```

Db      117 KP-GTRPVDYV 129
|| | ||||| |||
RESULT 12
KAD_VIBPA      STANDARD;      PRT;      214 AA.
AC  Q87RH4;
DT  15-SEP-2003 (Rel. 42, Created)
DT  15-SEP-2003 (Rel. 42, Last sequence update)
DT  15-SEP-2003 (Rel. 42, Last annotation update)
DE  Adenylate kinase (EC 2.7.4.3) (ATP-AMP transphosphorylase).
GN  ADK OR VP0822.
OS  Vibrio parahaemolyticus.
OC  Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC  Vibrionaceae; Vibrio.
OX  NCBI_TaxID=670;
RN  [1]
SEQUENCE FROM N.A.
RP  STRAIN=RMD 2210633 / Serotype O3:K6;
RX  MEDLINE=22508454; PubMed=12620739;
RA  Makino K., Oshima K., Kurokawa K., Yokoyama K., Uda T., Tagomori K.,
RA  Iijima Y., Najima M., Nakano M., Yamashita A., Kubota Y., Kimura S.,
RA  Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.;
RT  "Genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism
RT  distinct from that of V. cholerae.";
RL  Lancet 361:743-749(2003).
CC  -!- FUNCTION: This small ubiquitous enzyme is essential for
CC  maintenance and cell growth.
CC  -!- CATALYTIC ACTIVITY: ATP + AMP = ADP + ADP.
CC  -!- SUBUNIT: Monomer (By similarity).
CC  -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC  -!- SIMILARITY: Belongs to the adenylate kinase family.
CC
CC  This SWISS-PROT entry is copyright. It is produced through a collaboration
CC  between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC  the European Bioinformatics Institute. There are no restrictions on its
CC  use by non-profit institutions as long as its content is in no way
CC  modified and this statement is not removed. Usage by and for commercial
CC  entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC  or send an email to license@isb-sib.ch).
CC
CC  EMBL; AF005075; BAC59085.1; -.
CC  HAMAP; MF 00235; -i 1.
CC  PROSITE; PS00113; ADENYLATE KINASE; 1.
CC  Transferrase; Kinase; ATP-binding; Complete proteome.
FT  NP BIND 7 15 ATP (BY SIMILARITY).
SQ  SEQUENCE 214 AA; 23294 MW; 2229487FBA1C0D4D CRC64;
Query Match 34.2%; Score 47.5; DB 1; Length 214;
Best Local Similarity 46.2%; Pred. No. 3.7;
Matches 12; Conservative 5; Mismatches 8; Indels 1; Gaps 1;
Qy  3 LLTSRLRFPKPDGLRPI-VNMDYV 27
|| | ||||| |||
Db  82 LLDGFPRTIPQADGLKMGVEVDYVI 107
|| | ||||| |||
RESULT 13
CTBQ_XENLA      STANDARD;      PRT;      437 AA.
AC  Q9W758;
DT  16-OCT-2001 (Rel. 40, Created)
DT  16-OCT-2001 (Rel. 40, Last sequence update)
DT  16-OCT-2001 (Rel. 40, Last annotation update)
DE  C-terminal binding protein (TCF-3 co-repressor CtBP) (XctBP).
GN  CtBP.
OS  Xenopus laevis (African clawed frog).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC  Xenopodinae; Xenopus.
OX  NCBI_TaxID=8355;
RN  [1]
SEQUENCE FROM N.A.
RP  MEDLINE=99307079; PubMed=10375506;
RX  Brannon M., Brown J.D., Bates R., Kimelman D., Moon R.T.;
RT  "XctBP is a Xctf-3 co-repressor with roles throughout Xenopus
RT  development.";
RL  Development 126:3159-3170(1999).
CC  -!- FUNCTION: CO-REPRESSOR TARGETING DIVERSE TRANSCRIPTION REGULATORS.
CC  -!- SUBUNIT: INTERACTS WITH THE C-TERMINUS OF TCF-3 VIA THE CONSENSUS
CC  MOTIFS P-X-[DNS]-L-[STVA].
CC  -!- SUBCELLULAR LOCATION: Nuclear (Potential).
CC  -!- DEVELOPMENTAL STAGE: EXPRESSED THROUGHOUT DEVELOPMENT. LOCALIZED
CC  TO DISCRETE STRUCTURES DURING NEURALATION. THE PATTERN OF
CC  EXPRESSION IS INCREASINGLY REFINED TO INCLUDE THE HEAD, CENTRAL
CC  NERVOUS SYSTEM AND TISSUES ALONG THE DORSAL MIDLINE TO THE
CC  TAILBUD.
CC  -!- SIMILARITY: BELONGS TO THE D-ISOMER SPECIFIC 2-HYDROXYACID
CC  DEHYDROGENASES FAMILY. BUT HIGHLY DIVERGENT.
CC
CC  This SWISS-PROT entry is copyright. It is produced through a collaboration
CC  between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC  the European Bioinformatics Institute. There are no restrictions on its
CC  use by non-profit institutions as long as its content is in no way
CC  modified and this statement is not removed. Usage by and for commercial
CC  entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC  or send an email to license@isb-sib.ch).
CC
CC  EMBL; AF152006; AAD41370.1; -.
CC  HSSP; P17584; LDXY.
CC  TRANSFAC; T03243; -.
CC  InterPro; IPR006139; 2-Hacid DH.
CC  InterPro; IPR006140; 2-Hacid DH_C.
CC  Pfam; PF00389; 2-Hacid DH; 1.
CC  Pfam; PF02826; 2-Hacid DH_C; 1.
CC  PROSITE; PS00065; D_2_HYDROXYACID_DH_1; 1.
CC  PROSITE; PS00670; D_2_HYDROXYACID_DH_2; FALSE NEG.
CC  PROSITE; PS00671; D_2_HYDROXYACID_DH_3; FALSE NEG.
CC  Nuclear protein.
CC  SEQUENCE 437 AA; 47775 MW; 49D2FEFD82E2B010 CRC64;
Query Match 33.8%; Score 47; DB 1; Length 437;
Best Local Similarity 56.2%; Pred. No. 9.9;
Matches 9; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
Qy  12 PKPDGLRPIVNMDDYV 27
|| | ||||| |||
Db  345 PIPDSLRNCVKNKYLL 360
|| | ||||| |||
RESULT 14
SDP_EIMBO      STANDARD;      PRT;      596 AA.
AC  P42789;
DT  01-NOV-1995 (Rel. 32, Created)
DT  01-NOV-1995 (Rel. 32, Last sequence update)
DT  28-FEB-2003 (Rel. 41, Last annotation update)
DE  Sporozoite developmental protein (EC 3.4.99.-).
OS  Eimeria bovis.
OC  Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida; Eimeriidae;
OC  Eimeria.
OX  NCBI_TaxID=5803;
RN  [1]
SEQUENCE FROM N.A.
RP  TISSUE=Oocyst;
RX  MEDLINE=93149194; PubMed=8426605;
RA  Abrahamson M.S., Clark T.G., Mascolo P., Speer C.A., White M.W.;
RT  "Developmental gene expression in Eimeria bovis.";
RL  Mol. Biochem. Parasitol. 57:1-14(1993).
CC  -!- FUNCTION: MAY BE INVOLVED IN THE DEGRADATION OF A PROTEIN WHICH IS
CC  A COMPONENT OF THE SIGNAL TRANSDUCTION PATHWAY REGULATING OOCYST
CC  SPORULATION.
CC  -!- DEVELOPMENTAL STAGE: EXPRESSED IN SPORULATED OOCYSTS.
CC  -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M16.
CC

```


THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 12, 2003, 19:42:29 ; Search time 25.8113 Seconds
(without alignments)
269.937 Million cell updates/sec

Title: US-08-854-050-117

Perfect score: 139

Sequence: 1 PALLTSRLRFIPKPDGLRPIVNDYV 27

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL.23.*
1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phase.*
10: sp_plant.*
11: sp_rodent.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*
15: sp_rvirus.*
16: sp_bacteriap.*
17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	139	100.0	795	4	Q8NG38 homo sapien
2	139	100.0	807	4	Q8N6C3 homo sapien
3	139	100.0	1089	4	Q8NG46 homo sapien
4	100	71.9	1128	11	Q9QXZ4 mesocricetu
5	93	66.9	575	11	Q9JK99 rattus norv
6	93	60.4	1191	13	Q9DE32 xenopus lae
7	60	43.2	1474	5	Q962F9 cryptospori
8	57	41.0	582	2	Q8GN23 fischerella
9	57	41.0	2518	5	Q8IEH2 plasmodium
10	56	40.3	1259	10	Q9AU13 oryza sativ
11	56	40.3	1261	10	Q8LKW0 oryza sativ
12	50	36.0	355	3	Q8NIX1 neurospora
13	50	36.0	895	5	Q9GRCS paramecium
14	50	36.0	896	5	Q8MUQ8 paramecium
15	49	35.3	216	15	Q9IEA5 human immun
16	49	35.3	327	16	Q8UD25 agrobacteri

17	49	35.3	495	11	Q8CED6 mus musculu
18	49	35.3	495	11	Q8BNX2 mus musculu
19	49	35.3	544	15	Q9IED9 human immun
20	49	35.3	1412	11	Q8R3B0 mus musculu
21	49	35.3	2701	6	Q8WN96 bos taurus
22	48	34.5	232	10	Q9ZUD5 arabidopsis
23	48	34.5	646	10	Q9FKM4 arabidopsis
24	48	34.5	803	5	Q22343 caenorhabdi
25	48	34.5	3134	10	Q9LQC3 arabidopsis
26	47	33.8	119	10	Q8VYI6 arabidopsis
27	47	33.8	288	10	Q8LNP9 oryza sativ
28	47	33.8	484	11	Q9CS98 mus musculu
29	47	33.8	571	10	Q8GRS8 oryza sativ
30	47	33.8	595	11	Q8BK98 mus musculu
31	47	33.8	748	10	Q9ASG1 oryza sativ
32	47	33.8	872	15	Q900Y5 human immun
33	47	33.8	933	10	Q8W150 oryza sativ
34	47	33.8	1108	5	Q8I8Z6 sterkiella
35	47	33.8	1203	16	Q8D4Q6 vibrio vuln
36	47	33.8	1449	17	Q8PW15 methanosarc
37	46.5	33.5	203	2	Q50984 neisseria g
38	46.5	33.5	203	16	Q9KOD2 neisseria m
39	46.5	33.5	203	16	Q9JVD8 neisseria m
40	46.5	33.5	278	5	Q94873 drosophila
41	46.5	33.5	442	2	Q51880 phormidium
42	46.5	33.5	982	5	Q9VUA5 drosophila
43	46.5	33.5	6420	2	P95814 streptomyce
44	46	33.1	121	12	Q8VBS5 human adeno
45	46	33.1	339	5	Q8SSU8 dictyosteli

ALIGNMENTS

RESULT 1

Q8NG38 PRELIMINARY; PRT; 795 AA.
ID AC Q8NG38;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE ABG-deleted variant of telomerase reverse transcriptase.
GN TERT.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Stomach;
RA Hisatomi H., Nagao K., Kanamaru T., Hirata H., Miyachi K., Hikiji H.;
RT "Exon 11 deleted variant of human reverse transcriptase.";
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB086950; BAC11015.1; -
DR InterPro; IPR003545; Telomerase RT.
DR PRINTS; PR01365; TELOMERASERT.
KW RNA-directed DNA polymerase.
SQ SEQUENCE 795 AA; 88965 MW; 6BEAC8A6D1A2E8CB CRC64;

Query Match 100.0%; Score 139; DB 4; Length 795;
Best Local Similarity 100.0%; Pred. No. 5.5e-13;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PALLTSRLRFIPKPDGLRPIVNDYV 27

Db 614 PALLTSRLRFIPKPDGLRPIVNDYV 640

RESULT 2

Q8N6C3 PRELIMINARY; PRT; 807 AA.
ID Q8N6C3;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)

```

DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DE 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Beta and gamma deletion isoform of telomerase reverse
DE transcriptase.
GN HTERT.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Stomach cancer;
RA Hisatomi H., Nagao K., Kanamaru T., Sumida H., Hirata H., Yamamoto M.,
RA Kazumasa H.;
RT "Both beta and gamma deletion isoform of human telomerase reverse
RT transcriptase."
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB086379; BAC11014.1; -.
DR InterPro; IPR003545; Telomerase_RT.
DR PRINTS; PR01365; TELOMERASERT.
SQ SEQUENCE 807 AA; 90225 MW; 199664460CE6D763 CRC64;

Query Match 100.0%; Score 139; DB 4; Length 807;
Best Local Similarity 100.0%; Pred. No. 5.6e-13;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PALLTSRLRFIPKPDGLRPVNMDDYV 27
Db |||||
614 PALLTSRLRFIPKPDGLRPVNMDDYV 640

RESULT 3
Q8NG46 PRELIMINARY; PRT; 1069 AA.
ID Q8NG46
AC Q8NG46;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Telomerase reverse transcriptase.
GN HTERT.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Hisatomi H., Nagao K., Hirata H., Hikiji K., Kanamaru T.;
RT "Exon 11 deleted variant of the human telomerase reverse
RT transcriptase."
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB085628; BAC11010.1; -.
DR InterPro; IPR003545; Telomerase_RT.
DR PRINTS; PR01365; TELOMERASERT.
KW RNA-directed DNA polymerase.
SQ SEQUENCE 1069 AA; 120047 MW; BE1E77A653B1C666 CRC64;

Query Match 100.0%; Score 139; DB 4; Length 1069;
Best Local Similarity 100.0%; Pred. No. 7.7e-13;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PALLTSRLRFIPKPDGLRPVNMDDYV 27
Db |||||
614 PALLTSRLRFIPKPDGLRPVNMDDYV 640

RESULT 4
Q9QXZ4 PRELIMINARY; PRT; 1128 AA.
ID Q9QXZ4
AC Q9QXZ4;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Telomerase catalytic subunit.
GN

```

```

OS Mesocricetus auratus (Golden hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Mesocricetus.
OX NCBI_TaxID=10036;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21240330; PubMed=11342218;
RA Guo W., Okamoto M., Lee Y.M., Baluda M.A., Park N.H.;
RT "Enhanced activity of cloned hamster TERT gene promoter in transformed
RT cells."
RL Biochim. Biophys. Acta 1517:398-409 (2001).
DR EMBL; AF149012; AAF17334.1; -.
DR InterPro; IPR000477; RVTse.
DR InterPro; IPR003545; Telomerase_RT.
DR Pfam; PF00078; rvt; 1.
DR PRINTS; PR01365; TELOMERASERT.
KW RNA-directed DNA polymerase; Transferase.
SQ SEQUENCE 1128 AA; 128394 MW; 1D4F81249012174E CRC64;

Query Match 71.9%; Score 100; DB 11; Length 1128;
Best Local Similarity 73.1%; Pred. No. 1e-06;
Matches 19; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 PALLTSRLRFIPKPDGLRPVNMDDYV 26
Db |||||
608 PAMPICRLRFIPKPSGLRPVNMDDYV 633

RESULT 5
Q9JK99 PRELIMINARY; PRT; 575 AA.
ID Q9JK99
AC Q9JK99;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Telomerase catalytic subunit (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Wong S., Gao S., Xu X., Yu H.;
RT "Rat telomerase catalytic subunit, rTERT."
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF247818; AAF62177.1; -.
DR InterPro; IPR000477; RVTse.
DR InterPro; IPR003545; Telomerase_RT.
DR Pfam; PF00078; rvt; 1.
DR PRINTS; PR01365; TELOMERASERT.
KW RNA-directed DNA polymerase; Transferase.
FT NON_TER 1
SQ SEQUENCE 575 AA; 65672 MW; F80C81BD7F6A91A3 CRC64;

Query Match 66.9%; Score 93; DB 11; Length 575;
Best Local Similarity 75.0%; Pred. No. 6.1e-06;
Matches 18; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 ALLTSRLRFIPKPDGLRPVNMDDYV 25
Db |||||
58 AMPICRLRFIPKPSGLRPVNMDDYV 81

RESULT 6
Q9DE32 PRELIMINARY; PRT; 1191 AA.
ID Q9DE32
AC Q9DE32;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Telomerase reverse transcriptase.
GN TERT.

```



```

OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
[1]
RN SEQUENCE FROM N.A.
RA Kuramoto M., Ishikawa F.;
RT "Telomerase reverse transcriptase of Xenopus laevis.";
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF212299; AAG43537.1; -.
DR InterPro; IPR000477; RVTse.
DR Pfam; PF00078; rvt; 2.
DR PRINTS; PR01365; TELOMERASERT.
KW RNA-directed DNA polymerase; Transferase.
SQ SEQUENCE 1191 AA; 138016 MW; 9BD9D776869A57D6 CRC64;

Query Match 50.4%; Score 70; DB 13; Length 1191;
Best Local Similarity 82.4%; Pred. No. 0.055;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 LTSRLRFPKPDGLRPI 20
Db 672 LVSLRFPKPTNGLRPI 688

RESULT 7
Q962F9 ID Q962F9 PRELIMINARY; PRT; 1474 AA.
AC Q962F9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Telomerase reverse transcriptase.
GN TERT.
OS Cryptosporidium parvum.
OC Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;
OC Cryptosporidiidae; Cryptosporidium.
OX NCBI_TaxID=5807;
RN [1]
RP SEQUENCE FROM N.A.
RA Liu C., Abrahamson M.S.;
RT "Telomerase reverse transcriptase gene and telomerase activity in
RT Cryptosporidium parvum.";
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY034376; AAK60396.1; -.
DR InterPro; IPR001064; Crystallin.
DR PROSITE; PS00225; CRYSTALLIN_BETAGAMMA; 1.
KW RNA-directed DNA polymerase.
SQ SEQUENCE 1474 AA; 169954 MW; 5F2256F020E3BEF1 CRC64;

Query Match 43.2%; Score 60; DB 5; Length 1474;
Best Local Similarity 45.0%; Pred. No. 2.5;
Matches 9; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

QY 7 RLRFPKPDGLRPIVNDYV 26
Db 652 KIRWPKSKGLRPLINLSKV 671

RESULT 8
Q8GN23 ID Q8GN23 PRELIMINARY; PRT; 582 AA.
AC Q8GN23;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Peptide synthetase (Fragment).
OS Fischerella sp. CENA19.
OC Bacteria; Cyanobacteria; Stigonematales; Fischerella.
OX NCBI_TaxID=167040;
RN [1]

```

```

RP SEQUENCE FROM N.A.
RC STRAIN=CENA19;
RA Rabello E., Moon D.H., Teai S.M., Etchegaray A.;
RT "Peptide synthetase and polyketides synthase genes from Fischerella
RT sp. CENA 19.";
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF542135; AAN28671.1; -.
FT NON TER 1
SQ SEQUENCE 582 AA; 65720 MW; 09A0EDBA03D96E23 CRC64;

Query Match 41.0%; Score 57; DB 2; Length 582;
Best Local Similarity 58.8%; Pred. No. 2.7;
Matches 10; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 11 IPKPDGLRPIVNDYV 27
Db 457 LPKPDNLRLPIETAYVL 473

RESULT 9
Q8IEH2 ID Q8IEH2 PRELIMINARY; PRT; 2518 AA.
AC Q8IEH2;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein.
GN PF13_0080.
OS Plasmodium falciparum (isolate 3D7).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=36329;
RN [1]
RP SEQUENCE FROM N.A.
RA Harris B., Lennard N., Clark L., Line A., Barron A., Corton C.,
RA Berriman M., Pain A., Hall N., Atkin R., Chillingworth C., Doggett J.,
RA Omond D., Sanders M., Hayes R., Hall S., Quail M., Barrell B.;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL844509; CAD52286.1; -.
KW Hypothetical protein.
SQ SEQUENCE 2518 AA; 304135 MW; 8953AF19D54B7789 CRC64;

Query Match 41.0%; Score 57; DB 5; Length 2518;
Best Local Similarity 52.9%; Pred. No. 14;
Matches 9; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 7 RLRFPKPDGLRPIVNM 23
Db 1422 RINWPKKGLRPLINE 1438

RESULT 10
Q9AU13 ID Q9AU13 PRELIMINARY; PRT; 1259 AA.
AC Q9AU13;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Telomerase reverse transcriptase.
GN TERT.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RA Oguchi K., Tamura K., Takahashi H.;
RT "Molecular cloning and characterization of OsTERT, a telomerase
RT reverse transcriptase homolog in Oryza sativa.";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF288216; AAK35007.1; -.
KW Gramine; Q9AU13; -.
DR InterPro; IPR001209; Ribosomal_S14.

```


RT "A unique pause pattern during telomere addition by the error-prone
RL telomerase from the ciliate Paramecium tetraurelia.";

DR Gene 0:0-0(2002).
DR EMBL; AF515460; AAN03860.1; -.
DR InterPro; IPR000477; RVTse.
DR InterPro; IPR003545; Telomerase_RT.
DR Pfam; PF00078; rvt; 2.
DR PRINTS; PR01365; TELOMERASERT.
KW RNA-directed DNA polymerase; Transferase.
SQ SEQUENCE 896 AA; 107237 MW; 697031F9DD61A883 CRC64;

Query Match 36.0%; Score 50; DB 5; Length 896;
Best Local Similarity 60.0%; Pred. No. 54;
Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 7 RLRFPKPDGLRPV 21
: : : : :
Db 443 KLRVPGTFRDIV 457

RESULT 15

Q9IEA5 PRELIMINARY; PRT; 216 AA.
AC Q9IEA5;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-OCT-2000 (Tremblrel. 22, Last annotation update)
DE Gp41 (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=YBF26;
RA Roques P., Robertson D., Sandrine S., Christel D., Francois S.,
RT Philippe M.;
RT "Phylogenetic analysis and sub-typing of 47 HIV-1 group O isolates."
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ236415; CAB96263.1; -.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 216
SQ SEQUENCE 216 AA; 25003 MW; 0A5AC218BFA88932 CRC64;

Query Match 35.3%; Score 49; DB 15; Length 216;
Best Local Similarity 50.0%; Pred. No. 16;
Matches 9; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 7 RLRFPKPDGLRPV 24
: : : : :
Db 193 RLRIPSPQGLFLLYTD 210

Search completed: November 12, 2003, 19:50:46
Job time : 25.978 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 12, 2003, 19:41:04 ; Search time 34.8679 Seconds
(without alignments)
127.462 Million cell updates/sec

Title: US-08-854-050-115
Perfect score: 146
Sequence: 1 AKFLWMSVYVVELLSFFVYVTFQ 28

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_19Jun03:*
1: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1980.DAT:*
2: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:*
3: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:*
4: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1983.DAT:*
5: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1984.DAT:*
6: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1985.DAT:*
7: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1986.DAT:*
8: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1987.DAT:*
9: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1988.DAT:*
10: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1989.DAT:*
11: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1990.DAT:*
12: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1991.DAT:*
13: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1992.DAT:*
14: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1993.DAT:*
15: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1994.DAT:*
16: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1995.DAT:*
17: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1996.DAT:*
18: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1997.DAT:*
19: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1998.DAT:*
20: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1999.DAT:*
21: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:*
22: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*
23: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*
24: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	146	100.0	28	19	AAW57394 Human telomerase r
2	146	100.0	100	23	ABG71627 hTERT fragment wit
3	146	100.0	131	20	AAW57385 Amino acid sequenc
4	146	100.0	437	20	AAW25461 Human CRT-1 protei
5	146	100.0	438	20	AAW25462 Human CRT-1 protei
6	146	100.0	588	20	AAW00635 N-terminal truncat
7	146	100.0	588	20	AAW00644 N-terminal truncat
8	146	100.0	591	20	AAW57384 A catalytic telome
9	146	100.0	622	20	AAW25463 Human CRT-1 protei

10	146	100.0	807	19	AAW46997 Human telomerase r
11	146	100.0	807	20	AAW00637 N-terminal truncat
12	146	100.0	807	20	AAW00646 Truncated telomera
13	146	100.0	936	20	AAW00642 Truncated telomera
14	146	100.0	936	20	AAW00651 Truncated telomera
15	146	100.0	948	20	AAW00639 N-terminal truncat
16	146	100.0	948	20	AAW00648 Truncated telomera
17	146	100.0	949	19	AAW61349 Human telomerase p
18	146	100.0	1041	20	AAW00643 Altered C-terminus
19	146	100.0	1041	20	AAW00652 Altered C-terminus
20	146	100.0	1053	20	AAW00640 Altered C-terminus
21	146	100.0	1093	20	AAW00649 Altered C-terminus
22	146	100.0	1120	20	AAW00641 Telomerase protein
23	146	100.0	1120	20	AAW00650 Telomerase (ver. 2
24	146	100.0	1132	19	AAW71376 Human telomerase c
25	146	100.0	1132	19	AAW46957 Human telomerase r
26	146	100.0	1132	19	AAW56113 Human telomerase r
27	146	100.0	1132	20	AAW43621 A human telomerase
28	146	100.0	1132	20	AAW28881 Human telomerase r
29	146	100.0	1132	20	AAW32090 Human telomerase r
30	146	100.0	1132	20	AAW28401 Human EST2 protein
31	146	100.0	1132	20	AAW26580 Human telomerase r
32	146	100.0	1132	20	AAW00627 Human telomerase p
33	146	100.0	1132	20	AAW00638 Truncated telomera
34	146	100.0	1132	20	AAW90251 Human catalytic te
35	146	100.0	1132	21	AAW96566 hEST2, a human tel
36	146	100.0	1132	22	AAW82765 Human telomerase r
37	146	100.0	1132	22	AAW99930 Human telomerase p
38	146	100.0	1132	22	AAW64329 Human protein #2
39	146	100.0	1132	22	AAW64859 Heart muscle cell
40	146	100.0	1132	23	AAE29226 Human telomerase r
41	146	100.0	1132	23	AAU72735 Human telomerase r
42	146	100.0	1132	24	ABP56676 Human telomerase r
43	146	100.0	1154	19	AAW61350 Human telomerase p
44	146	100.0	1166	20	AAW00647 Telomerase (ver. 2
45	146	100.0	1189	19	AAW47008 Glutathione-S-tran

ALIGNMENTS

RESULT 1
AAW57394
ID AAW57394 standard; peptide; 28 AA.
XX
AC AAW57394;
XX
DT 13-AUG-1998 (first entry)
XX
DE Human telomerase reverse transcriptase antigenic peptide A-1.
XX
KW Human; telomerase reverse transcriptase; hTERT; TRT; diagnosis; prognosis; cell proliferation; cancer; ageing; ribonucleoprotein.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN GB2317891-A.
XX
PD 08-APR-1998.
XX
PF 01-OCT-1997; 97GB-0020890.
XX
PR 14-AUG-1997; 97US-0915503.
PR 01-OCT-1996; 96US-0724643.
PR 18-APR-1997; 97US-0844419.
PR 25-APR-1997; 97US-0846017.
PR 06-MAY-1997; 97US-0851843.
PR 09-MAY-1997; 97US-0854050.
PR 14-AUG-1997; 97US-0911312.
PR 14-AUG-1997; 97US-0912951.
XX
PA (GERO-) GERON CORP.

(UYTE-) UNIV TECHNOLOGY CORP.
 Andrews WH, Cech TR, Chapman KB, Harley C, Lingner J;
 Morin GB, Nakamura T, Harley CB;
 WPI; 1998-171633/16.
 Pure and recombinant human Telomerase Reverse Transcriptase and its
 variants - are useful in the diagnosis, prognosis and treatment of
 cell proliferation conditions especially cancer and ageing
 Example 8; Fig 54; 387pp; English.
 The present sequence represents an antigenic peptide from human
 telomerase reverse transcriptase (hTERT), from the present invention. The
 present invention also describes the following methods: (A) determining
 whether a test compound is a modulator of hTERT, by detecting the change
 in hTERT recombinant protein or polynucleotide, on administration of the
 compound; (B) preparation of recombinant telomerase by contacting a
 protein preparation of hTERT with a telomerase RNA component; (C)
 detection of the hTERT RNA or protein in a sample by binding a relevant
 probe to the sample and detecting the complex formed or in the case of
 RNA detection, amplifying the product and correlating the presence of
 complex or amplification product with presence of hTERT in the sample;
 and (D) increasing the proliferation of a vertebrate cell by increasing
 hTERT expression; and (E) the use of an agent that causes an increase in
 cell vertebrate cell proliferation to create a medicament that inhibits
 ageing. A protein preparation of hTERT and the polynucleotide encoding
 hTERT can be used in the manufacture of medicaments for inhibiting the
 effect of ageing or cancer. Inhibitors of telomerase activity can be
 used to treat conditions that are associated with high telomerase
 activity. A protein preparation of hTERT can also be used in the new
 methods.
 Query Match 100.0%; Score 146; DB 19; Length 28;
 Best Local Similarity 100.0%; Pred. No. 5.1e-14;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AKFLHLMMSVYVVELLSRFYVTTTFQ 28
 DB 1 AKFLHLMMSVYVVELLSRFYVTTTFQ 28
 RESULT 2
 ABG71627
 ID ABG71627 standard; protein; 100 AA.
 AC ABG71627;
 XX
 XX 09-JAN-2003 (first entry)
 DT
 DE hTERT fragment with HLA containing polypeptide at its N-terminus.
 KW Human; telomerase catalytic subunit; hTERT; human leukocyte antigen;
 KW human telomerase reverse transcriptase; HLA epitope; cancer;
 KW HLA profile; breast cancer; pancreatic cancer; colorectal cancer;
 KW lung cancer; ovarian cancer; cervical cancer; malignant melanoma;
 KW leukaemia; lymphoma; biliary tract carcinoma; anti-cancer; mutant;
 KW cytostatic; HLA class I epitope; HLA class II epitope; mutein.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 XX WO200270679-A2.
 PN
 XX
 PD 12-SEP-2002.
 XX
 XX 19-FEB-2002; 2002WO-N000069.
 PF
 XX
 XX 02-MAR-2001; 2001GB-0005238.
 PR
 XX

(GEMV-) GEMVAX AS.
 Eriksen JA, Gaudernack G, Moller M;
 WPI; 2002-750459/81.
 New polypeptide with an additional C-terminal and/or N-terminal
 sequence, useful for preparing anti-cancer vaccines -
 Disclosure; Fig 1; 62pp; English.
 The present invention relates to a polypeptide comprising a 20 amino
 acid sequence derived from human telomerase catalytic subunit
 (or human telomerase reverse transcriptase, hTERT) amino acid residues
 537-556, or fragments thereof comprising at least 10 amino acids and
 at least two human leukocyte antigen (HLA) class I or class II
 epitopes. The invention also describes a polypeptide having the above
 sequences on a fragment of hTERT which is not more than 100 amino
 acids of hTERT. The polypeptides of the invention are useful in a
 pharmaceutical composition or in a vaccine for preventing or treating
 cancer in populations of individuals having varying HLA profiles.
 The polypeptides are also useful in a diagnostic kit for diagnosing
 cancers such as breast, pancreatic, colorectal, lung, ovarian or
 cervical cancer, malignant melanoma, leukaemia, lymphoma or biliary
 tract carcinoma. The polypeptides or encoding polynucleotide
 sequences are useful for performing identity, sequence homology
 and/or hybridisation studies, for predicting structure and/or
 function (e.g. anti-cancer activity), or for screening methods in
 drug development or drug screening procedures. The present sequence
 represents a hTERT fragment with the 20 amino acid HLA epitope
 containing polypeptide at its N-terminus.
 Query Match 100.0%; Score 146; DB 23; Length 100;
 Best Local Similarity 100.0%; Pred. No. 1.9e-13;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AKFLHLMMSVYVVELLSRFYVTTTFQ 28
 DB 6 AKFLHLMMSVYVVELLSRFYVTTTFQ 33
 RESULT 3
 AA97385
 ID AA97385 standard; Protein; 131 AA.
 AC AA97385;
 XX
 XX 14-MAY-1999 (first entry)
 DT
 DE Amino acid sequence of the specification.
 DE Catalytic telomerase; diagnosis; disease; telomerase activity.
 KW Homo sapiens.
 OS
 XX JPI1046768-A.
 PN
 XX 23-FEB-1999.
 PD
 XX
 PF 01-AUG-1997; 97JP-0207708.
 XX
 XX 01-AUG-1997; 97JP-0207708.
 PR
 XX (MITU) MITSUBISHI CHEM CORP.
 PA
 XX WPI; 1999-208111/18.
 DR
 XX N-PSDB; AAX15924.
 DR
 XX New catalytic protein of telomerase of a higher animal and a gene in
 PT coding it - useful for diagnosis of diseases caused by the change in

PT activity of a telomerase
 XX Example 1; Page 14; 18pp; Japanese.
 CC The specification describes a human catalytic telomerase protein.
 CC The products are useful in drug compositions for the diagnosis
 CC of diseases caused by the change in activity of telomerase. The
 CC present sequence appears in the specification.
 XX Sequence 131 AA;
 SQ
 Query Match 100.0%; Score 146; DB 20; Length 131;
 Best Local Similarity 100.0%; Pred. No. 2.5e-13;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 AKFLHLMMSVYVVELLSFFYVTTTFQ 28
 DB 1 AKFLHLMMSVYVVELLSFFYVTTTFQ 28
 RESULT 4
 AAY25461
 ID AAY25461 standard; Protein; 437 AA.
 XX
 AC AAY25461;
 XX
 DT 22-SEP-1999 (first entry)
 DE Human CRT-1 protein #1.
 XX
 DE CRT-1; reverse transcriptase; telomerase; inhibitor; detection;
 KW telomerase activity; cancer cell; screening; human.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Protein 1..437
 FT /label= CRT-1
 FT /note= "Partial sequence, no stop codon given"
 XX
 PN WO9935261-A1.
 XX
 PD 15-JUL-1999.
 XX
 PF 08-JAN-1999; 99WO-JP00039.
 XX
 PR 06-MAY-1998; 98JP-0139177.
 PR 08-JAN-1998; 98JP-0013232.
 PR 30-JAN-1998; 98JP-0033584.
 XX
 PA (CHUS) CHUGAI SEIYAKU KK.
 XX
 PI Tsuchiya M, Yoshida K;
 XX
 DR WPI; 1999-430393/36.
 DR N-PSDB; AAX88243.
 XX
 PF 08-JAN-1999; 99WO-JP00039.
 XX
 PR 06-MAY-1998; 98JP-0139177.
 PR 08-JAN-1998; 98JP-0013232.
 PR 30-JAN-1998; 98JP-0033584.
 XX
 PA (CHUS) CHUGAI SEIYAKU KK.
 XX
 PI Tsuchiya M, Yoshida K;
 XX
 DR WPI; 1999-430393/36.
 DR N-PSDB; AAX88243.
 XX
 PT Novel Gene, useful in detection of telomerase activity and cancer
 PT cells as well as screening telomerase inhibitors for treatment of
 PT cancers
 XX
 PS Claim 2; Page 31-32; 44pp; Japanese.
 XX
 CC This invention describes novel human CRT-1 genes and their encoded
 CC proteins containing a reverse transcriptase motif, which act as
 CC telomerase inhibitors. The gene, its encoded protein and derived
 CC antibodies can be used to provide base sequence information, detect
 CC telomerase activity and cancer cells, and to screen telomerase
 CC inhibitors. The detection method is simple and effective.
 XX
 PT Novel Gene, useful in detection of telomerase activity and cancer
 PT cells as well as screening telomerase inhibitors for treatment of
 PT cancers
 XX
 PS Claim 2; Page 31-32; 44pp; Japanese.
 XX
 CC This invention describes novel human CRT-1 genes and their encoded
 CC proteins containing a reverse transcriptase motif, which act as
 CC telomerase inhibitors. The gene, its encoded protein and derived
 CC antibodies can be used to provide base sequence information, detect
 CC telomerase activity and cancer cells, and to screen telomerase
 CC inhibitors. The detection method is simple and effective.
 XX
 SQ Sequence 437 AA;
 Query Match 100.0%; Score 146; DB 20; Length 437;
 XX

Best Local Similarity 100.0%; Pred. No. 8.4e-13;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 AKFLHLMMSVYVVELLSFFYVTTTFQ 28
 DB 32 AKFLHLMMSVYVVELLSFFYVTTTFQ 59
 RESULT 5
 AAY25462
 ID AAY25462 standard; Protein; 438 AA.
 XX
 AC AAY25462;
 XX
 DT 22-SEP-1999 (first entry)
 DE Human CRT-1 protein #2.
 XX
 DE CRT-1; reverse transcriptase; telomerase; inhibitor; detection;
 KW telomerase activity; cancer cell; screening; human.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Protein 1..438
 FT /label= CRT-1
 FT /note= "Partial sequence, no stop codon given"
 XX
 PN WO9935261-A1.
 XX
 PD 15-JUL-1999.
 XX
 PF 08-JAN-1999; 99WO-JP00039.
 XX
 PR 06-MAY-1998; 98JP-0139177.
 PR 08-JAN-1998; 98JP-0013232.
 PR 30-JAN-1998; 98JP-0033584.
 XX
 PA (CHUS) CHUGAI SEIYAKU KK.
 XX
 PI Tsuchiya M, Yoshida K;
 XX
 DR WPI; 1999-430393/36.
 DR N-PSDB; AAX88250.
 XX
 PT Novel Gene, useful in detection of telomerase activity and cancer
 PT cells as well as screening telomerase inhibitors for treatment of
 PT cancers
 XX
 PS Example 1; Page 35-36; 44pp; Japanese.
 XX
 CC This invention describes novel human CRT-1 genes and their encoded
 CC proteins containing a reverse transcriptase motif, which act as
 CC telomerase inhibitors. The gene, its encoded protein and derived
 CC antibodies can be used to provide base sequence information, detect
 CC telomerase activity and cancer cells, and to screen telomerase
 CC inhibitors. The detection method is simple and effective.
 XX
 PT Novel Gene, useful in detection of telomerase activity and cancer
 PT cells as well as screening telomerase inhibitors for treatment of
 PT cancers
 XX
 PS Example 1; Page 35-36; 44pp; Japanese.
 XX
 CC This invention describes novel human CRT-1 genes and their encoded
 CC proteins containing a reverse transcriptase motif, which act as
 CC telomerase inhibitors. The gene, its encoded protein and derived
 CC antibodies can be used to provide base sequence information, detect
 CC telomerase activity and cancer cells, and to screen telomerase
 CC inhibitors. The detection method is simple and effective.
 XX
 SQ Sequence 438 AA;
 Query Match 100.0%; Score 146; DB 20; Length 438;
 Best Local Similarity 100.0%; Pred. No. 8.4e-13;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 AKFLHLMMSVYVVELLSFFYVTTTFQ 28
 DB 32 AKFLHLMMSVYVVELLSFFYVTTTFQ 59
 RESULT 6
 AAY00635
 ID AAY00635 standard; Protein; 588 AA.
 XX

AC AAY00635;
 XX
 DT 26-JUL-1999 (first entry)
 XX
 DE N-terminal truncated telomerase protein sequence.
 XX
 XX Telomerase; human; cancer; diagnosis; melanoma; skin cancer; leukaemia;
 KW neuroblastoma; breast carcinoma; colon carcinoma; lymphoma; osteosarcoma;
 KW smooth muscle cell hyperplasia; stem cell proliferation; Wilm's tumour;
 KW stem cell differentiation; organ regeneration; organ differentiation.
 XX
 OS Homo sapiens.
 OS Synthetic.
 PN WO9901560-A1.
 XX
 XX 14-JAN-1999.
 XX
 XX 01-JUL-1998; 98WO-US13835.
 XX
 PR 09-SEP-1997; 97US-0058287.
 PR 01-JUL-1997; 97US-0051410.
 PR 21-JUL-1997; 97US-0053018.
 PR 21-JUL-1997; 97US-0053329.
 PR 04-AUG-1997; 97US-0054642.
 XX
 XX (CAMB-) CAMBIA BIOSYSTEMS LLC.
 PA
 PI Bowtell D, Kilian A;
 XX
 DR WPI: 1999-106060/09.
 DR N-PSDB; AAX18263.
 XX
 XX New isolated vertebrate telomerase genes - used to develop products
 PT for treating cancers or for organ regeneration, nerve cell or brain
 PT cell growth following injury or bone marrow transplantation
 XX
 PS Claim 4; Fig 11a; 134pp; English.
 XX
 CC This sequence is a truncated human telomerase of the
 CC invention. Primers that amplify the telomerase coding sequence can be
 CC used in a method for diagnosing cancer in a patient. The telomerase can
 CC be used for detection, diagnosis and drug screening. Inhibitors of
 CC telomerase activity can be used to treat cancers such as melanomas, other
 CC skin cancers, neuroblastomas, breast carcinomas, colon carcinomas,
 CC leukaemias, lymphomas, osteosarcomas or smooth muscle cell hyperplasias
 CC or skin growths. Enhancers of telomerase may be used to stimulate stem
 CC cell proliferation and differentiation (expansion of haematopoietic stem
 CC cells could be administered in the bone marrow transplant context). As
 CC well, many tissues have stem cells. Proliferation of these cells may be
 CC useful in wound healing, hair growth, treatment of disease such as Wilm's
 CC tumour, organ regeneration or differentiation after injury or diseases,
 CC nerve cell or brain cell growth following injury.
 XX
 SQ Sequence 588 AA;
 Query Match 100.0%; Score 146; DB 20; Length 588;
 Best Local Similarity 100.0%; Pred. No. 1.1e-12;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AKFLHLMMSVYVVELLSFFVVTETTFQ 28
 |||||
 Db 542 AKFLHLMMSVYVVELLSFFVVTETTFQ 569
 RESULT 7
 AAY00644
 ID AAY00644 standard; Protein; 588 AA.
 XX
 AC AAY00644;
 XX
 DT 26-JUL-1999 (first entry)
 XX

DE N-terminal truncated telomerase (ver. 2) protein sequence.
 XX
 KW Telomerase; human; cancer; diagnosis; melanoma; skin cancer; leukaemia;
 KW neuroblastoma; breast carcinoma; colon carcinoma; lymphoma; osteosarcoma;
 KW smooth muscle cell hyperplasia; stem cell proliferation; Wilm's tumour;
 KW stem cell differentiation; organ regeneration; organ differentiation.
 XX
 OS Homo sapiens.
 OS Synthetic.
 PN WO9901560-A1.
 XX
 XX 14-JAN-1999.
 XX
 XX 01-JUL-1998; 98WO-US13835.
 XX
 PR 09-SEP-1997; 97US-0058287.
 PR 01-JUL-1997; 97US-0051410.
 PR 21-JUL-1997; 97US-0053018.
 PR 21-JUL-1997; 97US-0053329.
 PR 04-AUG-1997; 97US-0054642.
 XX
 XX (CAMB-) CAMBIA BIOSYSTEMS LLC.
 PA
 PI Bowtell D, Kilian A;
 XX
 DR WPI: 1999-106060/09.
 DR N-PSDB; AAX18272.
 XX
 XX New isolated vertebrate telomerase genes - used to develop products
 PT for treating cancers or for organ regeneration, nerve cell or brain
 PT cell growth following injury or bone marrow transplantation
 XX
 PS Claim 4; Fig 11t-u; 134pp; English.
 XX
 CC This sequence is a truncated human telomerase of the
 CC invention. Primers that amplify the telomerase coding sequence can be
 CC used in a method for diagnosing cancer in a patient. The telomerase can
 CC be used for detection, diagnosis and drug screening. Inhibitors of
 CC telomerase activity can be used to treat cancers such as melanomas,
 CC other skin cancers, neuroblastomas, breast carcinomas, colon carcinomas,
 CC leukaemias, lymphomas, osteosarcomas or smooth muscle cell hyperplasias
 CC or skin growths. Enhancers of telomerase may be used to stimulate stem
 CC cell proliferation and differentiation (expansion of haematopoietic stem
 CC cells could be administered in the bone marrow transplant context). As
 CC well, many tissues have stem cells. Proliferation of these cells may be
 CC useful in wound healing, hair growth, treatment of disease such as
 CC Wilm's tumour, organ regeneration or differentiation after injury or
 CC diseases, nerve cell or brain cell growth following injury.
 CC Note: The N-terminus of this sequence can be replaced by the sequences
 CC shown in AAY00656-Y00658.
 XX
 SQ Sequence 588 AA;
 Query Match 100.0%; Score 146; DB 20; Length 588;
 Best Local Similarity 100.0%; Pred. No. 1.1e-12;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AKFLHLMMSVYVVELLSFFVVTETTFQ 28
 |||||
 Db 542 AKFLHLMMSVYVVELLSFFVVTETTFQ 569
 RESULT 8
 AAY97384
 ID AAY97384 standard; Protein; 591 AA.
 XX
 AC AAY97384;
 XX
 DT 14-MAY-1999 (first entry)
 XX
 DE A catalytic telomerase protein.
 XX

KW Catalytic telomerase; diagnosis; disease; telomerase activity.
 XX
 OS Homo sapiens.
 XX JP11046768-A.
 PN
 XX 23-FEB-1999.
 PD
 XX
 PF 01-AUG-1997; 97JP-0207708.
 XX
 PR 01-AUG-1997; 97JP-0207708.
 XX
 PA (MITU) MITSUBISHI CHEM CORP.
 XX
 DR WPI; 1999-208111/18.
 DR N-PSDB; AAX15923.
 XX
 XX New catalytic protein of telomerase of a higher animal and a gene
 PT coding it - useful for diagnosis of diseases caused by the change in
 PT activity of a telomerase
 XX
 PS Claim 1; Page 11-14; 18pp; Japanese.
 XX
 CC The present sequence represents a catalytic telomerase protein.
 CC The products are useful in drug compositions for the diagnosis
 CC of diseases caused by the change in activity of telomerase.
 XX
 SQ Sequence 591 AA;
 Query Match 100.0%; Score 146; DB 20; Length 591;
 Best Local Similarity 100.0%; Pred. No. 1.1e-12;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AKFLHMLMSVYVVELLRSPFYVTETTFQ 28
 |||||
 Db 1 AKFLHMLMSVYVVELLRSPFYVTETTFQ 28
 |||||
 RESULT 9
 AAY25463
 ID AAY25463 standard; Protein; 622 AA.
 AC
 XX AAY25463;
 XX
 DT 22-SEP-1999 (first entry)
 XX
 DE Human CRT-1 protein #3.
 XX
 KW CRT-1; reverse transcriptase; telomerase; inhibitor; detection;
 KW telomerase activity; cancer cell; screening; human.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Protein 1..622
 FT /label= CRT-1
 FT /note= "Partial sequence, no stop codon given"
 XX
 XX WO9935261-A1.
 PN
 XX
 PD 15-JUL-1999.
 XX
 PF 08-JAN-1999; 99WO-JP00039.
 XX
 PR 06-MAY-1998; 98JP-0139177.
 PR 08-JAN-1998; 98JP-0013232.
 PR 30-JAN-1998; 98JP-0033584.
 XX
 XX (CHUS) CHUGAI SEIYAKU KK.
 PA
 XX
 PI Tsuchiya M, Yoshida K;
 XX
 DR WPI; 1999-430393/36.

DR N-PSDB; AAX88251.
 XX
 PT Novel gene, useful in detection of telomerase activity and cancer
 PT cells as well as screening telomerase inhibitors for treatment of
 PT cancers
 XX
 PS Example 1; Page 37-39; 44pp; Japanese.
 XX
 CC This invention describes novel human CRT-1 genes and their encoded
 CC proteins containing a reverse transcriptase motif, which act as
 CC telomerase inhibitors. The gene, its encoded protein and derived
 CC antibodies can be used to provide base sequence information, detect
 CC telomerase activity and cancer cells, and to screen telomerase
 CC inhibitors. The detection method is simple and effective.
 XX
 SQ Sequence 622 AA;
 Query Match 100.0%; Score 146; DB 20; Length 622;
 Best Local Similarity 100.0%; Pred. No. 1.2e-12;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AKFLHMLMSVYVVELLRSPFYVTETTFQ 28
 |||||
 Db 32 AKFLHMLMSVYVVELLRSPFYVTETTFQ 59
 |||||
 RESULT 10
 AAW46997
 ID AAW46997 standard; Protein; 807 AA.
 XX
 AC AAW46997;
 XX
 DT 13-AUG-1998 (first entry)
 XX
 DE Human telomerase reverse transcriptase Deltal82 variant.
 XX
 KW Human; telomerase reverse transcriptase; hTERT; TRT; diagnosis;
 KW prognosis; cell proliferation; cancer; ageing; ribonucleoprotein.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 XX GB2317891-A.
 PN
 PD 08-APR-1998.
 XX
 PF 01-OCT-1997; 97GB-0020890.
 XX
 PR 14-AUG-1997; 97US-0915503.
 PR 01-OCT-1996; 96US-0724643.
 PR 18-APR-1997; 97US-0844419.
 PR 25-APR-1997; 97US-0846017.
 PR 06-MAY-1997; 97US-0851843.
 PR 09-MAY-1997; 97US-0854050.
 PR 14-AUG-1997; 97US-0911312.
 PR 14-AUG-1997; 97US-0912951.
 XX
 PA (GERO-) GERON CORP.
 PA (UYTE-) UNIV TECHNOLOGY CORP.
 XX
 PI Andrews WH, Cech TR, Chapman KB, Harley C, Lingner J;
 PI Morin GS, Nakamura T, Harley CB;
 XX
 DR WPI; 1998-171633/16.
 DR N-PSDB; AAV22382.
 XX
 PT Pure and recombinant human Telomerase Reverse Transcriptase and its
 PT variants - are useful in the diagnosis, prognosis and treatment of
 PT cell proliferation conditions especially cancer and ageing
 XX
 PS Disclosure; Fig 20; 387pp; English.
 XX
 CC The present sequence represents a human telomerase reverse transcriptase

CC (hTERT) variant from the present invention. The present invention also
 CC describes the following methods: (A) determining whether a test compound
 CC is a modulator of hTERT, by detecting the change in hTERT recombinant
 CC protein or polynucleotide, on administration of the compound; (B)
 CC preparation of recombinant telomerase by contacting a protein
 CC preparation of hTERT with a telomerase RNA component; (C) detection of
 CC the hTERT RNA or protein in a sample by binding a relevant probe to the
 CC sample and detecting the complex formed or in the case of RNA detection,
 CC amplifying the product and correlating the presence of complex or
 CC amplification product with presence of hTERT in the sample; and (D)
 CC increasing the proliferation of a vertebrate cell by increasing hTERT
 CC expression; and (E) the use of an agent that causes an increase in cell
 CC vertebrate cell proliferation to create a medicament that inhibits
 CC ageing. A protein preparation of hTERT and the polynucleotide encoding
 CC hTERT can be used in the manufacture of medicaments for inhibiting the
 CC effect of ageing or cancer. Inhibitors of telomerase activity can be
 CC used to treat conditions that are associated with high telomerase
 CC activity. A protein preparation of hTERT can also be used in the new
 CC methods.

XX SQ Sequence 807 AA;

Query Match 100.0%; Score 146; DB 19; Length 807;
 Best Local Similarity 100.0%; Pred. No. 1.6e-12;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKFLHLMMSVYVVELLSFFVYVTTTFQ 28
 |||||
 Db 542 AKFLHLMMSVYVVELLSFFVYVTTTFQ 569

RESULT 11

AAAY00637
 ID AAY00637 standard; Protein; 807 AA.

XX AC AAY00637;

XX DT 26-JUL-1999 (first entry)

XX DE N-terminal truncated telomerase protein sequence.

XX KW Telomerase; human; cancer; diagnosis; melanoma; skin cancer; leukaemia;
 KW neuroblastoma; breast carcinoma; colon carcinoma; lymphoma; osteosarcoma;
 KW smooth muscle cell hyperplasia; stem cell proliferation; Wilm's tumour;
 KW stem cell differentiation; organ regeneration; organ differentiation.

XX OS Homo sapiens.

OS Synthetic.

XX PN WO9901560-A1.

XX PD 14-JAN-1999.

XX PF 01-JUL-1998; 98WO-US13835.

XX PR 09-SEP-1997; 97US-0058287.

XX PR 01-JUL-1997; 97US-0051410.

XX PR 21-JUL-1997; 97US-0053018.

XX PR 21-JUL-1997; 97US-0053329.

XX PR 04-AUG-1997; 97US-0054642.

XX PA (CAMB-) CAMBIA BIOSYSTEMS LLC.

XX PI Bowtell D, Kilian A;

XX DR WPI; 1999-106060/09.

XX DR N-PSDB; AAX18265.

XX PT New isolated vertebrate telomerase genes - used to develop products
 PT for treating cancers or for organ regeneration, nerve cell or brain
 PT cell growth following injury or bone marrow transplantation

XX PS Claim 4; Fig 11d-e; 134pp; English.

XX CC This sequence is a truncated human telomerase of the
 CC invention. Primers that amplify the telomerase coding sequence can be
 CC used in a method for diagnosing cancer in a patient. The telomerase can
 CC be used for detection, diagnosis and drug screening. Inhibitors of
 CC telomerase activity can be used to treat cancers such as melanomas, other
 CC skin cancers, neuroblastomas, breast carcinomas, colon carcinomas,
 CC leukaemias, lymphomas, osteosarcomas or smooth muscle cell hyperplasias
 CC or skin growths. Enhancers of telomerase may be used to stimulate stem
 CC cell proliferation and differentiation (expansion of haematopoietic stem
 CC cells could be administered in the bone marrow transplant context). As
 CC well, many tissues have stem cells. Proliferation of these cells may be
 CC useful in wound healing, hair growth, treatment of disease such as Wilm's
 CC tumour, organ regeneration or differentiation after injury or diseases,
 CC nerve cell or brain cell growth following injury.

XX SQ Sequence 807 AA;

Query Match 100.0%; Score 146; DB 20; Length 807;
 Best Local Similarity 100.0%; Pred. No. 1.6e-12;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKFLHLMMSVYVVELLSFFVYVTTTFQ 28
 |||||
 Db 542 AKFLHLMMSVYVVELLSFFVYVTTTFQ 569

RESULT 12

AAAY00646

ID AAY00646 standard; Protein; 807 AA.

XX AC AAY00646;

XX DT 26-JUL-1999 (first entry)

XX DE Truncated telomerase (ver. 2) protein sequence.

XX KW Telomerase; human; cancer; diagnosis; melanoma; skin cancer; leukaemia;
 KW neuroblastoma; breast carcinoma; colon carcinoma; lymphoma; osteosarcoma;
 KW smooth muscle cell hyperplasia; stem cell proliferation; Wilm's tumour;
 KW stem cell differentiation; organ regeneration; organ differentiation.

XX OS Homo sapiens.

OS Synthetic.

XX PN WO9901560-A1.

XX PD 14-JAN-1999.

XX PF 01-JUL-1998; 98WO-US13835.

XX PR 09-SEP-1997; 97US-0058287.

XX PR 01-JUL-1997; 97US-0051410.

XX PR 21-JUL-1997; 97US-0053018.

XX PR 21-JUL-1997; 97US-0053329.

XX PR 04-AUG-1997; 97US-0054642.

XX PA (CAMB-) CAMBIA BIOSYSTEMS LLC.

XX PI Bowtell D, Kilian A;

XX DR WPI; 1999-106060/09.

XX DR N-PSDB; AAX18274.

XX PT New isolated vertebrate telomerase genes - used to develop products
 PT for treating cancers or for organ regeneration, nerve cell or brain
 PT cell growth following injury or bone marrow transplantation

XX PS Claim 4; Fig 11x-y; 134pp; English.

XX CC This sequence is a truncated human telomerase of the
 CC invention. Primers that amplify the telomerase coding sequence can be
 CC used in a method for diagnosing cancer in a patient. The telomerase can

CC be used for detection, diagnosis and drug screening. Inhibitors of
 CC telomerase activity can be used to treat cancers such as melanomas,
 CC other skin cancers, neuroblastomas, breast carcinomas, colon carcinomas,
 CC leukaemias, lymphomas, osteosarcomas or smooth muscle cell hyperplasias
 CC or skin growths. Enhancers of telomerase may be used to stimulate stem
 CC cell proliferation and differentiation (expansion of haematopoietic stem
 CC cells could be administered in the bone marrow transplant context). As
 CC well, many tissues have stem cells. Proliferation of these cells may be
 CC useful in wound healing, hair growth, treatment of disease such as
 CC Wilm's tumour, organ regeneration or differentiation after injury or
 CC diseases, nerve cell or brain cell growth following injury.
 CC Note: The N-terminus of this sequence can be replaced by the sequences
 CC shown in AAY00656-Y00658.

XX SQ Sequence 807 AA;
 Query Match 100.0%; Score 146; DB 20; Length 807;
 Best Local Similarity 100.0%; Pred. No. 1.6e-12;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKFLHMLMSVYVVELLSFFVYVTTTFQ 28
 DB 542 AKFLHMLMSVYVVELLSFFVYVTTTFQ 569

RESULT 13
 AAY00642
 ID AAY00642 standard; Protein; 936 AA.

XX AC AAY00642;
 XX DT 26-JUL-1999 (first entry)
 XX DE Truncated telomerase protein sequence lacking motif A.

XX KW Telomerase; human; cancer; diagnosis; melanoma; skin cancer; leukaemia;
 KW neuroblastoma; breast carcinoma; colon carcinoma; lymphoma; osteosarcoma;
 KW smooth muscle cell hyperplasia; stem cell proliferation; Wilm's tumour;
 KW stem cell differentiation; organ regeneration; organ differentiation.

XX OS Homo sapiens.
 OS Synthetic.

XX PN WO9901560-A1.
 XX PD 14-JAN-1999.
 XX PF 01-JUL-1998; 98WO-US13835.

XX PR 09-SEP-1997; 97US-0058287.
 PR 01-JUL-1997; 97US-0051410.
 PR 21-JUL-1997; 97US-0053018.
 PR 21-JUL-1997; 97US-0053329.
 PR 04-AUG-1997; 97US-0054642.

XX PA (CAMB-) CAMBIA BIOSYSTEMS LLC.
 XX PI Bowtell D, Kilian A;
 XX DR WPI; 1999-106060/09.
 DR N-PSDB; AAX18270.

XX PT New isolated vertebrate telomerase genes - used to develop products
 PT for treating cancers or for organ regeneration, nerve cell or brain
 PT cell growth following injury or bone marrow transplantation
 XX PS Claim 4; Fig 11p-q; 134pp; English.

XX CC This sequence is a truncated human telomerase of the
 CC invention. Primers that amplify the telomerase coding sequence can be
 CC used in a method for diagnosing cancer in a patient. The telomerase can
 CC be used for detection, diagnosis and drug screening. Inhibitors of
 CC telomerase activity can be used to treat cancers such as melanomas, other

CC skin cancers, neuroblastomas, breast carcinomas, colon carcinomas,
 CC leukaemias, lymphomas, osteosarcomas or smooth muscle cell hyperplasias
 CC or skin growths. Enhancers of telomerase may be used to stimulate stem
 CC cell proliferation and differentiation (expansion of haematopoietic stem
 CC cells could be administered in the bone marrow transplant context). As
 CC well, many tissues have stem cells. Proliferation of these cells may be
 CC useful in wound healing, hair growth, treatment of disease such as Wilm's
 CC tumour, organ regeneration or differentiation after injury or diseases,
 CC nerve cell or brain cell growth following injury.

XX SQ Sequence 936 AA;

Query Match 100.0%; Score 146; DB 20; Length 936;
 Best Local Similarity 100.0%; Pred. No. 1.8e-12;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKFLHMLMSVYVVELLSFFVYVTTTFQ 28
 DB 542 AKFLHMLMSVYVVELLSFFVYVTTTFQ 569

RESULT 14
 AAY00651
 ID AAY00651 standard; Protein; 936 AA.

XX AC AAY00651;
 XX DT 26-JUL-1999 (first entry)
 XX DE Truncated telomerase (ver. 2) protein sequence lacking motif A.

XX KW Telomerase; human; cancer; diagnosis; melanoma; skin cancer; leukaemia;
 KW neuroblastoma; breast carcinoma; colon carcinoma; lymphoma; osteosarcoma;
 KW smooth muscle cell hyperplasia; stem cell proliferation; Wilm's tumour;
 KW stem cell differentiation; organ regeneration; organ differentiation.

XX OS Homo sapiens.
 OS Synthetic.

XX PN WO9901560-A1.
 XX PD 14-JAN-1999.
 XX PF 01-JUL-1998; 98WO-US13835.

XX PR 09-SEP-1997; 97US-0058287.
 PR 01-JUL-1997; 97US-0051410.
 PR 21-JUL-1997; 97US-0053018.
 PR 21-JUL-1997; 97US-0053329.
 PR 04-AUG-1997; 97US-0054642.

XX PA (CAMB-) CAMBIA BIOSYSTEMS LLC.
 XX PI Bowtell D, Kilian A;
 XX DR WPI; 1999-106060/09.
 DR N-PSDB; AAX18279.

XX PT New isolated vertebrate telomerase genes - used to develop products
 PT for treating cancers or for organ regeneration, nerve cell or brain
 PT cell growth following injury or bone marrow transplantation
 XX PS Claim 4; Fig 11ak-al; 134pp; English.

XX CC This sequence is a truncated human telomerase of the
 CC invention. Primers that amplify the telomerase coding sequence can be
 CC used in a method for diagnosing cancer in a patient. The telomerase can
 CC be used for detection, diagnosis and drug screening. Inhibitors of
 CC telomerase activity can be used to treat cancers such as melanomas,
 CC other skin cancers, neuroblastomas, breast carcinomas, colon carcinomas,
 CC leukaemias, lymphomas, osteosarcomas or smooth muscle cell hyperplasias
 CC or skin growths. Enhancers of telomerase may be used to stimulate stem
 CC cell proliferation and differentiation (expansion of haematopoietic stem

CC cells could be administered in the bone marrow transplant context). As
CC well, many tissues have stem cells. Proliferation of these cells may be
CC useful in wound healing, hair growth, treatment of disease such as
CC Wilm's tumour, organ regeneration or differentiation after injury or
CC diseases, nerve cell or brain cell growth following injury.
CC Note: The N-terminus of this sequence can be replaced by the sequences
CC shown in AAY00656-Y00658.

XX SQ Sequence 936 AA;

Query Match 100.0%; Score 146; DB 20; Length 936;
Best Local Similarity 100.0%; Pred. No. 1.8e-12;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKFLHLMMSVYVVELLSRFFVYVTTTFQ 28
|||
Db 542 AKFLHLMMSVYVVELLSRFFVYVTTTFQ 569

RESULT 15

AAV00639
ID AAY00639 standard; Protein; 948 AA.

XX AC AAY00639;

XX DT 26-JUL-1999 (first entry)

XX DE N-terminal truncated telomerase protein sequence.

XX KW Telomerase; human; cancer; diagnosis; melanoma; skin cancer; leukaemia;
XX KW neuroblastoma; breast carcinoma; colon carcinoma; lymphoma; osteosarcoma;
XX KW smooth muscle cell hyperplasia; stem cell proliferation; Wilm's tumour;
XX KW stem cell differentiation; organ regeneration; organ differentiation.

XX OS Homo sapiens.

XX OS Synthetic.

XX PN WO9901560-A1.

XX PD 14-JAN-1999.

XX PF 01-JUL-1998; 98WO-US13835.

XX PR 09-SEP-1997; 97US-0058287.

XX PR 01-JUL-1997; 97US-0051410.

XX PR 21-JUL-1997; 97US-0053018.

XX PR 21-JUL-1997; 97US-0053329.

XX PR 04-AUG-1997; 97US-0054642.

XX PA (CAMB-) CAMBIA BIOSYSTEMS LLC.

XX PI Bowtell D, Kilian A;

XX DR WPI; 1999-106060/09.

XX DR N-PSDB; AAY00639.

XX PT New isolated vertebrate telomerase genes - used to develop products
XX PT for treating cancers or for organ regeneration, nerve cell or brain
XX PT cell growth following injury or bone marrow transplantation

XX PS Claim 4; Fig 11j-k; 134pp; English.

XX This sequence is a truncated human telomerase of the
CC invention. Primers that amplify the telomerase coding sequence can be
CC used in a method for diagnosing cancer in a patient. The telomerase can
CC be used for detection, diagnosis and drug screening. Inhibitors of
CC telomerase activity can be used to treat cancers such as melanomas, other
CC skin cancers, neuroblastomas, breast carcinomas, colon carcinomas,
CC leukaemias, lymphomas, osteosarcomas or smooth muscle cell hyperplasias
CC or skin growths. Enhancers of telomerase may be used to stimulate stem
CC cell proliferation and differentiation (expansion of haematopoietic stem
CC cells could be administered in the bone marrow transplant context). As
CC well, many tissues have stem cells. Proliferation of these cells may be

CC useful in wound healing, hair growth, treatment of disease such as Wilm's
CC tumour, organ regeneration or differentiation after injury or diseases,
CC nerve cell or brain cell growth following injury.

XX SQ Sequence 948 AA;

Query Match 100.0%; Score 146; DB 20; Length 948;
Best Local Similarity 100.0%; Pred. No. 1.8e-12;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKFLHLMMSVYVVELLSRFFVYVTTTFQ 28
|||
Db 542 AKFLHLMMSVYVVELLSRFFVYVTTTFQ 569

Search completed: November 12, 2003, 19:47:14
Job time : 35.8679 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 12, 2003, 19:43:04 ; Search time 10.9182 Seconds
(without alignments)
246.626 Million cell updates/sec

Title: US-08-854-050-115
Perfect score: 146
Sequence: 1 AKFLHLMMSVYVVELLSRFYVTTTFQ 28
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 76.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	146	100.0	1132	2 T03844	telomerase catalyt
2	81	55.5	989	2 T03838	telomerase catalyt
3	54	37.0	427	2 A49518	kallistatin precu
4	54	37.0	884	2 S53396	telomerase catalyt
5	53.5	36.6	521	2 T41134	aspartic acid prot
6	52	35.6	102	2 B97775	hypothetical prote
7	52	35.6	465	2 C97751	cationic amino aci
8	51	34.9	470	2 F71686	cationic amino aci
9	51	34.9	1132	2 T31107	telomerase reverse
10	50.5	34.6	302	2 B71543	probable benzoate
11	50.5	34.6	653	2 T08621	hypothetical prote
12	50	34.2	500	2 F88921	protein F56E10.3
13	49	33.6	148	2 T39949	probable copper tr
14	48	32.9	231	2 D97248	conserved membrane
15	48	32.9	340	2 E75436	conserved hypothet
16	48	32.9	398	1 E64112	bicyclomycin resis
17	47.5	32.5	163	2 S21858	hypothetical 18.7K
18	47.5	32.5	267	2 D58933	hypothetical prote
19	47	32.2	224	1 A64599	hydrogenase (EC 1
20	47	32.2	224	2 D71915	hydrogenase, cytoc
21	47	32.2	258	1 C69175	heat shock protein
22	47	32.2	316	2 AC3102	hypothetical prote
23	47	32.2	316	2 G98184	oligopeptide ABC t
24	47	32.2	835	2 E72305	hypothetical prote
25	47	32.2	1125	2 S67794	probable membrane
26	46.5	31.8	456	2 A85139	hypothetical prote
27	46	31.5	187	1 IVHUB1	interferon beta-1
28	46	31.5	301	2 T44011	G protein-coupled
29	46	31.5	554	2 S52967	NADH2 dehydrogenas

30 46 31.5 570 2 S07744 NADH2 dehydrogenas
31 45.5 31.2 371 2 B86489 protein T32E20.25
32 45.5 31.2 652 2 A84461 probable fibrin [br/>33 45 30.8 96 2 F70578 hypothetical prote
34 45 30.8 120 2 S39340 hypothetical prote
35 45 30.8 203 2 H86713 hypothetical prote
36 45 30.8 214 2 A86670 hypothetical prote
37 45 30.8 268 2 F71712 prolipoprotein dia
38 45 30.8 277 2 G72357 sugar ABC transpor
39 45 30.8 405 2 S42371 hypothetical prote
40 45 30.8 441 2 G64492 hypothetical prote
41 45 30.8 544 2 S75109 cytochrome-c oxida
42 45 30.8 744 2 T13682 NADH2 dehydrogenas
43 45 30.8 971 2 D70128 conserved hypothet
44 44.5 30.5 710 2 T04979 hypothetical prote
45 44 30.1 62 2 T08028 ycf9 protein - Chl

ALIGNMENTS

RESULT 1

T03844
telomerase catalytic chain - human
N;Alternate names: telomerase reverse transcriptase
C;Species: Homo sapiens (man)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 08-Oct-1999
C;Accession: T03844
R;Nakamura, T.M.; Morin, G.B.; Chapman, K.B.; Weinrich, S.L.; Andrews, W.H.; Lingner, J
Science 277, 955-959, 1997
A;Title: Telomerase catalytic subunit homologs from fission yeast and human.
A;Reference number: Z15111; MUID:97400623; PMID:9252327
A;Accession: T03844
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1132 <NA>
A;Cross-references: EMBL:AF015950; NID:g2330016; PIDN:AAC51672.1; PID:g2330017
A;Experimental source: kidney
C;Genetics:
A;Gene: TRT
A;Map position: 5p

Query Match 100.0%; Score 146; DB 2; Length 1132;
Best Local Similarity 100.0%; Pred. No. 2.8e-13;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKFLHLMMSVYVVELLSRFYVTTTFQ 28
Db 542 AKFLHLMMSVYVVELLSRFYVTTTFQ 569

RESULT 2

T03838
telomerase catalytic chain - fission yeast (Schizosaccharomyces pombe)
N;Alternate names: telomerase reverse transcriptase 1
C;Species: Schizosaccharomyces pombe
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 01-Dec-2000
C;Accession: T03838; T04085
R;Nakamura, T.M.; Morin, G.B.; Chapman, K.B.; Weinrich, S.L.; Andrews, W.H.; Lingner, J
Science 277, 955-959, 1997
A;Title: Telomerase catalytic subunit homologs from fission yeast and human.
A;Reference number: Z15111; MUID:97400623; PMID:9252327
A;Accession: T03838
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-989 <NA>
A;Cross-references: EMBL:AF015783; NID:g2340167; PIDN:AAC49803.1; PID:g2340169
A;Experimental source: strain 972h(-)
A;Accession: T03839
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-524,526-989 <NA2>
A;Cross-references: EMBL:AF015783; NID:g2340167; PIDN:AAC49802.1; PID:g2340168

R.;Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Volckaert, G.
submitted to the EMBL Data Library, March 1998

A;Reference number: Z21904
A;Accession: T40085
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-524,526-989 <LYN>
A;Cross-references: EMBL:AL022299; PIDN:CAA18391.1; GSPDB:GN00067; SPDB:SPBC29A3.14C
A;Experimental source: strain 972h-; cosmid c29A3
C;Genetics:
A;Gene: trt1; SPBC29A3.14C
A;Map position: 2
A;Introns: 8673; 11373; 15372; 24171; 37271; 39573; 48573; 52473; 58272; 64471; 69373; 77775
C;Keywords: alternative splicing

Query Match 55.5%; Score 81; DB 2; Length 989;
Best Local Similarity 42.3%; Pred. No. 0.00079;
Matches 11; Conservative 12; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AKFLHLMSSVVVVELLSFFVVTET 26
Db 425 AEFYWLNSFIIFILQSFFVITSS 450

RESULT 3

A49518
kallistatin precursor - human
N;Alternate names: proteinase inhibitor 4; tissue kallikrein inhibitor
C;Species: Homo sapiens (man)
C;Date: 10-Nov-1995 #sequence_revision 10-Nov-1995 #text_change 26-May-2000
C;Accession: A49518; A55560; A45093
R;Chai, K.X.; Chen, L.M.; Chao, J.; Chao, L.
J. Biol. Chem. 268, 24498-24505, 1993
A;Title: Kallistatin: a novel human serine proteinase inhibitor. Molecular cloning, ties
A;Reference number: A49518; MUID:94043294; PMID:8227002
A;Accession: A49518
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-427 <CHA>
A;Cross-references: GB:L19684; NID:G425145; PIDN:AA59454.1; PID:G425146
R;Chai, K.X.; Ward, D.C.; Chao, J.; Chao, L.
Genomics 23, 370-378, 1994
A;Title: Molecular cloning, sequence analysis, and chromosomal localization of the human
A;Reference number: A55560; MUID:95137583; PMID:7835886
A;Accession: A55560
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-427 <CH2>
A;Cross-references: GB:L28101; NID:G609489; PIDN:AAC41706.1; PID:G619783
R;Zhou, G.X.; Chao, L.; Chao, J.
J. Biol. Chem. 267, 25873-25880, 1992

A;Title: Kallistatin: a novel human tissue kallikrein inhibitor. Purification, character
A;Reference number: A45093; MUID:93100304; PMID:1334488
A;Accession: A45093
A;Molecule type: protein
A;Residues: 389-403 <ZHO>
A;Cross-references: PIDN:AA24557.1; PID:G261993
A;Note: sequence extracted from NCBI backbone (NCBIP:120847)
C;Genetics:
A;Gene: GDB:P14; KIST
A;Cross-references: GDB:266537; OMIM:147935
A;Map position: 14q31-14q32.1
C;Superfamily: antithrombin III
C;Keywords: blocked amino end; glycoprotein; pyroglutamic acid; serine proteinase inhibi
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-427/Product: kallistatin #status predicted <MAT>
F:21/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predicted
F:33,108,157,238/Binding site: carboxylate (Asn) [covalent] #status predicted
F:388/Inhibitory site: Phe (tissue kallikrein) #status experimental

Query Match 37.0%; Score 54; DB 2; Length 427;
Best Local Similarity 46.4%; Pred. No. 3.2;
Matches 13; Conservative 4; Mismatches 11; Indels 0; Gaps 0;

Qy 1 AKFLHLMSSVVVVELLSFFVVTET 28
Db 153 AKFLNDTMAVEAKLPHTNFYDTVGTIQ 180

RESULT 4

S53396
telomerase catalytic chain EST2 - yeast (Saccharomyces cerevisiae)
N;Alternate names: protein L8543.12; protein YLR318W
C;Species: Saccharomyces cerevisiae
C;Date: 05-May-1995 #sequence_revision 01-Sep-1995 #text_change 05-Nov-1999
C;Accession: S53396
R;Du, Z.

submitted to the EMBL Data Library, February 1995
A;Description: The sequence of S. cerevisiae cosmid 8543.
A;Reference number: S53390
A;Accession: S53396
A;Molecule type: DNA
A;Residues: 1-884 <DUZ>
A;Cross-references: EMBL:U20618; NID:G2258165; PID:G662136; GSPDB:GN00012; MIPS:YLR318W
A;Experimental source: strain S288C (AB972)
C;Genetics:
A;Gene: SGD:EST2; MIPS:YLR318W
A;Cross-references: SGD:S0004310; MIPS:YLR318W
A;Map position: 12R

Query Match 37.0%; Score 54; DB 2; Length 884;
Best Local Similarity 36.4%; Pred. No. 6.3; 7; Indels 0; Gaps 0;
Matches 8; Conservative 7; Mismatches 7;

Qy 3 FLHLMSSVVVVELLSFFVVTET 24
Db 364 FLSLFRQLIPKIQIFFYCTE 385

RESULT 5

T41134
aspartic acid proteinase - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
C;Accession: T41134
R;Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Oliver, K.; Harris, D.
submitted to the EMBL Data Library, April 1998
A;Reference number: Z21971
A;Accession: T41134
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-521 <LYN>
A;Cross-references: EMBL:AL022598; PIDN:CAA18644.1; GSPDB:GN00068; SPDB:SPCC1795.09
A;Experimental source: strain 972h-; cosmid c1795
C;Genetics:
A;Gene: SPDB:SPCC1795.09
A;Map position: 3
C;Superfamily: aspartic proteinase MKC7

Query Match 36.6%; Score 53.5; DB 2; Length 521;
Best Local Similarity 34.4%; Pred. No. 4.5;
Matches 11; Conservative 7; Mismatches 9; Indels 5; Gaps 1;

Qy 2 KFLHLMSSVVVVELLSFFY----VTET 28
Db 274 KLTHYAVSIYVQFLNSTFFSNYSIITDAVFQ 305

RESULT 6

B97775
hypothetical protein RC0602 [imported] - Rickettsia conorii (strain Malish 7)
C;Species: Rickettsia conorii
C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 30-Sep-2001
C;Accession: B97775
R;Ogata, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, D.;
Science 293, 2093-2098, 2001

A;Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii.

A;Reference number: A97700; MUID:21442074; PMID:11557893

A;Accession: B97775

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-102 <KUR>

A;Cross-references: GB:AE006914; PIDN:AAL03140.1; PID:gl5619686; GSPDB:GN00173

C;Genetics:

A;Gene: RC0602

Query Match 35.6%; Score 52; DB 2; Length 102;
Best Local Similarity 50.0%; Pred. No. 1.6;
Matches 8; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 AKFLHLMMSVYVVELL 16

||| :||: ||: ||

Db 18 AKLFHWMISIVIVML 33

RESULT 7

cationic amino acid transporter-1 atrCl (imported) - Rickettsia conorii (strain Malish 7

C;Species: Rickettsia conorii

C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 17-May-2002

C;Accession: C97751

R;Ogata, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, D.; Ro

Science 293, 2093-2098, 2001

A;Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii.

A;Reference number: A97700; MUID:21442074; PMID:11557893

A;Accession: C97751

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-465 <KUR>

A;Cross-references: GB:AE006914; PIDN:AAL02949.1; PID:gl5619479; GSPDB:GN00173

C;Genetics:

A;Gene: atrCl

C;Superfamily: arginine permease

Query Match 35.6%; Score 52; DB 2; Length 465;
Best Local Similarity 33.3%; Pred. No. 6.7;
Matches 7; Conservative 9; Mismatches 5; Indels 0; Gaps 0;

QY 4 LHWLMSVYVVELLSFFVYTE 24

::| :||: ||: ||| |

Db 443 IYWFITIFLYLIRSFPMQKE 463

RESULT 8

F71686

cationic amino acid transporter-1 (atrCl) RP307 - Rickettsia prowazekii

C;Species: Rickettsia prowazekii

C;Date: 21-Nov-1998 #sequence_revision 21-Nov-1998 #text_change 03-Nov-2000

C;Accession: F71686

R;Andersson, S.G.E.; Zomorodipour, A.; Andersson, J.O.; Sichert-Ponten, T.; Alsmark, D

Nature 396, 133-140, 1998

A;Title: The genome sequence of Rickettsia prowazekii and the origin of mitochondria.

A;Reference number: A71630; MUID:99039499; PMID:9823893

A;Accession: F71686

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-470 <AND>

A;Cross-references: GB:AJ235271; GB:AJ235269; NID:g3868717; PIDN:CAA14768.1; PID:g386086

A;Experimental source: strain Madrid E

C;Genetics:

A;Gene: atrCl; RP307

C;Superfamily: arginine permease

Query Match 34.9%; Score 51; DB 2; Length 470;
Best Local Similarity 35.3%; Pred. No. 9.5;
Matches 6; Conservative 9; Mismatches 2; Indels 0; Gaps 0;

QY 4 LHWLMSVYVVELLSFF 20

::| :||: ||: ||| |

Db 448 IYWFITIFLYLVRSPFF 464

RESULT 9

T31107

telomerase reverse transcriptase - Oxytricha trifallax

C;Species: Oxytricha trifallax

C;Date: 02-Sep-2000 #sequence_revision 02-Sep-2000 #text_change 02-Sep-2000

C;Accession: T31107

R;Bryan, T.M.; Sperger, J.M.; Chapman, K.B.; Cech, T.R.

Proc. Natl. Acad. Sci. U.S.A. 95, 8479-8484, 1998

A;Title: Telomerase reverse transcriptase genes in Tetrahymena thermophila and Oxytrich

A;Reference number: Z20985; MUID:98337940; PMID:9671703

A;Accession: T31107

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-1132

A;Cross-references: EMBL:AF060230; NID:g3342795; PID:g3342796; PIDN:AAC39163.1

C;Genetics:

A;Gene: TEXT

Query Match 34.9%; Score 51; DB 2; Length 1132;
Best Local Similarity 39.1%; Pred. No. 22;
Matches 9; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

QY 2 KFLHLMMSVYVVELLSFFVYTE 24

||| :||: ||: ||| |

Db 542 KVLKWWFEDLAITLMRCYFSTE 564

RESULT 10

B71543

probable benzoate octaphenyltransferase - Chlamydia trachomatis (serotype D, strain UW3

C;Species: Chlamydia trachomatis

C;Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 20-Apr-2000

C;Accession: B71543

R;Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitchell

Science 282, 754-759, 1998

A;Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia tra

A;Reference number: A71570; MUID:9900809; PMID:9784136

A;Accession: B71543

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-302 <ARN>

A;Cross-references: GB:AE001295; GB:AE001273; NID:g3328617; PIDN:AAC67811.1; PID:g33286

A;Experimental source: serotype D, strain UW-3/Cx

C;Genetics:

A;Gene: ubiA

C;Superfamily: 4-hydroxybenzoate octaprenyltransferase

Query Match 34.6%; Score 50.5; DB 2; Length 302;
Best Local Similarity 40.9%; Pred. No. 7.4;
Matches 9; Conservative 6; Mismatches 6; Indels 1; Gaps 1;

QY 5 HWLMS-VYVVELLSFFVYTET 25

||| :||: ||: ||| |

Db 143 HWILGLVYVYLAITLMNFFAIET 164

RESULT 11

T30621

hypothetical protein 19L - Molluscum contagiosum virus 1

N;Alternate names: MC019L

C;Species: Molluscum contagiosum virus 1

C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 11-May-2000

C;Accession: T30621

R;Senkevitch, T.G.; Bugert, J.J.; Sisler, J.R.; Koonin, E.V.; Darai, G.; Moss, B.

Science 273, 813-816, 1996

A;Title: Genome sequence of a human tumorigenic poxvirus: Prediction of specific host r

A;Reference number: Z20876; MUID:96325459; PMID:8670425

A;Accession: T30621

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

Search completed: November 12, 2003, 19:52:00
Job time : 10.9182 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 12, 2003, 19:41:59 ; Search time 5.81132 Seconds
(without alignments)
226.583 Million cell updates/sec

Title: US-08-854-050-115
Perfect score: 146
Sequence: 1 AKFLHWMVYVVELLSFFYVTTTFQ 28

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	146	100.0	1132	1 TERT_HUMAN	O14746 homo sapien
2	115	78.8	1122	1 TERT_MOUSE	O70372 mus musculu
3	81	55.5	988	1 TERT_SCHPO	O13339 schizosacch
4	69	47.3	1031	1 TERT_EUPAE	O00939 euploates ae
5	54	37.0	427	1 KAIN_HUMAN	P29622 homo sapien
6	54	37.0	884	1 TERT_YEAST	O06163 saccharomyc
7	51	34.9	1132	1 TERT_OXYTR	O76332 oxytricha t
8	49	33.6	148	1 CTRC_SCHPO	Q9usv7 schizosacch
9	48	32.9	398	1 BCR_HAEIN	P45123 haemophilus
10	47	32.2	258	1 HTPX_METTH	O26659 methanobact
11	46	31.5	187	1 INB_HUMAN	P01574 homo sapien
12	46	31.5	301	1 VUS1_HSV62	P52542 human herpe
13	46	31.5	554	1 NUSM_APILI	P34855 apis mellif
14	46	31.5	570	1 NUSM_PARTE	P15584 paramecium
15	46	31.5	720	1 LCFC_HUMAN	O95573 homo sapien
16	45	30.8	268	1 LGT_RICPR	Q9ze99 rickettsia
17	45	30.8	456	1 YNX4_CABEL	P34577 caenorhabdi
18	45	30.8	971	1 Y228_BORBU	O51246 borrelia bu
19	44	30.1	62	1 PSB2_CHLRE	P92276 chlamydomon
20	44	30.1	260	1 Y940_XYLFA	Q9p6t8 xyloella fas
21	44	30.1	314	1 ELO4_HUMAN	O95473 macaca fasc
22	44	30.1	314	1 ELO4_MACFA	O95473 macaca fasc
23	44	30.1	501	1 LYSI_CORGL	P35865 corynebacte
24	44	30.1	505	1 MATK_RHISY	O9gfn8 rhizophora
25	44	30.1	605	1 VEL_HPV14	P36721 human papil
26	44	30.1	720	1 LCFC_MOUSE	Q9c2w4 mus musculu
27	44	30.1	720	1 LCFC_RAT	O63151 rattus norv
28	44	30.1	831	1 PRIA_SYNY3	P74397 synchocyst
29	44	30.1	836	1 YGL1_SCHPO	O9y7j8 schizosacch
30	44	30.1	7073	1 RIAB_CVHSA	P59641 h replicase
31	43.5	29.8	396	1 CGEI_RAT	P39949 rattus norv
32	43.5	29.8	407	1 CGEI_CHICK	P49707 gallus gall
33	43.5	29.8	425	1 SECY_ODOSI	P49461 odontella s

RESULT 1

TERT_HUMAN
ID TERT_HUMAN STANDARD; PRT; 1132 AA.
AC O14746; O14783;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Telomerase reverse transcriptase (EC 2.7.7.-) (Telomerase catalytic subunit) (HEST2).
DE subunit (HEST2).
GN TERT OR TRT OR EST2 OR TCS1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=97400623; PubMed=9252327;
RA Nakamura T.M., Morin G.B., Chapman K.B., Weinrich S.L., Andrews W.H., Lingner J., Harley C.B., Cech T.R.;
RT "Telomerase catalytic subunit homologs from fission yeast and human."; Science 277:955-959(1997).
RL [2]
RN [2]
RP SEQUENCE FROM N.A.
RC MEDLINE=97433088; PubMed=9288757;
RA Meyerson M., Counter C.M., Eaton E.N., Ellison L.W., Steiner P., Caddle S.D., Ziaugra L., Beijersbergen R.L., Davidoff M.J., Liu Q., Bacchetti S., Haber D.A., Weinberg R.A.;
RT "hEST2, the putative human telomerase catalytic subunit gene, is up-regulated in tumor cells and during immortalization."; Cell 90:785-795(1997).
RL [3]
RN [3]
RP SEQUENCE FROM N.A.
RC MEDLINE=99267414; PubMed=10333526;
RA Wick M., Zubov D., Hagen G.;
RT "Genomic organization and promoter characterization of the gene encoding the human telomerase reverse transcriptase (hTERT)."; Gene 232:97-106(1999).
RL [4]
RN [4]
RP SEQUENCE FROM N.A.
RC Londono-Vallejo J.A.;
RT "Sequence of a BAC carrying the entire hTERT gene."; Submitted (Oct-2001) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: TELOMERASE IS A RIBONUCLEOPROTEIN ENZYME ESSENTIAL FOR THE REPLICATION OF CHROMOSOME TERMINI IN MOST EUKARYOTES. IT ELONGATES TELOMERES. IT IS A REVERSE TRANSCRIPTASE THAT ADDS SIMPLE SEQUENCE REPEATS TO CHROMOSOME ENDS BY COPYING A TEMPLATE SEQUENCE WITHIN THE RNA COMPONENT OF THE ENZYME.
CC -!- SUBUNIT: Interacts with PINK1.
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- DISEASE: ACTIVATION OF TELOMERASE HAS BEEN IMPLICATED IN CELL IMMORTALIZATION AND CANCER CELL PATHOGENESIS.
CC -!- SIMILARITY: BELONGS TO THE REVERSE TRANSCRIPTASE FAMILY.
CC TELOMERASE SUBFAMILY.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration

34 43.5 29.8 482 1 FUKC_ECO57
35 43.5 29.8 482 1 FUKC_ECOLI
36 43.5 29.8 491 1 CGEI_MOUSE
37 43.5 29.8 909 1 CNG4_HUMAN
38 43 29.5 139 1 PNA8_RHOU
39 43 29.5 190 1 KCY_THREVO
40 43 29.5 252 1 MODA_RHOCA
41 43 29.5 339 1 RML1_ACACA
42 43 29.5 400 1 OPRM_WACMU
43 43 29.5 743 1 NUSC_CARTI
44 43 29.5 744 1 NUSC_GERJA
45 43 29.5 1047 1 AT9A_HUMAN
O8x6r3 escherichia
P11553 escherichia
Q61457 mus musculu
Q14028 homo sapien
Q59764 r nad(p) tr
Q97bv0 thermoplasma
Q08383 rhodobacter
P46766 acanthamoeb
Q9myw9 macaca mula
Q32091 carthamus t
P51100 gerbera jam
O75110 homo sapien


```

DE subunit) (Telomerase subunit P123) .
OS Euplates aediculatus.
OC Eukaryota; Alveolata; Ciliophora; Spirotrichea; Hypotrichia;
OC Euplotida; Euplotidae; Euplates.
OX NCBI_TaxID=5940;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97274210; PubMed=9110970;
RA Lingner J., Hughes T.R., Shevchenko A., Mann M., Lundblad V.,
RA Cech T.R.;
RT "Reverse transcriptase motifs in the catalytic subunit of
RT telomerase.";
RL Science 276:561-567(1997).
CC -1- FUNCTION: TELOMERASE IS A RIBONUCLEOPROTEIN ENZYME ESSENTIAL FOR
CC THE REPLICATION OF CHROMOSOME TERMINI IN MOST EUKARYOTES. IT
CC ELONGATES TELOMERES. IT IS A REVERSE TRANSCRIPTASE THAT ADDS
CC SIMPLE SEQUENCE REPEATS TO CHROMOSOME ENDS BY COPYING A TEMPLATE
CC SEQUENCE WITHIN THE RNA COMPONENT OF THE ENZYME.
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- SIMILARITY: BELONGS TO THE REVERSE TRANSCRIPTASE FAMILY.
CC TELOMERASE SUBFAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U95964; AAC47515.1; -.
CC InterPro; IPR000477; RVTse.
CC Pfam; IPR003545; Telomerase_RT.
CC Pfam; PF000078; rvt; 1.
CC PRINTS; PR01365; TELOMERASERT.
CC Transferrase; RNA-directed DNA polymerase; Telomere; Nuclear protein;
CC DNA-binding.
CC KW
CC SEQUENCE 1031 AA; 122562 MW; 57B87A63A1PED60F CRC64;
CC -----
Query Match 47.3%; Score 69; DB 1; Length 1031;
Best Local Similarity 56.5%; Pred.No. 0.017;
Matches 13; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 2 KFLHLWLSVVVVELLSFFYVTE 24
DB 438 KULRWTFEDLVSLRCFFYVTE 460
| | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | |

RESULT 5
KAIN_HUMAN STANDARD; PRT; 427 AA.
ID KAIN_HUMAN
AC P29622; Q9EBZ5.
DT 01-APR-1993 (Rel. 25, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE The Kallistatin precursor (Kallikrein inhibitor) (Protease inhibitor 4).
GN SERPIN4 OR P14 OR KST.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94043294; PubMed=8227002;
RA Chai K.X., Chen L.-M., Chao J., Chao L.;
RT "Kallistatin: a novel human serine proteinase inhibitor. Molecular
RT cloning, tissue distribution, and expression in Escherichia coli.";
RT J. Biol. Chem. 268:24498-24505(1993).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=95137583; PubMed=7835886;
RA Chai K.X., Ward D.C., Chao J., Chao L.;
RT "Molecular cloning, sequence analysis, and chromosomal localization

```

of the human protease inhibitor 4 (kallistatin) gene (PI4).";
 Genomics 23:370-378(1994).
 [3]
 SEQUENCE FROM N.A.
 RC MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udén T.B., Tohiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Vallalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 [4]
 RN SEQUENCE OF 388-403.
 RP TISSUE=Plasma;
 RX MEDLINE=93100304; PubMed=1334488;
 RC Zhou G.X., Chao L., Chao J.;
 RT "Kallistatin: a novel human tissue kallikrein inhibitor."
 RT Purification, characterization, and reactive center sequence.";
 RL J. Biol. Chem. 267:25873-25880(1992).
 CC -1- FUNCTION: INHIBITS HUMAN AMIDOLYTIC AND KININOGENASE ACTIVITIES OF
 CC HUMAN TISSUE KALLIKREIN. INHIBITION IS ACHIEVED BY FORMATION OF AN
 CC EQUI-MOLAR, HEAT- AND SDS-STABLE COMPLEX BETWEEN THE INHIBITOR AND
 CC THE ENZYME, AND GENERATION OF A SMALL C-TERMINAL FRAGMENT OF THE
 CC INHIBITOR DUE TO CLEAVAGE AT THE REACTIVE SITE BY TISSUE
 CC KALLIKREIN.
 CC -1- SUBUNIT: MONOMER AND SOME HOMODIMERS.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: Synthesized by liver and secreted in plasma.
 CC -1- PM: THE N-TERMINUS IS BLOCKED.
 CC -1- MISCELLANEOUS: HEPARIN BLOCKS KALLISTATIN'S COMPLEX FORMATION WITH
 CC TISSUE KALLIKREIN AND ABOLISHES ITS INHIBITORY EFFECT ON TISSUE
 CC KALLIKREIN'S ACTIVITY.
 CC -1- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; L19684; AAA59454.1; --
 CC EMBL; L28101; AAC41706.1; --
 CC EMBL; BC014992; AAH14992.1; --
 CC PIR; A49518; A49518.
 CC HSP; P05154; 1PA1.
 CC Genew; HGNC:8948; SERPINA4.
 CC MM; 147935; --
 CC GO; GO:0005209; F:plasma protein; TAS.
 CC GO; GO:000515; F:protein binding activity; TAS.
 CC GO; GO:0004868; F:serpin; TAS.
 CC InterPro; IPR000215; Serpin.
 CC Pfam; PF00079; serpin; 1.
 CC SMART; SM00093; SERPIN; 1.
 CC PROSITE; PS00284; SERPIN; 1.
 KW Serpin; Serine protease inhibitor; Plasma; Glycoprotein; Signal.
 FT SIGNAL 1 20 POTENTIAL.

FT CHAIN 21 427
 FT ACT SITE 388 389 KALLISTATIN.
 FT CARBOHYD 33 33 REACTIVE BOND.
 FT CARBOHYD 108 108 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 157 157 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 238 238 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CONFLICT 382 382 T -> S (IN REF. 3).
 SQ SEQUENCE 427 AA; 48556 MW; 3DBBE7AF956D4DAC CRC64;
 Query Match 37.0%; Score 54; DB 1; Length 427;
 Best Local Similarity 46.4%; Pred. No. 1.2;
 Matches 13; Conservative 4; Mismatches 11; Indels 0; Gaps 0;
 QY 1 AKFLHMLWSVVVVELLSFFVYVTFQ 28
 DB 153 AKFLNDTMAVYEAKLFHTNFYDVTGTTQ 180
 RESULT 6
 TERT YEAST
 ID TERT YEAST STANDARD; PRT; 884 AA.
 AC Q06163;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Telomerase reverse transcriptase (EC 2.7.7.-) (Telomerase catalytic
 DE subunit).
 GN EST2 OR YLR318W OR L8543.12.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
 OX NCBI TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=S288c / AB972;
 RX MEDLINE=97313267; PubMed=9169871;
 RA Johnston M., Hillier L., Riles L., Albermann K., Andre B., Ansorge W.,
 RA Benes V., Brueckner M., Delius H., Dubois E., Duesterhoeft A.,
 RA Entian K.-D., Floeth M., Goffeau A., Hebling U., Heumann K.,
 RA Heuss-Neitzel D., Hilbert H., Hilger F., Kleine K., Koetter P.,
 RA Louis E.J., Messinguy F., Mewes H.-W., Miosga T., Moesl D.,
 RA Mueller-Auer S., Nentwich U., Obermaier B., Pirawski E., Pohl T.M.,
 RA Portetle D., Purnelle B., Rechmann S., Rieger M., Rinke M., Rose M.,
 RA Scharte M., Scherens B., Scholler P., Schwager C., Schwarz S.,
 RA Underwood A.P., Urrestazu L.A., Vandenbol M., Verhasselt P.,
 RA Vierendeels P., Voet M., Volckaert G., Voss H., Wambutt R., Wedler E.,
 RA Wedler H., Zimmermann F.K., Zollner A., Hani J., Hebeisel J.D.;
 RT "The nucleotide sequence of Saccharomyces cerevisiae chromosome XII.";
 RL Nature 387:87-90(1997).
 [2]
 RN CHARACTERIZATION.
 RP MEDLINE=97274210; PubMed=9110970;
 RX Lingner J., Hughes T.R., Shevchenko A., Mann M., Lundblad V.,
 RA Cech T.R.;
 RT "Reverse transcriptase motifs in the catalytic subunit of
 RT telomerase.";
 RL Science 276:561-567(1997).
 CC -1- FUNCTION: TELOMERASE IS A RIBONUCLEOPROTEIN ENZYME ESSENTIAL FOR
 CC THE REPLICATION OF CHROMOSOME TERMINI IN MOST EUKARYOTES. IT
 CC ELONGATES TELOMERES. IT IS A REVERSE TRANSCRIPTASE THAT ADDS
 CC SIMPLE SEQUENCE REPEATS TO CHROMOSOME ENDS BY COPYING A TEMPLATE
 CC SEQUENCE WITHIN THE RNA COMPONENT OF THE ENZYME.
 CC -1- SUBCELLULAR LOCATION: Nuclear.
 CC -1- MISCELLANEOUS: DELETION CAUSES TELOMERE SHORTENING AND SENESCENCE.
 CC -1- SIMILARITY: BELONGS TO THE REVERSE TRANSCRIPTASE FAMILY.
 CC TELOMERASE SUBFAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----

CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; U20618; AAB64520.1; -.
 DR PIR; S53396; S53396.
 DR SGD; S0004310; EST2.
 DR GO; GO:0005730; C:nucleolus; IDA.
 DR InterPro; IPR000477; RVTS.
 DR InterPro; IPR003545; Telomerase_RT.
 DR Pfam; PF00078; rvt; 1.
 DR PRINTS; PR01365; TLEOMERASERT.
 KW Transferase; RNA-directed DNA polymerase; Telomere; Nuclear protein;
 KW DNA-binding.
 SQ SEQUENCE 884 AA; 102663 MW; 788334BB49592340 CRC64;
 Query Match 37.0%; Score 54; DB 1; Length 884;
 Best Local Similarity 36.4%; Pred. No. 2.4;
 Matches 8; Conservative 7; Mismatches 7; Indels 0; Gaps 0;
 QY 3 FLHLMSVYVVELLSRFFVYTE 24
 Db :|||:|||||
 364 FISWLFRLPKIIQTFYCTE 385
 RESULT 7
 TERT_OXYTR
 ID TERT_OXYTR STANDARD; PRT; 1132 AA.
 AC O76332;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DE Telomerase reverse transcriptase (EC 2.7.7.-) (Telomerase catalytic
 subunit) (Telomerase subunit P133).
 DE TERT.
 OS Oxytricha trifallax.
 GN Eukaryota; Alveolata; Ciliophora; Spirotrichea; Stichotrichia;
 OC Stichotrichida; Oxytrichidae; Oxytricha.
 OX NCBI_TaxID=5946;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98337940; PubMed=9671703;
 RA Bryan T.M., Sperger J.M., Chapman K.B., Cech T.R.;
 RT "Telomerase reverse transcriptase genes identified in Tetrahymena
 thermophila and Oxytricha trifallax."
 RL Proc. Natl. Acad. Sci. U.S.A. 95:8479-8484(1998).
 CC -!- FUNCTION: TELOMERASE IS A RIBONUCLEOPROTEIN ENZYME ESSENTIAL FOR
 CC THE REPLICATION OF CHROMOSOME TERMINI IN MOST EUKARYOTES. IT
 CC ELONGATES TELOMERES. IT IS A REVERSE TRANSCRIPTASE THAT ADDS
 CC SIMPLE SEQUENCE REPEATS TO CHROMOSOME ENDS BY COPYING A TEMPLATE
 CC SEQUENCE WITHIN THE RNA COMPONENT OF THE ENZYME.
 CC -!- SUBCELLULAR LOCATION: Nuclear.
 CC -!- SIMILARITY: BELONGS TO THE REVERSE TRANSCRIPTASE FAMILY.
 CC TELOMERASE SUBFAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; AF060230; AAC39163.1; -.
 DR PIR; T31107; T31107.
 DR InterPro; IPR003545; Telomerase_RT.
 DR PRINTS; PR01365; TLEOMERASERT.
 KW Transferase; RNA-directed DNA polymerase; Telomere; Nuclear protein;
 KW DNA-binding.
 SQ SEQUENCE 1132 AA; 134124 MW; 81E145F5F24392DC CRC64;
 Query Match 34.9%; Score 51; DB 1; Length 1132;
 Best Local Similarity 39.1%; Pred. No. 8.8;
 Matches 9; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

QY 2 KFLHLMMSVYVVELLSRFFVYTE 24
 Db :|||:|||||
 542 KVLKWFEDLAITMRCYFYTE 564
 RESULT 8
 CTR6_SCHPO
 ID CTR6_SCHPO STANDARD; PRT; 148 AA.
 AC Q9USV7;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Copper transport protein ctr6 (Copper transporter 6).
 GN CTR6 OR SPBC23G7.16.
 OS Schizosaccharomyces pombe (Fission yeast).
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;
 OC Schizosaccharomycetes.
 OX NCBI_TaxID=4896;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=972;
 RX MEDLINE=21848401; PubMed=11859360;
 RA Wood V., Gilliam R., Rajadream M.A., Lyne M., Lyne R., Stewart A.,
 RA Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
 RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
 RA Collins M., Connor R., Cronin A., Davis P., Fellwell T., Fraser A.,
 RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
 RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
 RA James K., Jones L., Jones M., Leather S., McDonald S., McJeun J.,
 RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
 RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,
 RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
 RA Skellon J., Simmonds M., Squares R., Squares S., Stevens K.,
 RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
 RA Woodward J., Voickaert G., Aert R., Robben J., Grymonprez B.,
 RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
 RA Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H.,
 RA Borzym K., Langer I., Beck A., Leirach H., Reinhardt R., Pohl T.M.,
 RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
 RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
 RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
 RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
 RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
 RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
 RA Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
 RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
 RT "The genome sequence of Schizosaccharomyces pombe."
 RL Nature 415:871-880(2002).
 RN [2]
 RP FUNCTION, SUBUNIT, SUBCELLULAR LOCATION, AND INDUCTION.
 RX MEDLINE=22336382; PubMed=12244050;
 RA Bellemare D.R., Shaner L., Morano K.A., Beaudoin J., Langlois R.,
 RA Labbe S.;
 RT "Ctr6, a vacuolar membrane copper transporter in Schizosaccharomyces
 RT pombe."
 RL J. Biol. Chem. 277:46676-46686(2002).
 CC -!- FUNCTION: Mobilizes stored copper from the vacuole to the
 CC cytoplasm under conditions of copper limitation.
 CC -!- SUBUNIT: Homotrimer.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Vacuolar.
 CC -!- INDUCTION: By copper deprivation.
 CC -!- SIMILARITY: BELONGS TO THE SLC31A FAMILY OF TRANSPORTERS.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; AL035065; CAB58134.1; -.

```

DR PIR; T39949; T39949.
DR GeneDB SPombe: SPBG23G7.16; -.
DR Pfam; PF04145; Ctr; 1.
KW Transmembrane; Transport; Copper transport.
FT DOMAIN 1 31 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 32 54 POTENTIAL.
FT DOMAIN 55 104 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 105 127 POTENTIAL.
FT DOMAIN 128 148 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 149 16747 MW; D5E214905DDB0491 CRC64;
SQ SEQUENCE 148 AA; 16747 MW; D5E214905DDB0491 CRC64;

Query Match 33.6%; Score 49; DB 1; Length 148;
Best Local Similarity 40.6%; Pred. No. 2.2;
Matches 13; Conservative 7; Mismatches 8; Indels 4; Gaps 1;

QY 1 AKFLHMLMSV-----YVVELLRSPFYVTETTFQ 28
DB 38 SQFLLSLALAILGYLFLRLRSFTSLKETEFQ 69

RESULT 9
BCR_HAEN
ID - BCR_HAEN STANDARD; PRT; 398 AA.
AC P45123;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Bicyclomycin resistance protein homolog.
GN BCR OR H1242.
OS Haemophilus influenzae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Haemophilus.
OX NCBI_TaxID=727;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Rd / KW20 / ATCC 51907;
RX MEDLINE=95350630; PubMed=7542800;
RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
RA Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
RA McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
RA Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
RA Usterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
RA Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,
RA Gnehm C.L., McDonald L.A., Small K.V., Frazer C.M., Smith H.O.,
RA Venter J.C.;
RT "Whole-genome random sequencing and assembly of Haemophilus influenzae Rd."
RL Science 269:496-512(1995).
CC -1- FUNCTION: INVOLVED IN SULFONAMIDE (SULFATHIAZOLE) AND
CC BICYCLOMYCIN RESISTANCE. PROBABLE MEMBRANE TRANSLOCASE
CC (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
CC (Potential).
CC -1- SIMILARITY: BELONGS TO THE MAJOR FACILITATOR FAMILY (ALSO KNOWN
CC AS THE DRUG RESISTANCE TRANSLOCASE FAMILY). BELONGS TO THE
CC BCR/CMA SUBFAMILY.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U32804; AAC22894.1; -.
CC PIR; E64112; E64112.
CC TIGR; H1242.
CC InterPro; IPR004812; Efflux_Bcr_CflA.
CC InterPro; IPR007114; MFS.
CC InterPro; IPR005828; Sub_transporter.
CC Pfam; PF00083; sugar_tr; 1.
DR

```

```

DR PIR; TIGR00710; efflux_Bcr_CflA; 1.
KW Antibiotic resistance; Transport; Transmembrane; Inner membrane;
KW Complete proteome.
FT TRANSMEM 8 28 POTENTIAL.
FT TRANSMEM 52 72 POTENTIAL.
FT TRANSMEM 75 95 POTENTIAL.
FT TRANSMEM 102 122 POTENTIAL.
FT TRANSMEM 137 157 POTENTIAL.
FT TRANSMEM 164 184 POTENTIAL.
FT TRANSMEM 225 245 POTENTIAL.
FT TRANSMEM 247 267 POTENTIAL.
FT TRANSMEM 275 295 POTENTIAL.
FT TRANSMEM 296 316 POTENTIAL.
FT TRANSMEM 343 363 POTENTIAL.
FT TRANSMEM 369 389 POTENTIAL.
SQ SEQUENCE 398 AA; 43459 MW; F681C5C654675216 CRC64;

Query Match 32.9%; Score 48; DB 1; Length 398;
Best Local Similarity 36.7%; Pred. No. 8.5;
Matches 11; Conservative 3; Mismatches 10; Indels 6; Gaps 1;

QY 2 KFLHMLMSVYVVELL-----RSFFYVTET 25
DB 158 KFFHWHAFYVISLVGLAALVFFIIPET 187

RESULT 10
HTPX_METH
ID - HTPX_METH STANDARD; PRT; 258 AA.
AC O26669;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Probable protease htpx homolog (EC 3.4.24.-).
GN HTPX OR MTH569.
OS Methanobacterium thermoautotrophicum.
OC Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;
OC Methanobacteriaceae; Methanothermobacter.
OX NCBI_TaxID=187420;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Delta H;
RX MEDLINE=98037514; PubMed=9371463;
RA Smith D.R., Doucette-Stamm L.A., Deloughery C., Lee H.-M., Dubois J.,
RA Alldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K.,
RA Harrison D., Hoang L., Keagle P., Lumm W., Pothier B., Qiu D.,
RA Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R.,
RA McDougall S., Shimer G., Goyal A., Pietrowski S., Church G.M.,
RA Daniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N.;
RT "Complete genome sequence of Methanobacterium thermoautotrophicum
RT deltaH: functional analysis and comparative genomics."
RL J. Bacteriol. 179:7135-7155(1997).
CC -1- COFACTOR: Binds 1 zinc ion per subunit (By similarity).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M48.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AE000839; AAB85075.1; -.
CC PIR; C69175; C69175.
CC MEROPS; M48.004; -.
CC HAMAP; MF 00188; atypical; 1.
CC InterPro; IPR001915; Peptidase_M48.
CC InterPro; IPR006025; Zn_MpPeptidase.
CC Pfam; PF01435; Peptidase_M48; 1.
CC PROSITE; PS00142; ZINC_PROTEASE; FALSE_NEG.
DR

```



```

DR GO: GO:0006919; P: caspase activation; NAS.
DR GO: GO:0007166; P: cell surface receptor linked signal transdu. .; TAS.
DR GO: GO:0030101; P: natural killer cell activation; NAS.
DR GO: GO:0008285; P: negative regulation of cell proliferation; NAS.
DR GO: GO:0046597; P: negative regulation of virion penetration; NAS.
DR GO: GO:0045089; P: positive regulation of innate immune response; NAS.
DR GO: GO:0045343; P: regulation of MHC class I biosynthesis; NAS.
DR GO: GO:0009615; P: response to viruses; NAS.
DR InterPro: IPR000471; Interferon_abd.
DR Pfam: PF00143; Interferon_1.
DR PRINTS: PR00266; INTERFERONAB.
DR ProDom: PD000550; Interferon_abd; 1.
DR SMART: SM00076; IFabd; 1.
DR PROSITE: PS00252; INTERFERON_A_B_D; 1.
KW Cytokine; Glycoprotein; Antiviral; Signal; Pharmaceutical;
KW 3D-structure.
FT SIGNAL 1 21
FT CHAIN 22 187
FT CARBOHYD 101 101
FT DISULFID 52 162
FT VARIANT 162 162
FT FT
FT FT
FT HELIX 24 44
FT HELIX 63 66
FT HELIX 73 92
FT TURN 96 97
FT HELIX 102 125
FT TURN 126 128
FT HELIX 134 156
FT TURN 157 159
FT HELIX 161 182
FT TURN 183 184
SQ SEQUENCE 187 AA; 22294 MW; 0B013D4087723CEC CRC64;

Query Match 31.5%; Score 46; DB 1; Length 187;
Best Local Similarity 28.0%; Pred. No. 7.8;
Matches 7; Conservative 9; Mismatches 9; Indels 0; Gaps 0;

Oy 2 KFLHLMSSVYVVELLRSPFFVYTTT 26
Db 158 EYSHCAWTVIRVEILRNFYFINRLT 182

RESULT 12
VU51_HSV62
ID VU51_HSV62 STANDARD; PRT; 301 AA.
AC P25242;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE G-protein coupled receptor homolog U51.
GN U51 OR KAL2R.
OS Human herpesvirus (type 6 / strain 229) (HHV6).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Betaherpesvirinae; Roseolovirus.
OX NCBI_TaxID=36351;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=95074921; PubMed=7983761;
RA Stamey F.R., Dominguez G., Black J.B., Dambaugh T.R., Pellett P.E.;
RT "Intragenomic linear amplification of human herpesvirus 6B orlyt
RT suggests acquisition of orlyt by transposition."
CC J. Virol. 69:589-596(1995).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch)
CC -----
CC EMBL: L06178; AAB96805.1;
DR InterPro: IPR003916; NADhub_oxred5.
DR InterPro: IPR001750; Oxidored_q1.
DR InterPro: IPR001516; Oxidored_q1_N.

```



```

DR Pfam; PF00361; oxidored_q1; 1.
DR Pfam; PF00662; oxidored_q1_N; 1.
DR PRINTS; PR01434; NADHDBGNASES.
KW Oxidoreductase; NAD; Ubiquinone; Mitochondrion.
SQ SEQUENCE 554 AA; 65590 MW; 0C8ECCB99CD756B3 CRC64;

Query Match 31.5%; Score 46; DB 1; Length 554;
Best Local Similarity 47.4%; Pred. No. 24;
Matches 9; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 3 FLHMLSVYVVELLRSPFFYT 21
Db 16 FLMLMSLYLLYLNKRRFF 34

RESULT 14
NUSM PARTE STANDARD; PRT; 570 AA.
AC P15584;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE NADH-ubiquinone oxidoreductase chain 5 (EC 1.6.5.3).
GN NDS OR NDH5.
OS Paramecium tetraurelia.
OC Mitochondrion.
OC Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Peniculida;
OC Paramecium.
OX NCBI_TaxID=5888;
RN 1;
RP SEQUENCE FROM N.A.
RC STRAIN=Stock 51;
RX MEDLINE=90174913; PubMed=2308823;
RA Pritchard A.E., Sellhauer J.J., Mahalingam R., Sable C.L.,
RA Venuti S.E., Cummings D.J.;
RT "Nucleotide sequence of the mitochondrial genome of Paramecium.";
RL Nucleic Acids Res. 18:173-180(1990).
CC -!- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X15917; CAA34053.1; -.
CC PIR; S07744; S07744.
CC DR InterPro; IPR003916; NADhub_oxred5.
CC DR InterPro; IPR001750; Oxidored_q1.
CC DR InterPro; IPR001516; Oxidored_q1_N.
CC DR Pfam; PF00361; oxidored_q1; 1_N.
CC DR Pfam; PF00662; oxidored_q1; 1.
CC DR PRINTS; PR01434; NADHDBGNASES.
KW Oxidoreductase; NAD; Ubiquinone; Mitochondrion.
SQ SEQUENCE 570 AA; 65196 MW; 23636CFDC1B0BC4C CRC64;

Query Match 31.5%; Score 46; DB 1; Length 570;
Best Local Similarity 29.2%; Pred. No. 24;
Matches 7; Conservative 9; Mismatches 8; Indels 0; Gaps 0;

QY 3 FLHMLSVYVVELLRSPFFYTET 26
Db 529 FFYWIATFFVILVLFYQKKT 552

RESULT 15
LCFC HUMAN STANDARD; PRT; 720 AA.
AC O95573;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)

```

```

DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Long-chain-fatty-acid--CoA ligase 3 (EC 6.2.1.3) (Long-chain acyl-CoA
DE synthetase 3) (LACS 3).
GN FACL3 OR ACS3 OR LACS3.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN 1;
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=97321062; PubMed=9177793;
RA Minekura H., Fujino T., Kang M.-J., Fujita T., Endo Y., Yamamoto T.T.;
RT "Human acyl-coenzyme A synthetase 3 cDNA and localization of its gene
RT (ACS3) to chromosome band 2q34-q35.";
RL Genomics 42:180-181(1997).
RN 2;
RP SEQUENCE FROM N.A.
RX MEDLINE=21564184; PubMed=11707336;
RA Minekura H., Kang M.-J., Inagaki Y., Suzuki H., Sato H., Fujino T.,
RA Yamamoto T.T.;
RT "Genomic organization and transcription units of the human acyl-CoA
RT synthetase 3 gene.";
RL Gene 278:185-192(2001).
CC -!- FUNCTION: ACTIVATION OF LONG-CHAIN FATTY ACIDS FOR BOTH SYNTHESIS
CC OF CELLULAR LIPIDS, AND DEGRADATION VIA BETA-OXIDATION.
CC PREFERENTIALLY USES MYRISTATE, LAURATE, ARACHIDONATE AND
CC BICOSAPENTAENOATE AS SUBSTRATES (BY SIMILARITY).
CC -!- CATALYTIC ACTIVITY: ATP + a long-chain carboxylic acid + CoA = AMP
CC + diphosphate + an acyl-CoA.
CC -!- COFACTOR: MAGNESIUM (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: MICROSOMES, OUTER MITOCHONDRIAL MEMBRANE
CC AND PEROXISOMAL MEMBRANE.
CC -!- SIMILARITY: BELONGS TO THE ATP-DEPENDENT AMP-BINDING ENZYME
CC FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; D89053; BAA37142.1; -.
CC DR EMBL; AB061712; BAB72074.1; -.
CC DR Genew; HGNC:3570; FACL3.
CC DR MIM; 602371; -.
CC DR GO; GO:0004321; F.fatty-acyl-CoA synthase activity; TAS.
CC DR InterPro; IPR000873; AMP-bind.
CC DR Pfam; PF00501; AMP-binding; 1.
CC DR PRINTS; PR00154; AMPBINDING.
CC DR PROSITE; PS00455; AMP_BINDING; 1.
KW Ligase; Fatty acid metabolism; Magnesium; Multigene family.
SQ SEQUENCE 720 AA; 80345 MW; 845959A765B6B6 CRC64;

Query Match 31.5%; Score 46; DB 1; Length 720;
Best Local Similarity 30.4%; Pred. No. 31;
Matches 7; Conservative 9; Mismatches 7; Indels 0; Gaps 0;

QY 3 FLHMLSVYVVELLRSPFFYTET 25
Db 25 FIHFLISLYLTLYIPFFYFSES 47

Search completed: November 12, 2003, 19:48:02
Job time : 6.81132 secs

```

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 12, 2003, 19:42:29 ; Search time 26.7673 Seconds
(without alignments)
269.937 Million cell updates/sec

Title: US-08-854-050-115
Perfect score: 146
Sequence: 1 AKFLHLMMSVYVVELLSRFYVTTTFQ 28

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 23:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mmc:*
- 8: sp_organelle:*
- 9: sp_phase:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rvirus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	146	100.0	795	4 Q8NG38	Q8ng38 homo sapien
2	146	100.0	807	4 Q8N6C3	Q8n6c3 homo sapien
3	146	100.0	1059	4 Q8NG46	Q8ng46 homo sapien
4	122	83.6	1128	11 Q9QX24	Q9qx24 mesocricetu
5	113	77.4	1191	13 Q9DE32	Q9de32 xenopus lae
6	66	45.2	1032	5 Q8MUB3	Q8mub3 euplotes cr
7	63	43.2	867	3 Q9P8T2	Q9p8t2 candida alb
8	63	43.2	867	3 Q9P8T3	Q9p8t3 candida alb
9	61	41.8	1259	10 Q9AU13	Q9au13 oryza sativ
10	61	41.8	1261	10 Q8LKW0	Q8lkw0 oryza sativ
11	58	39.7	575	11 Q9JK99	Q9jk99 rattus norv
12	55	37.7	823	5 Q8SQ00	Q8sq00 encephalito
13	53.5	36.6	521	3 Q59774	Q59774 schizosacch
14	52.5	36.0	1475	5 Q8T678	Q8t678 dictyosteli
15	52	35.6	102	16 Q92I18	Q92i18 rickettsia
16	52	35.6	465	16 Q92IK9	Q92ik9 rickettsia

Q8i2w8 plasmodium
Q9zdm0 rickettsia
Q8i8z6 sterkiella
Q8i8z7 sterkiella
Q84221 chlamydia t
Q9188 molluscum c
Q8xxw8 raistonia s
Q77812 macaca fasc
O11310 molluscum c
Q9txp1 caenorhabdi
Q8i5r4 plasmodium
Q8ieh2 plasmodium
Q8ria9 lactobacill
Q8nm7 corynebacte
Q9haa6 methanosarc
Q9rvb1 deinococcus
Q84531 vibrio vuln
Q9nu29 caenorhabdi
Q9z2n6 cyanidiosch
Q8lqd2 oryza sativ
Q25150 helicobacte
Q921k3 helicobacte
Q9v9g5 drosophila
Q8u710 agrobacteri
Q9mnk3 galathealin
Q9en28 ansacta moo
Q8u268 pyrococcus

17 51 34.9 160 5 Q8I2W8
18 51 34.9 470 16 Q9ZDM0
19 51 34.9 1108 5 Q8I8Z6
20 51 34.9 1135 5 Q8I8Z7
21 50.5 34.6 302 16 Q84221
22 50.5 34.6 663 12 Q9188
23 50 34.2 121 16 Q8XXW8
24 50 34.2 187 6 Q77812
25 50 34.2 301 12 O11310
26 50 34.2 475 5 Q9TXP1
27 50 34.2 1283 5 Q8I5R4
28 50 34.2 2518 5 Q8IEH2
29 49 33.6 210 2 Q8RLA9
30 48 32.9 95 16 Q8NNN7
31 48 32.9 180 1 Q9HHA6
32 48 32.9 231 16 Q97FA9
33 48 32.9 340 16 Q9RVB1
34 48 32.9 541 16 Q8D531
35 48 32.9 739 5 Q9N2U9
36 47.5 32.5 163 12 Q04392
37 47.5 32.5 267 8 Q9Z2N6
38 47 32.2 113 10 Q8LQD2
39 47 32.2 224 16 Q25350
40 47 32.2 224 16 Q9ZLK3
41 47 32.2 256 5 Q9V5G5
42 47 32.2 316 16 Q8U7L0
43 47 32.2 333 8 Q9MNK3
44 47 32.2 400 12 Q9EN28
45 47 32.2 417 17 Q8U268

ALIGNMENTS

RESULT 1
Q8NG38 PRELIMINARY; PRT; 795 AA.
AC Q8NG38;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE ABG-deleted variant of telomerase reverse transcriptase.
GN TERT.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Stomach;
RA Hisatomi H., Nagao K., Kanamaru T., Hirata H., Miyachi K., Hikiiji H.;
RT "Exon 11 deleted variant of human reverse transcriptase."
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB086950; BAC11015.1; -
DR InterPro; IPR003545; Telomerase RT.
DR PRINTS; PR01365; TELOMERASERT.
KW RNA-directed DNA polymerase.
SQ SEQUENCE 795 AA; 88965 MW; 6BEAC8A6D1A2E8CB CRC64;

Query Match 100.0%; Score 146; DB 4; Length 795;
Best Local Similarity 100.0%; Pred. No. 1.3e-13;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKFLHLMMSVYVVELLSRFYVTTTFQ 28
Db 542 AKFLHLMMSVYVVELLSRFYVTTTFQ 569

RESULT 2
Q8N6C3 PRELIMINARY; PRT; 807 AA.
ID Q8N6C3
AC Q8N6C3;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)

```

OS Mesocricetus auratus (Golden hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Mesocricetus.
OX NCBI_TaxID=10036;
RN [1]_SEQUENCE FROM N.A.
RP SEQUENCE 1128 AA; 128394 MW; 1D4F81249012174E CRC64;
RX MEDLINE=21340330; PubMed=11342218;
RT Guo W., Okamoto M., Lee Y.M., Baluda M.A., Park N.H.;
RA "Enhanced activity of cloned hamster TERT gene promoter in transformed
RL cells.";
RR Biochim. Biophys. Acta 1517:398-409(2001).
DR EMBL; AF149012; AAF17334.1; -.
DR InterPro; IPR000477; RVTse.
DR IntronPro; IPR003545; Telomerase_RT.
DR Pfam; PF00078; rvt; 1.
DR PRINTS; PR01365; TELOMERASERT.
KW RNA-directed DNA polymerase; Transferase.
SQ SEQUENCE 1128 AA; 128394 MW; 1D4F81249012174E CRC64;

Query Match      83.6%; Score 122; DB 11; Length 1128;
Best Local Similarity 85.7%; Pred. No. 7.5e-10;
Matches 24; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 AKFLHLMMSVYVVLLRSFFYVTTTFQ 28
DB 536 AVLEFWLMDAYVELLRSPFYVTTTFQ 563
||||| ||||| ||||| ||||| ||||| |||||

RESULT 5
Q9DE32 PRELIMINARY; PRT; 1191 AA.
ID AC Q9DE32;
DT 01-WAR-2001 (TrEMBLrel. 16, Created)
DT 01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-WAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Telomerase reverse transcriptase.
GN TERT.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]_SEQUENCE FROM N.A.
RA Kuramoto M., Ishikawa F.;
RT "Telomerase reverse transcriptase of Xenopus laevis.";
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF212299; AAG43537.1; -.
DR InterPro; IPR000477; RVTse.
DR IntronPro; IPR003545; Telomerase_RT.
DR Pfam; PF00078; rvt; 2.
DR PRINTS; PR01365; TELOMERASERT.
KW RNA-directed DNA polymerase; Transferase.
SQ SEQUENCE 1191 AA; 138016 MW; 9BD9D776869A57D6 CRC64;

Query Match      77.4%; Score 113; DB 13; Length 1191;
Best Local Similarity 71.4%; Pred. No. 1.8e-08;
Matches 20; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 AKFLHLMMSVYVVLLRSFFYVTTTFQ 28
DB 597 AKFVFWMDDTYIQLLKSFYVTTTFQ 624
||||| ||||| ||||| ||||| ||||| |||||

RESULT 6
Q8MUB3 PRELIMINARY; PRT; 1032 AA.
ID AC Q8MUB3;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Telomerase reverse transcriptase.
```

```

GN      Candida albicans (Yeast).
OS      Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC      Saccharomycetales; mitosporic Saccharomycetales; Candida.
OX      NCBI_TaxID=5476;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=3153;
RT      Metz A.M., Love R.A., Strobel G.A., Long D.M.;
RL      "Two Expressed Telomerase Reverse Transcriptase Genes Identified in
RT      Candida albicans";
RL      Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR      EMBL; AF216871; AAF26732.1; -.
DR      InterPro; IPR000477; RVTse.
DR      Pfam; PF00078; rvt; 1.
KW      RNA-directed DNA polymerase; Transference.
SQ      SEQUENCE      867 AA; 100872 MW; EB67BEC54340E10F CRC64;

Query Match      43.2%; Score 63; DB 3; Length 867;
Best Local Similarity 45.8%; Pred. No. 0.5;
Matches 11; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY      3 FLHWMSSVVVVELLRSEFFVYVTE 26
DB      333 YLWMLPEHLKNILRSFWYTETS 356

RESULT 9
O9AU13 PRELIMINARY; PRT; 1259 AA.
ID      Q9AU13
AC      AC
DT      01-JUN-2001 (TEMBLrel. 17, Created)
DT      01-JUN-2001 (TEMBLrel. 17, Last sequence update)
DT      01-MAR-2003 (TEMBLrel. 23, Last annotation update)
DE      Telomerase reverse transcriptase.
OS      Oryza sativa (Rice).
OC      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC      Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC      Ehrhartoideae; Oryzaceae; Oryza.
OX      NCBI_TaxID=4530;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      Oguchi K., Tamura K., Takahashi H.;
RT      "Molecular cloning and characterization of OsTERT, a telomerase
RT      reverse transcriptase homolog in Oryza sativa.";
RL      Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR      EMBL; AF282216; AAK35007.1; -.
DR      Gramene; Q9AU13; -.
DR      InterPro; IPR001209; Ribosomal_S14.
DR      InterPro; IPR000477; RVTse.
DR      InterPro; IPR003545; Telomerase_RT.
DR      Pfam; PF00078; rvt; 2.
DR      PRINTS; PR01365; TELOMERASERT.
DR      PROSITE; PS00527; RIBOSOMAL_S14; 1.
KW      RNA-directed DNA polymerase; Transference.
SQ      SEQUENCE      1259 AA; 143710 MW; 15B041789F2D5CAD CRC64;

Query Match      41.8%; Score 61; DB 10; Length 1259;
Best Local Similarity 45.5%; Pred. No. 1.4;
Matches 10; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY      3 FLHWMSSVVVVELLRSEFFVYVTE 24
DB      695 WISWLFSDIVPVRTFYVTE 706

RESULT 10
O8LKW0 PRELIMINARY; PRT; 1261 AA.
ID      O8LKW0
AC      AC
DT      01-OCT-2002 (TEMBLrel. 22, Created)
DT      01-OCT-2002 (TEMBLrel. 22, Last sequence update)

```

```

DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Telomerase reverse transcriptase.
GN TERT.
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=cv. Nipponbare;
RX MEDLINE=22096152; PubMed=12100484;
RA Heller-Uzysnka K., Schnippenkoetter W., Kilian A.;
RT "Cloning and characterization of rice (Oryza sativa L) telomerase
reverse transcriptase, which reveals complex splicing patterns.";
RL Plant J. 31:75-86(2002).
DR EMBL; AF494453; AAW21641.1; -.
DR Gramene; Q8LKW0; -.
DR InterPro; IPR001209; Ribosomal_S14.
DR InterPro; IPR000477; RVTse.
DR InterPro; IPR003545; Telomerase_RT.
DR Pfam; PF00078; rvt; 2.
DR PRINTS; PR01365; TELOMERASERT.
DR PROSITE; PS00527; RIBOSOMAL_S14; 1.
KW RNA-directed DNA polymerase; Transferase.
SQ SEQUENCE 1261 AA; 143715 MW; 353153D1C8B7D5CB CRC64;

Query Match 41.8%; Score 61; DB 10; Length 1261;
Best Local Similarity 45.5%; Pred. No. 1.4;
Matches 10; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY 3 FLHWMMSVYVVELLRSPFYVTE 24
DB 685 WISLFSFDIVPVVTVTFYVTE 706

RESULT 11
Q9JK99 PRELIMINARY; PRT; 575 AA.
ID Q9JK99
AC Q9JK99
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Telomerase catalytic subunit (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RN SEQUENCE FROM N.A.
RA Wong S., Gao S., Xu X., Yu H.;
RT "Rat telomerase catalytic subunit, rTERT.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF247818; AAF62177.1; -.
DR InterPro; IPR000477; RVTse.
DR InterPro; IPR003545; Telomerase_RT.
DR Pfam; PF00078; rvt; 1.
DR PRINTS; PR01365; TELOMERASERT.
KW RNA-directed DNA polymerase; Transferase.
FT NON TER
SQ SEQUENCE 575 AA; 65672 MW; F80C81BD7F6A91A3 CRC64;

Query Match 39.7%; Score 58; DB 11; Length 575;
Best Local Similarity 83.3%; Pred. No. 1.9;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 17 RSFFYVTVTFQ 28
DB 1 RSFFYITESTFQ 12

RESULT 12
Q8SQ00 PRELIMINARY; PRT; 823 AA.
ID Q8SQ00
AC Q8SQ00
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Telomerase reverse transcriptase.
GN ECU09 0310.
OS Encephalitozoon cuniculi.
OC Eukaryota; Fungi; Microsporidia; Unikaryonidae; Encephalitozoon.
OX NCBI_TaxID=6035;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=GB-M1;
RX MEDLINE=21576510; PubMed=11719806;
RA Katinka M.D., Duprat S., Cornillot E., Metenier G., Thomarat P.,
RA Prensier G., Barbe V., Peyretailade E., Brottier P., Wincker P.,
RA Delbac F., El Alaoui H., Peyret P., Saurin W., Gouy M.,
RA Weissenbach J., Vivares C.P.;
RT "Genome sequence and gene compaction of the eukaryote parasite
Encephalitozoon cuniculi.";
RL Nature 414:450-453(2001).
DR EMBL; AL590451; CAD27002.1; -.
DR InterPro; IPR000477; RVTse.
DR Pfam; PF00078; rvt; 1.
DR RNA-directed DNA polymerase; Transferase.
KW RNA-directed DNA polymerase; Transferase.
SQ SEQUENCE 823 AA; 95280 MW; 8FD1BED4CCE68354 CRC64;

Query Match 37.7%; Score 55; DB 5; Length 823;
Best Local Similarity 29.6%; Pred. No. 7.7;
Matches 8; Conservative 10; Mismatches 9; Indels 0; Gaps 0;

QY 1 AKFLHWMMSVYVVELLRSPFYVTE 27
DB 326 SRFLVYITEKLIPIISKYFYCTETSF 352

RESULT 13
Q59774 PRELIMINARY; PRT; 521 AA.
ID Q59774
AC Q59774
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Aspartic protease.
GN SPC1795.09.
OS Schizosaccharomyces pombe (Fission Yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=972h-;
RA Lyne M., Rajandream M.A., Barrell B.G., Oliver K., Harris D.;
RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL022598; CAA18644.1; -.
DR GeneDB SPombe; SPC1795.09; -.
DR InterPro; IPR001461; AsproteaseA1.
DR Pfam; PF00026; asp; 1.
DR PRINTS; PR00792; PEPSIN.
KW Protease.
SQ SEQUENCE 521 AA; 57623 MW; 21F002CF829175EC CRC64;

Query Match 36.6%; Score 53.5; DB 3; Length 521;
Best Local Similarity 34.4%; Pred. No. 8.4;
Matches 11; Conservative 7; Mismatches 9; Indels 5; Gaps 1;

QY 2 KFLHWMMSVYVVELLRSPFYVTE 28

```

Db 274 KLTHYAVSIYSVQVFLNSTFFFNYSIITDAYFQ 305

RESULT 14
Q8T678
ID Q8T678 PRELIMINARY; PRT; 1475 AA.
AC Q8T678;

ID	Q8T678	PRELIMINARY;	FRT; 1475 AA.
AC	Q8T678;		

DE ABC transporter AbcG15.
CN ABCG15

OS Dictyostelium discoideum (Slime mold).

CC Eukaryota; Mycetozoa; Dictyostelida; Dictyostelium.
OX NCBI_TaxID=44689;

RN	[1]	RP	SEQUENCE FROM N.A.
1	1	1	1
2	2	2	2
3	3	3	3
4	4	4	4
5	5	5	5
6	6	6	6
7	7	7	7
8	8	8	8
9	9	9	9
10	10	10	10
11	11	11	11
12	12	12	12
13	13	13	13
14	14	14	14
15	15	15	15
16	16	16	16
17	17	17	17
18	18	18	18
19	19	19	19
20	20	20	20
21	21	21	21
22	22	22	22
23	23	23	23
24	24	24	24
25	25	25	25
26	26	26	26
27	27	27	27
28	28	28	28
29	29	29	29
30	30	30	30
31	31	31	31
32	32	32	32
33	33	33	33
34	34	34	34
35	35	35	35
36	36	36	36
37	37	37	37
38	38	38	38
39	39	39	39
40	40	40	40
41	41	41	41
42	42	42	42
43	43	43	43
44	44	44	44
45	45	45	45
46	46	46	46
47	47	47	47
48	48	48	48
49	49	49	49
50	50	50	50
51	51	51	51
52	52	52	52
53	53	53	53
54	54	54	54
55	55	55	55
56	56	56	56
57	57	57	57
58	58	58	58
59	59	59	59
60	60	60	60
61	61	61	61
62	62	62	62
63	63	63	63
64	64	64	64
65	65	65	65
66	66	66	66
67	67	67	67
68	68	68	68
69	69	69	69
70	70	70	70
71	71	71	71
72	72	72	72
73	73	73	73
74	74	74	74
75	75	75	75
76	76	76	76
77	77	77	77
78	78	78	78
79	79	79	79
80	80	80	80
81	81	81	81
82	82	82	82
83	83	83	83
84	84	84	84
85	85	85	85
86	86	86	86
87	87	87	87
88	88	88	88
89	89	89	89
90	90	90	90
91	91	91	91
92	92	92	92
93	93	93	93
94	94	94	94
95	95	95	95
96	96	96	96
97	97	97	97
98	98	98	98
99	99	99	99
100	100	100	100

RC STRAIN=AX4;
PA Anard C Locis WE .

RT "Evolution of the ABC transporters of Dictyostelium." ;

CC -!- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY.

DR EMBL; AF482393; AAL91500.1; - .
DR InterPro: IPR003593: AAA ATPase.

DR InterPro; IPR003439; ABC_transporter.
 DP Pfam: PF00005; ABC_4.
 DP

DR PD000006; ABC transporter; 2.

DR SMART; SM00382; AAA; 2.
DR PROSITE; PS00211; ABC TRANSPORTER; 1.

KW ATP-binding; Transport.
SO SEQUENCE 1475 AA: 166858 MW: 214258402BE60E0C CPC64.

Country	Year	Value	Unit
Algeria	1970	1.0	1000
Algeria	1971	1.0	1000
Algeria	1972	1.0	1000
Algeria	1973	1.0	1000
Algeria	1974	1.0	1000
Algeria	1975	1.0	1000
Algeria	1976	1.0	1000
Algeria	1977	1.0	1000
Algeria	1978	1.0	1000
Algeria	1979	1.0	1000
Algeria	1980	1.0	1000
Algeria	1981	1.0	1000
Algeria	1982	1.0	1000
Algeria	1983	1.0	1000
Algeria	1984	1.0	1000
Algeria	1985	1.0	1000
Algeria	1986	1.0	1000
Algeria	1987	1.0	1000
Algeria	1988	1.0	1000
Algeria	1989	1.0	1000
Algeria	1990	1.0	1000
Algeria	1991	1.0	1000
Algeria	1992	1.0	1000
Algeria	1993	1.0	1000
Algeria	1994	1.0	1000
Algeria	1995	1.0	1000
Algeria	1996	1.0	1000
Algeria	1997	1.0	1000
Algeria	1998	1.0	1000
Algeria	1999	1.0	1000
Algeria	2000	1.0	1000
Algeria	2001	1.0	1000
Algeria	2002	1.0	1000
Algeria	2003	1.0	1000
Algeria	2004	1.0	1000
Algeria	2005	1.0	1000
Algeria	2006	1.0	1000
Algeria	2007	1.0	1000
Algeria	2008	1.0	1000
Algeria	2009	1.0	1000
Algeria	2010	1.0	1000
Algeria	2011	1.0	1000
Algeria	2012	1.0	1000
Algeria	2013	1.0	1000
Algeria	2014	1.0	1000
Algeria	2015	1.0	1000
Algeria	2016	1.0	1000
Algeria	2017	1.0	1000
Algeria	2018	1.0	1000
Algeria	2019	1.0	1000
Algeria	2020	1.0	1000
Algeria	2021	1.0	1000
Algeria	2022	1.0	1000
Algeria	2023	1.0	1000
Algeria	2024	1.0	1000
Algeria	2025	1.0	1000
Algeria	2026	1.0	1000
Algeria	2027	1.0	1000
Algeria	2028	1.0	1000
Algeria	2029	1.0	1000
Algeria	2030	1.0	1000
Algeria	2031	1.0	1000
Algeria	2032	1.0	1000
Algeria	2033	1.0	1000
Algeria	2034	1.0	1000
Algeria	2035	1.0	1000
Algeria	2036	1.0	1000
Algeria	2037	1.0	1000
Algeria	2038	1.0	1000
Algeria	2039	1.0	1000
Algeria	2040	1.0	1000
Algeria	2041	1.0	1000
Algeria	2042	1.0	1000
Algeria	2043	1.0	1000
Algeria	2044	1.0	1000
Algeria	2045	1.0	1000
Algeria	2046	1.0	1000
Algeria	2047	1.0	1000
Algeria	2048	1.0	1000
Algeria	2049	1.0	1000
Algeria	2050	1.0	1000
Algeria	2051	1.0	1000
Algeria	2052	1.0	1000
Algeria	2053	1.0	1000
Algeria	2054	1.0	1000
Algeria	2055	1.0	1000
Algeria	2056	1.0	1000
Algeria	2057	1.0	1000
Algeria	2058	1.0	1000
Algeria	2059	1.0	1000

Accuracy: 56.0%; Score: 32.5; DB: 3; Length: 14/3;
Best Local Similarity: 46.7%; Pred. No. 32;

Matches 14; Conservative 4; Mismatches 7; Indels 5; Gaps 2;

QY 1 AKFLHWL---MSVYVVELLRSSFYVTTTF 27

Db 1248 SKFYHWLPFALSIIWEL--PFVLVSGTIF 1275

RESULT 15
Q92I18

ID	Q92I18	PRELIMINARY;	PRT;	102 AA.
AC	Q92I18:			

DT 01-DEC-2001 (TremblLrel. 19, Created)

DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)

DE Hypothetical protein RC0602.
GN RC0602.

OS Rickettsia conorii.
QC Bacteria: Proteobacteria: Alphaproteobacteria: Rickettsiales

Rickettsiaceae; Rickettsiae; Rickettsia.

```

OC NCBI_taxID=701;
RN [1]

```

RP SEQUENCE FROM N.A.
RC STRAIN=Malish 7;

RX	MEDLINE=21442074; PubMed=11557893;
RA	Ogata H, Audic S, Benestou-Audiffren D, Bourjoux P, Esposito W

Samson D., Roux V., Cossart P., Weissenbach J., Claverie J.-M.,

RT "Mechanisms of evolution in *Rickettsia conorii* and *R. prowazekii*."; RA RAOUT D.;

RL Science 293:2093-2098(2001).
DR EMBL; AE008621; AAL03140.1; -.

DR InterPro; IPR000516; Ni_hydr_CytB.
DR Pfam: PF01292. Ni_hydr_CytB_1

KW Hypothetical protein; Complete proteome.

SQ SEQUENCE 102 AA; 11898 MW; D65104E/E81886C5 CRC64;

Query Match	35.6%;	Score 52;	DB 16;	Length 102;
Best Local Similarity	50.0%;	Pred. No. 3;		

Matches	8;	Conservative	4;	Mismatches	4;	Indels	0;	Gaps	0;
---------	----	--------------	----	------------	----	--------	----	------	----

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 12, 2003, 19:41:04 ; Search time 29.8868 Seconds
(without alignments)
127.462 Million cell updates/sec

Title: US-08-854-050-112

Perfect score: 131

Sequence: 1 FFYVTEFTQKRLFFYRKSWSK 24

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_19Jun03.*
1: /SIDSI/gcgdata/geneseq/geneseq-embl/AA1980.DAT.*
2: /SIDSI/gcgdata/geneseq/geneseq-embl/AA1981.DAT.*
3: /SIDSI/gcgdata/geneseq/geneseq-embl/AA1982.DAT.*
4: /SIDSI/gcgdata/geneseq/geneseq-embl/AA1983.DAT.*
5: /SIDSI/gcgdata/geneseq/geneseq-embl/AA1984.DAT.*
6: /SIDSI/gcgdata/geneseq/geneseq-embl/AA1985.DAT.*
7: /SIDSI/gcgdata/geneseq/geneseq-embl/AA1986.DAT.*
8: /SIDSI/gcgdata/geneseq/geneseq-embl/AA1987.DAT.*
9: /SIDSI/gcgdata/geneseq/geneseq-embl/AA1988.DAT.*
10: /SIDSI/gcgdata/geneseq/geneseq-embl/AA1989.DAT.*
11: /SIDSI/gcgdata/geneseq/geneseq-embl/AA1990.DAT.*
12: /SIDSI/gcgdata/geneseq/geneseq-embl/AA1991.DAT.*
13: /SIDSI/gcgdata/geneseq/geneseq-embl/AA1992.DAT.*
14: /SIDSI/gcgdata/geneseq/geneseq-embl/AA1993.DAT.*
15: /SIDSI/gcgdata/geneseq/geneseq-embl/AA1994.DAT.*
16: /SIDSI/gcgdata/geneseq/geneseq-embl/AA1995.DAT.*
17: /SIDSI/gcgdata/geneseq/geneseq-embl/AA1996.DAT.*
18: /SIDSI/gcgdata/geneseq/geneseq-embl/AA1997.DAT.*
19: /SIDSI/gcgdata/geneseq/geneseq-embl/AA1998.DAT.*
20: /SIDSI/gcgdata/geneseq/geneseq-embl/AA1999.DAT.*
21: /SIDSI/gcgdata/geneseq/geneseq-embl/AA2000.DAT.*
22: /SIDSI/gcgdata/geneseq/geneseq-embl/AA2001.DAT.*
23: /SIDSI/gcgdata/geneseq/geneseq-embl/AA2002.DAT.*
24: /SIDSI/gcgdata/geneseq/geneseq-embl/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	131	100.0	24	19 AAW57391	Human telomerase r
2	131	100.0	24	19 AAW57387	Human telomerase r
3	131	100.0	48	21 AAY86593	Telomerase peptide
4	131	100.0	100	23 ABG71627	hTERT fragment wit
5	131	100.0	131	20 AAW97385	Amino acid sequenc
6	131	100.0	259	19 AAW46998	Human telomerase r
7	131	100.0	283	20 AAY43128	Human telomerase r
8	131	100.0	437	20 AAY25461	Human CRT-1 protei
9	131	100.0	438	20 AAY25462	Human CRT-1 protei

10	131	100.0	564	19 AAW56109	Human telomerase r
11	131	100.0	588	20 AAY00635	N-terminal truncat
12	131	100.0	588	20 AAY00644	N-terminal truncat
13	131	100.0	591	20 AAW97384	A catalytic telome
14	131	100.0	622	20 AAY25463	Human CRT-1 protei
15	131	100.0	807	19 AAW46997	Human telomerase r
16	131	100.0	807	20 AAY00637	N-terminal truncat
17	131	100.0	807	20 AAY00646	Truncated telomera
18	131	100.0	936	20 AAY00642	Truncated telomera
19	131	100.0	936	20 AAY00651	Truncated telomera
20	131	100.0	948	20 AAY00639	N-terminal truncat
21	131	100.0	948	20 AAY00648	Truncated telomera
22	131	100.0	949	19 AAW61349	Human telomerase p
23	131	100.0	1041	20 AAY00643	Altered C-terminus
24	131	100.0	1041	20 AAY00652	Altered C-terminus
25	131	100.0	1053	20 AAY00640	Altered C-terminus
26	131	100.0	1093	20 AAY00649	Altered C-terminus
27	131	100.0	1120	20 AAY00641	Telomerase protein
28	131	100.0	1120	20 AAY00650	Telomerase (ver. 2
29	131	100.0	1132	19 AAW71376	Human telomerase c
30	131	100.0	1132	19 AAW46957	Human telomerase r
31	131	100.0	1132	20 AAY43821	A human telomerase
32	131	100.0	1132	20 AAY28881	Human telomerase r
33	131	100.0	1132	20 AAY32090	Human telomerase r
34	131	100.0	1132	20 AAY28401	Human EST2 protein
35	131	100.0	1132	20 AAY26580	Human telomerase r
36	131	100.0	1132	20 AAY00627	Human telomerase p
37	131	100.0	1132	20 AAY00638	Truncated telomera
38	131	100.0	1132	20 AAY90251	Human catalytic te
39	131	100.0	1132	21 AAY96566	hEST2, a human tel
40	131	100.0	1132	22 AAB82765	Human telomerase r
41	131	100.0	1132	22 AAB82765	Human telomerase r
42	131	100.0	1132	22 AAG64329	Human protein #2.
43	131	100.0	1132	22 AAG64329	Human protein #2.
44	131	100.0	1132	22 AAG64329	Heart muscle cell
45	131	100.0	1132	23 AAE29226	Human telomerase r
	131	100.0	1132	23 AAU72735	Human telomerase r

ALIGNMENTS

RESULT 1

AAW57391
ID AAW57391 standard; peptide; 24 AA.
XX
AC AAW57391;
XX
AC AAW57391;
XX
DT 13-AUG-1998 (first entry)
XX
DE Human telomerase reverse transcriptase antigenic peptide S-1.
XX
KW Human; telomerase reverse transcriptase; hTERT; TRT; diagnosis;
KW prognosis; cell proliferation; cancer; ageing; ribonucleoprotein.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN GB2317891-A.
XX
PD 08-APR-1998.
XX
PF 01-OCT-1997; 97GB-0020890.
XX
PR 14-AUG-1997; 97US-0915503.
PR 01-OCT-1996; 96US-0724643.
PR 18-APR-1997; 97US-0844419.
PR 25-APR-1997; 97US-0846017.
PR 06-MAY-1997; 97US-0851843.
PR 09-MAY-1997; 97US-0854050.
PR 14-AUG-1997; 97US-0911312.
PR 14-AUG-1997; 97US-0912951.
XX
PA (GERO-) GERON CORP.

THIS PAGE BLANK (USPTO)

PA (UYTE-) UNIV TECHNOLOGY CORP.
 XX Andrews WH, Cech TR, Chapman KB, Harley C, Lingner J;
 PI Morin GB, Nakamura T, Harley CB;
 XX WPI; 1998-171633/16.
 XX Pure and recombinant human Telomerase Reverse Transcriptase and its
 PT variants - are useful in the diagnosis, prognosis and treatment of
 PT cell proliferation conditions especially cancer and ageing
 XX Example 8; Fig 54; 387pp; English.
 XX The present sequence represents an antigenic peptide from human
 CC telomerase reverse transcriptase (hTERT), from the present invention. The
 CC present invention also describes the following methods: (A) determining
 CC whether a test compound is a modulator of hTERT, by detecting the change
 CC in hTERT recombinant protein or polynucleotide, on administration of the
 CC compound; (B) preparation of recombinant telomerase by contacting a
 CC protein preparation of hTERT with a telomerase RNA component; (C)
 CC detection of the hTERT RNA or protein in a sample by binding a relevant
 CC probe to the sample and detecting the complex formed or in the case of
 CC RNA detection, amplifying the product and correlating the presence of
 CC complex or amplification product with presence of hTERT in the sample;
 CC and (D) increasing the proliferation of a vertebrate cell by increasing
 CC hTERT expression; and (E) the use of an agent that causes an increase in
 CC cell vertebrate cell proliferation to create a medicament that inhibits
 CC ageing. A protein preparation of hTERT and the polynucleotide encoding
 CC hTERT can be used in the manufacture of medicaments for inhibiting the
 CC effect of ageing or cancer. Inhibitors of telomerase activity can be
 CC used to treat conditions that are associated with high telomerase
 CC activity. A protein preparation of hTERT can also be used in the new
 CC methods.
 XX Sequence. 24 AA;
 SQ Query Match 100.0%; Score 131; DB 19; Length 24;
 Best Local Similarity 100.0%; Pred. NO. 6.4e-13;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 FFYVTTTFQKNRLFFYRKSWSK 24
 Db 1 FFYVTTTFQKNRLFFYRKSWSK 24
 RESULT 2
 AAW57387
 ID AAW57387 standard; peptide; 24 AA.
 XX AAW57387;
 XX 13-AUG-1998 (first entry)
 XX Human telomerase reverse transcriptase antigenic peptide.
 DE Human; telomerase reverse transcriptase; hTERT; TRT; diagnosis;
 KW prognosis; cell proliferation; cancer; ageing; ribonucleoprotein;
 KW antigenic.
 XX Synthetic.
 OS Homo sapiens.
 XX GB2317891-A.
 XX 08-APR-1998.
 XX 01-OCT-1997; 97GB-0020890.
 XX 14-AUG-1997; 97US-0915503.
 PR 01-OCT-1996; 96US-0724643.
 PR 18-APR-1997; 97US-0844419.
 PR 25-APR-1997; 97US-0846017.
 PR 06-MAY-1997; 97US-0851843.

PR 09-MAY-1997; 97US-0854050.
 PR 14-AUG-1997; 97US-0911312.
 PR 14-AUG-1997; 97US-0912951.
 XX (GERO-) GERON CORP.
 PA (UYTE-) UNIV TECHNOLOGY CORP.
 XX Andrews WH, Cech TR, Chapman KB, Harley C, Lingner J;
 PI Morin GB, Nakamura T, Harley CB;
 XX WPI; 1998-171633/16.
 XX Pure and recombinant human Telomerase Reverse Transcriptase and its
 PT variants - are useful in the diagnosis, prognosis and treatment of
 PT cell proliferation conditions especially cancer and ageing
 XX Example 8; Page 259; 387pp; English.
 XX The present sequence represents an antigenic peptide from human
 CC telomerase reverse transcriptase (hTERT), from the present invention. The
 CC present invention also describes the following methods: (A) determining
 CC whether a test compound is a modulator of hTERT, by detecting the change
 CC in hTERT recombinant protein or polynucleotide, on administration of the
 CC compound; (B) preparation of recombinant telomerase by contacting a
 CC protein preparation of hTERT with a telomerase RNA component; (C)
 CC detection of the hTERT RNA or protein in a sample by binding a relevant
 CC probe to the sample and detecting the complex formed or in the case of
 CC RNA detection, amplifying the product and correlating the presence of
 CC complex or amplification product with presence of hTERT in the sample;
 CC and (D) increasing the proliferation of a vertebrate cell by increasing
 CC hTERT expression; and (E) the use of an agent that causes an increase in
 CC cell vertebrate cell proliferation to create a medicament that inhibits
 CC ageing. A protein preparation of hTERT and the polynucleotide encoding
 CC hTERT can be used in the manufacture of medicaments for inhibiting the
 CC effect of ageing or cancer. Inhibitors of telomerase activity can be
 CC used to treat conditions that are associated with high telomerase
 CC activity. A protein preparation of hTERT can also be used in the new
 CC methods.
 XX Sequence 24 AA;
 SQ Query Match 100.0%; Score 131; DB 19; Length 24;
 Best Local Similarity 100.0%; Pred. NO. 6.4e-13;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 FFYVTTTFQKNRLFFYRKSWSK 24
 Db 1 FFYVTTTFQKNRLFFYRKSWSK 24
 RESULT 3
 AAY86593
 ID AAY86593 standard; Peptide; 48 AA.
 XX AAY86593;
 XX 05-MAY-2000 (first entry)
 XX Telomerase peptide #8.
 DE Telomerase; antigenic peptide; cancer; therapy; human; tumour cell;
 KW malignant melanoma; leukaemia; lymphoma; biliary tract carcinoma;
 KW telomerase T lymphocyte.
 XX Homo sapiens.
 OS WO200002581-A1.
 XX 20-JAN-2000.
 XX 30-JUN-1999; 99WO-NO00220.
 XX 08-JUL-1998; 98NO-0003141.

THIS PAGE BLANK (USPTO)

XX PA (NHYD) NORSK HYDRO AS.
 XX PI Gaudernack G, Eriksen JA, Moller M, Gjertsen MK, Saeterdal I;
 XX PI Saebøe-Larsen S;
 XX DR WPI; 2000-145727/13.
 XX PT Protein or peptide fragments useful in the treatment and prophylaxis of
 XX PT cancer in mammals -
 XX PS Claim 9; Page 34; 53pp; English.
 XX CC This sequence represents a telomerase peptide of the invention, and can
 CC be used in a method for the treatment or prophylaxis of cancer. The
 CC sequences are useful in the treatment or prophylaxis of cancer
 CC especially, breast, lung, ovarian, cervical, colorectal, prostate or
 CC pancreatic cancers, malignant melanoma, leukaemias, lymphomas, or biliary
 CC tract carcinomas. They are useful for generating telomerase T lymphocytes
 CC capable of recognising and destroying tumour cells in a mammal.
 CC comprising culturing T lymphocytes obtained from the mammal with the
 CC peptides. Telomerase protein is expressed only by tumour cells, hence,
 CC other body cells are not targeted or destroyed by telomerase specific T
 CC cells.
 CC Note: This sequence was indexed from WO200002581, which is the first
 CC major country equivalent to NO9803141.
 XX CC

SQ Sequence 48 AA;

Query Match 100.0%; Score 131; DB 21; Length 48;
 Best Local Similarity 100.0%; Pred. NO. 1.3e-12;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FFYVTETTFQKNRLFFYRKSWWSK 24
 |||||
 Db 14 FFYVTETTFQKNRLFFYRKSWWSK 37

RESULT 4

ID ABG71627 standard; protein; 100 AA.

AC ABG71627;

DT 09-JAN-2003 (first entry)

DE hTERT fragment with HLA containing polypeptide at its N-terminus.

XX Human; telomerase catalytic subunit; hTERT; human leukocyte antigen;
 KW human telomerase reverse transcriptase; HLA epitope; cancer;
 KW HLA profile; breast cancer; pancreatic cancer; colorectal cancer;
 KW lung cancer; ovarian cancer; cervical cancer; malignant melanoma;
 KW leukaemia; lymphoma; biliary tract carcinoma; anti-cancer; mutant;
 KW cytostatic; HLA class I epitope; HLA class II epitope; mutein.

XX Homo sapiens.

OS Synthetic.

FN WO200270679-A2.

PD 12-SEP-2002.

PF 19-FEB-2002; 2002WO-NO00069.

XX 02-MAR-2001; 2001GB-0005238.

XX (GEMV-) GEMWAX AS.

PI Eriksen JA, Gaudernack G, Moller M;

XX WPI; 2002-750459/81.

XX New polypeptide with an additional C-terminal and/or N-terminal

PT sequence, useful for preparing anti-cancer vaccines -
 XX Disclosure; Fig 1; 62pp; English.

XX The present invention relates to a polypeptide comprising a 20 amino
 CC acid sequence derived from human telomerase catalytic subunit
 CC (or human telomerase reverse transcriptase, hTERT) amino acid residues
 CC 537-556, or fragments thereof comprising at least 10 amino acids and
 CC at least two human leukocyte antigen (HLA) class I or class II
 CC epitopes. The invention also describes a polypeptide having the above
 CC 20 amino acid peptide sequence as additional C- and/or N-terminal
 CC sequences on a fragment of hTERT which is not more than 100 amino
 CC acids of hTERT. The polypeptides of the invention are useful in a
 CC pharmaceutical composition or in a vaccine for preventing or treating
 CC cancer in populations of individuals having varying HLA profiles.
 CC The polypeptides are also useful in a diagnostic kit for diagnosing
 CC cancers such as breast, pancreatic, colorectal, lung, ovarian or
 CC cervical cancer, malignant melanoma, leukaemia, lymphoma or biliary
 CC tract carcinoma. The polypeptides or encoding polynucleotide
 CC sequences are useful for performing identity, sequence homology
 CC and/or hybridisation studies, for predicting structure and/or
 CC function (e.g. anti-cancer activity), or for screening methods in
 CC drug development or drug screening procedures. The present sequence
 CC represents a hTERT fragment with the 20 amino acid HLA epitope
 CC containing polypeptide at its N-terminus.

XX Sequence 100 AA;

Query Match 100.0%; Score 131; DB 23; Length 100;
 Best Local Similarity 100.0%; Pred. NO. 2.8e-12;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FFYVTETTFQKNRLFFYRKSWWSK 24
 |||||
 Db 24 FFYVTETTFQKNRLFFYRKSWWSK 47

RESULT 5

AAW97385

ID AAW97385 standard; Protein; 131 AA.

AC AAW97385;

DT 14-MAY-1999 (first entry)

DE Amino acid sequence of the specification.

XX Catalytic telomerase; diagnosis; disease; telomerase activity.

XX Homo sapiens.

XX JP11046768-A.

XX 23-FEB-1999.

XX 01-AUG-1997; 97JP-0207708.

XX 01-AUG-1997; 97JP-0207708.

XX (MITU) MITSUBISHI CHEM CORP.

XX WPI; 1999-208111/18.

XX N-PSDB; AAX15924.

XX New catalytic protein of telomerase of a higher animal and a gene
 PT coding it - useful for diagnosis of diseases caused by the change in
 PT activity of a telomerase

XX Example 1; Page 14; 18pp; Japanese.

XX The specification describes a human catalytic telomerase protein.
 CC The products are useful in drug compositions for the diagnosis
 CC of diseases caused by the change in activity of telomerase. The

THIS PAGE BLANK (USPTO)

CC present sequence appears in the specification.

XX Sequence 131 AA;
SQ Query Match 100.0%; Score 131; DB 20; Length 131;
Best Local Similarity 100.0%; Pred. No. 3.8e-12;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FFYVTTTFOKNRLFFYRKSWSK 24
Db 19 FFYVTTTFOKNRLFFYRKSWSK 42

RESULT 6
AAW46998
ID AAW46998 standard; Protein; 259 AA.

XX AAW46998;

XX 13-AUG-1998 (first entry)

XX Human telomerase reverse transcriptase protein from cDNA clone 712562.

XX Human; telomerase reverse transcriptase; hTERT; TRT; diagnosis;

KW prognosis; cell proliferation; cancer; ageing; ribonucleoprotein.

XX Homo sapiens.

XX GB2317891-A.

XX 08-APR-1998.

XX 01-OCT-1997; 97GB-0020890.

XX 14-AUG-1997; 97US-0915503.

XX 01-OCT-1996; 96US-0724643.

XX 18-APR-1997; 97US-0844419.

XX 25-APR-1997; 97US-0846017.

XX 06-MAY-1997; 97US-0851843.

XX 09-MAY-1997; 97US-0854050.

XX 14-AUG-1997; 97US-0911312.

XX 14-AUG-1997; 97US-0912951.

XX (GERO-) GERON CORP.

PA (UVTE-) UNIV TECHNOLOGY CORP.

XX Andrews WH, Cech TR, Chapman KB, Harley C, Lingner J;

PI Morin GB, Nakamura T, Harley CB;

XX WPI; 1998-171633/16.

DR N-PSDB; AAV22379.

XX Pure and recombinant human Telomerase Reverse Transcriptase and its

PT variants - are useful in the diagnosis, prognosis and treatment of

PT cell proliferation conditions especially cancer and ageing

XX Example 1; Fig 19; 387pp; English.

XX The present sequence represents a human telomerase reverse transcriptase

CC (hTERT) protein from a cDNA clone from the present invention. The present

CC invention also describes the following methods: (A) determining whether

CC a test compound is a modulator of hTERT, by detecting the change in hTERT

CC recombinant protein or polynucleotide, on administration of the compound;

CC (B) preparation of recombinant telomerase by contacting a protein

CC hTERT can be used in the manufacture of medicaments for inhibiting the

CC effect of ageing or cancer. Inhibitors of telomerase activity can be

CC used to treat conditions that are associated with high telomerase

CC activity. A protein preparation of hTERT can also be used in the new

CC methods.

XX SQ Sequence 259 AA;

Query Match 100.0%; Score 131; DB 19; Length 259;

Best Local Similarity 100.0%; Pred. No. 7.7e-12;

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FFYVTTTFOKNRLFFYRKSWSK 24

Db 12 FFYVTTTFOKNRLFFYRKSWSK 35

RESULT 7

AAW43128

ID AAW43128 standard; Protein; 283 AA.

XX AAW43128;

XX 20-DEC-1999 (first entry)

XX Human telomerase reverse transcriptase.

XX Human telomerase reverse transcriptase; hTERT; antibody; diagnosis;

KW telomerase-related disease; cancer.

XX Homo sapiens.

XX WO9950407-A1.

XX 07-OCT-1999.

XX 26-MAR-1999; 99WO-JP01557.

XX 26-MAR-1998; 98JP-0098486.

XX (KYOW) KYOWA HAKKO KOGYO KK.

XX Hanai N, Yamasaki M, Shibata K, Furuya A, Mikuni O, Anazawa H;

XX WPI; 1999-591316/50.

XX New monoclonal antibody recognizing human telomerase catalytic subunit

PT (hTERT) useful for treating and diagnosing cancer -

XX Claim 2; Page 72-73; 78pp; Japanese.

XX This sequence represents the human telomerase reverse transcriptase

CC (hTERT). The invention relates to a monoclonal antibody recognising the

CC hTERT. The antibody can be used for the investigation, diagnosis and

CC treatment of telomerase-related diseases, especially diseases in which

CC telomerase expression is up-regulated e.g. cancers.

XX SQ Sequence 283 AA;

Query Match 100.0%; Score 131; DB 20; Length 283;

Best Local Similarity 100.0%; Pred. No. 8.5e-12;

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FFYVTTTFOKNRLFFYRKSWSK 24

Db 12 FFYVTTTFOKNRLFFYRKSWSK 35

RESULT 8

AAW25461

ID AAW25461 standard; Protein; 437 AA.

XX AAW25461;

THIS PAGE BLANK (USPTO)


```

XX DT 22-SEP-1999 (first entry)
XX DE Human CRT-1 protein #1.
XX KW CRT-1; reverse transcriptase; telomerase; inhibitor; detection;
XX KW telomerase activity; cancer cell; screening; human.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX FT Protein 1..437
XX FT /label= CRT-1
XX FT /note= "Partial sequence, no stop codon given"
XX PN WO9935261-A1.
XX PD 15-JUL-1999.
XX PF 08-JAN-1999; 99WO-JP00039.
XX PR 06-MAY-1998; 98JP-0139177.
XX PR 08-JAN-1998; 98JP-0013232.
XX PR 30-JAN-1998; 98JP-0033584.
XX PA (CHUS ) CHUGAI SEIYAKU KK.
XX PI Tsuchiya M, Yoshida K;
XX DR WPI; 1999-430393/36.
XX DR N-PSDB; AAX88243.
XX PS Novel gene, useful in detection of telomerase activity and cancer
XX PT cells as well as screening telomerase inhibitors for treatment of
XX PT cancers
XX SQ Sequence 437 AA;
XX Query Match 100.0%; Score 131; DB 20; Length 437;
XX Best Local Similarity 100.0%; Pred. No. 1.3e-11;
XX Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX DT 1 FFYVTETTFQKNRLFFYRKSVWSK 24
XX DB |||||||
XX
XX RESULT 9
XX ID AAY25462
XX AC AAY25462;
XX DT 22-SEP-1999 (first entry)
XX DE Human CRT-1 protein #2.
XX KW CRT-1; reverse transcriptase; telomerase; inhibitor; detection;
XX KW telomerase activity; cancer cell; screening; human.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX FT Protein 1..438

```

```

FT /label= CRT-1
FT /note= "Partial sequence, no stop codon given"
XX PN WO9935261-A1.
XX PD 15-JUL-1999.
XX PF 08-JAN-1999; 99WO-JP00039.
XX PR 06-MAY-1998; 98JP-0139177.
XX PR 08-JAN-1998; 98JP-0013232.
XX PR 30-JAN-1998; 98JP-0033584.
XX PA (CHUS ) CHUGAI SEIYAKU KK.
XX PI Tsuchiya M, Yoshida K;
XX DR WPI; 1999-430393/36.
XX DR N-PSDB; AAX88250.
XX PS Novel gene, useful in detection of telomerase activity and cancer
XX PT cells as well as screening telomerase inhibitors for treatment of
XX PT cancers
XX PS Example 1; Page 35-36; 44pp; Japanese.
XX CC This invention describes novel human CRT-1 genes and their encoded
XX CC proteins containing a reverse transcriptase motif, which act as
XX CC telomerase inhibitors. The gene, its encoded protein and derived
XX CC antibodies can be used to provide base sequence information, detect
XX CC telomerase activity and cancer cells, and to screen telomerase
XX CC inhibitors. The detection method is simple and effective.
XX SQ Sequence 438 AA;
XX Query Match 100.0%; Score 131; DB 20; Length 438;
XX Best Local Similarity 100.0%; Pred. No. 1.3e-11;
XX Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 FFYVTETTFQKNRLFFYRKSVWSK 24
XX DB |||||||
XX DB 50 FFYVTETTFQKNRLFFYRKSVWSK 73
XX
XX RESULT 10
XX ID AAW56109
XX AC AAW56109 standard; Protein; 564 AA.
XX DT 13-AUG-1998 (first entry)
XX DE Human telomerase reverse transcriptase 63 kDa clone 712562 protein.
XX KW Human; telomerase reverse transcriptase; hTERT; diagnosis;
XX KW prognosis; cell proliferation; cancer; ageing; ribonucleoprotein.
XX OS Synthetic.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX FT Misc-difference 102
XX FT /label= encoded by ARG
XX PN GB2317891-A.
XX PD 08-APR-1998.
XX PF 01-OCT-1997; 97GB-0020890.
XX PR 14-AUG-1997; 97US-0915503.
XX PR 01-OCT-1996; 96US-0724643.
XX PR 18-APR-1997; 97US-0844419.

```

THIS PAGE BLANK (USPTO)

PR 25-APR-1997; 97US-0846017.
 PR 06-MAY-1997; 97US-0851843.
 PR 09-MAY-1997; 97US-0854050.
 PR 14-AUG-1997; 97US-0911312.
 PR 14-AUG-1997; 97US-0912951.
 XX (GRO-) GERON CORP.
 PA (UYTE-) UNIV TECHNOLOGY CORP.
 XX Andrews WH, Cech TR, Chapman KB, Harley C, Lingner J;
 PI Morin GB, Nakamura T, Harley CB;
 XX WPI; 1998-171633/16.
 DR N-ESDB; AAV22426.
 XX Pure and recombinant human Telomerase Reverse Transcriptase and its
 PT variants - are useful in the diagnosis, prognosis and treatment of
 PT cell proliferation conditions especially cancer and ageing
 XX Example 1; Fig 68; 387pp; English.
 XX The present sequence is a human telomerase reverse transcriptase (hTERT)
 CC clone protein from the present invention. The present invention also
 CC describes the following methods: (A) determining whether a test compound
 CC is a modulator of hTERT, by detecting the change in hTERT recombinant
 CC protein or polynucleotide, on administration of the compound; (B)
 CC preparation of recombinant telomerase by contacting a protein
 CC preparation of hTERT with a telomerase RNA component; (C) detection of
 CC the hTERT RNA or protein in a sample by binding a relevant probe to the
 CC sample and detecting the complex formed or in the case of RNA detection,
 CC amplifying the product and correlating the presence of complex or
 CC amplification product with presence of hTERT in the sample; and (D)
 CC increasing the proliferation of a vertebrate cell by increasing hTERT
 CC expression; and (E) the use of an agent that causes an increase in cell
 CC vertebrate cell proliferation to create a medicament that inhibits
 CC ageing. A protein preparation of hTERT and the polynucleotide encoding
 CC hTERT can be used in the manufacture of medicaments for inhibiting the
 CC effect of ageing or cancer. Inhibitors of telomerase activity can be
 CC used to treat conditions that are associated with high telomerase
 CC activity. A protein preparation of hTERT can also be used in the new
 CC methods.
 XX SQ Sequence 564 AA;
 Query Match 100.0%; Score 131; DB 19; Length 564;
 Best Local Similarity 100.0%; Pred. No. 1.7e-11;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 FFYVTETTFQKNRLFFYRKSVWSK 24
 DB 12 FFYVTETTFQKNRLFFYRKSVWSK 35
 RESULT 11
 AAY00635
 ID AAY00635 standard; Protein; 588 AA.
 XX AC AAY00635;
 XX 26-JUL-1999 (first entry)
 DT N-terminal truncated telomerase protein sequence.
 DE Telomerase; human; cancer; diagnosis; melanoma; skin cancer; leukaemia;
 KW neuroblastoma; breast carcinoma; colon carcinoma; lymphoma; osteosarcoma;
 KW smooth muscle cell hyperplasia; stem cell proliferation; Wilm's tumour;
 KW stem cell differentiation; organ regeneration; organ differentiation.
 XX Homo sapiens.
 OS Synthetic.
 XX WO9901560-A1.
 PN 14-JAN-1999.
 PD 01-JUL-1998; 98WO-US13835.
 XX

PD 14-JAN-1999.
 XX 01-JUL-1998; 98WO-US13835.
 XX 09-SEP-1997; 97US-0058287.
 PR 01-JUL-1997; 97US-0051410.
 PR 21-JUL-1997; 97US-0053018.
 PR 21-JUL-1997; 97US-0053329.
 PR 04-AUG-1997; 97US-0054642.
 XX (CAMB-) CAMBIA BIOSYSTEMS LLC.
 PA Bowtell D, Kilian A;
 PI WPI; 1999-106060/09.
 DR N-PSDB; AAX18263.
 XX New isolated vertebrate telomerase genes - used to develop products
 PT for treating cancers or for organ regeneration, nerve cell or brain
 PT cell growth following injury or bone marrow transplantation
 XX Claim 4; Fig 11a; 134pp; English.
 XX This sequence is a truncated human telomerase of the
 CC invention. Primers that amplify the telomerase coding sequence can be
 CC used in a method for diagnosing cancer in a patient. The telomerase can
 CC be used for detection, diagnosis and drug screening. Inhibitors of
 CC telomerase activity can be used to treat cancers such as melanomas, other
 CC skin cancers, neuroblastomas, breast carcinomas, colon carcinomas,
 CC leukaemias, lymphomas, osteosarcomas or smooth muscle cell hyperplasias
 CC or skin growths. Enhancers of telomerase may be used to stimulate stem
 CC cell proliferation and differentiation (expansion of haematopoietic stem
 CC cells could be administered in the bone marrow transplant context). As
 CC well, many tissues have stem cells. Proliferation of these cells may be
 CC useful in wound healing, hair growth, treatment of disease such as Wilm's
 CC tumour, organ regeneration or differentiation after injury or diseases,
 CC nerve cell or brain cell growth following injury.
 XX SQ Sequence 588 AA;
 Query Match 100.0%; Score 131; DB 20; Length 588;
 Best Local Similarity 100.0%; Pred. No. 1.8e-11;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 FFYVTETTFQKNRLFFYRKSVWSK 24
 DB 560 FFYVTETTFQKNRLFFYRKSVWSK 583
 RESULT 12
 AAY00644
 ID AAY00644 standard; Protein; 588 AA.
 XX AC AAY00644;
 XX 26-JUL-1999 (first entry)
 DT N-terminal truncated telomerase (ver. 2) protein sequence.
 DE Telomerase; human; cancer; diagnosis; melanoma; skin cancer; leukaemia;
 KW neuroblastoma; breast carcinoma; colon carcinoma; lymphoma; osteosarcoma;
 KW smooth muscle cell hyperplasia; stem cell proliferation; Wilm's tumour;
 KW stem cell differentiation; organ regeneration; organ differentiation.
 XX Homo sapiens.
 OS Synthetic.
 XX WO9901560-A1.
 PN 14-JAN-1999.
 PD 01-JUL-1998; 98WO-US13835.
 XX

THIS PAGE BLANK (USPTO)

PR 09-SEP-1997; 97US-0058287.
 PR 01-JUL-1997; 97US-0051410.
 PR 21-JUL-1997; 97US-0053018.
 PR 21-JUL-1997; 97US-0053329.
 PR 04-AUG-1997; 97US-0054642.
 XX (CAMB-) CAMBIA BIOSYSTEMS LLC.
 PA Bowtell D, Killian A;
 XX WPI; 1999-106060/09.
 DR N-PSDB; AAX18272.
 XX New isolated vertebrate telomerase genes - used to develop products
 PT for treating cancers or for organ regeneration, nerve cell or brain
 PT cell growth following injury or bone marrow transplantation
 XX Claim 4; Fig.11t-u; 134pp; English.
 XX This sequence is a truncated human telomerase of the
 CC invention. Primers that amplify the telomerase coding sequence can be
 CC used in a method for diagnosing cancer in a patient. The telomerase can
 CC be used for detection, diagnosis and drug screening. Inhibitors of
 CC telomerase activity can be used to treat cancers such as melanomas,
 CC other skin cancers, neuroblastomas, breast carcinomas, colon carcinomas,
 CC leukaemias, lymphomas, osteosarcomas or smooth muscle cell hyperplasias
 CC or skin growths. Enhancers of telomerase may be used to stimulate stem
 CC cell proliferation and differentiation (expansion of haematopoietic stem
 CC cells could be administered in the bone marrow transplant context). As
 CC well, many tissues have stem cells. Proliferation of these cells may be
 CC useful in wound healing, hair growth, treatment of disease such as
 CC wilm's tumour, organ regeneration or differentiation after injury or
 CC diseases, nerve cell or brain cell growth following injury.
 CC Note: The N-terminus of this sequence can be replaced by the sequences
 CC shown in AAY00656-Y00658.
 XX Query Match 100.0%; Score 131; DB 20; Length 588;
 XX Best Local Similarity 100.0%; Pred. No. 1.8e-11;
 XX Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 FFYVTETTFQKNRLFFYRKSVWSK 24
 DB 560 FFYVTETTFQKNRLFFYRKSVWSK 583
 RESULT 13
 AAW97384
 ID AAW97384 standard; Protein; 591 AA.
 XX AC AAW97384;
 XX 14-MAY-1999 (first entry)
 DT A catalytic telomerase protein.
 DE Catalytic telomerase; diagnosis; disease; telomerase activity.
 KW Homo sapiens.
 XX JP11046768-A.
 XX 23-FEB-1999.
 XX 01-AUG-1997; 97JP-0207708.
 XX 01-AUG-1997; 97JP-0207708.
 XX (MITU) MITSUBISHI CHEM CORP.
 PA WPI; 1999-208111/18.
 XX N-PSDB; AAX15923.
 DR

XX New catalytic protein of telomerase of a higher animal and a gene
 PT coding it - useful for diagnosis of diseases caused by the change in
 PT activity of a telomerase
 XX Claim 1; Page 11-14; 18pp; Japanese.
 XX The present sequence represents a catalytic telomerase protein.
 CC The products are useful in drug compositions for the diagnosis
 CC of diseases caused by the change in activity of telomerase.
 XX Sequence 591 AA;
 SQ Query Match 100.0%; Score 131; DB 20; Length 591;
 Best Local Similarity 100.0%; Pred. No. 1.8e-11;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 FFYVTETTFQKNRLFFYRKSVWSK 24
 DB 19 FFYVTETTFQKNRLFFYRKSVWSK 42
 RESULT 14
 AAY25463
 ID AAY25463 standard; Protein; 622 AA.
 XX AC AAY25463;
 XX 22-SEP-1999 (first entry)
 DT Human CRT-1 protein #3.
 DE CRT-1; reverse transcriptase; telomerase; inhibitor; detection;
 KW telomerase activity; cancer cell; screening; human.
 XX Homo sapiens.
 OS Key Location/Qualifiers
 FH Protein 1..622
 FT /label= CRT-1
 FT /note= "Partial sequence, no stop codon given"
 XX WO9935261-A1.
 XX 15-JUL-1999.
 XX 08-JAN-1999; 99WO-JP00039.
 XX 06-MAY-1998; 98JP-0139177.
 XX 08-JAN-1998; 98JP-0013232.
 XX 30-JAN-1998; 98JP-0033594.
 XX (CHUS) CHUGAI SEIYAKU KK.
 XX Tsuchiya M, Yoshida K;
 XX WPI; 1999-430393/36.
 XX N-PSDB; AAX88251.
 XX Novel gene, useful in detection of telomerase activity and cancer
 PT cells as well as screening telomerase inhibitors for treatment of
 PT cancers
 XX Example 1; Page 37-39; 44pp; Japanese.
 XX This invention describes novel human CRT-1 genes and their encoded
 CC proteins containing a reverse transcriptase motif, which act as
 CC telomerase inhibitors. The gene, its encoded protein and derived
 CC antibodies can be used to provide base sequence information, detect
 CC telomerase activity and cancer cells, and to screen telomerase
 CC inhibitors. The detection method is simple and effective.
 XX Sequence 622 AA;
 SQ

THIS PAGE BLANK (USPTO)

Query Match 100.0%; Score 131; DB 20; Length 622;
Best Local Similarity 100.0%; Pred. No. 1.9e-11;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 FFYVTETTFQKNRLFFYRKSWSK 24
Db 50 FFYVTETTFQKNRLFFYRKSWSK 73

RESULT 15
AAW46997
ID AAW46997 standard; Protein; 807 AA.
XX AC AAW46997;
XX DT 13-AUG-1998 (first entry)
XX DE Human telomerase reverse transcriptase Delta182 variant.
XX KW Human; telomerase reverse transcriptase; hTERT; TRT; diagnosis;
XX KW prognosis; cell proliferation; cancer; ageing; ribonucleoprotein.
XX OS Synthetic.
XX OS Homo sapiens.
XX PN GB2317891-A.
XX PD 08-APR-1998.
XX PF 01-OCT-1997; 97GB-0020890.
XX PR 14-AUG-1997; 97US-0915503.
XX PR 01-OCT-1996; 96US-0724643.
XX PR 18-APR-1997; 97US-0844419.
XX PR 25-APR-1997; 97US-0846017.
XX PR 06-MAY-1997; 97US-0851843.
XX PR 09-MAY-1997; 97US-0854050.
XX PR 14-AUG-1997; 97US-0911312.
XX PR 14-AUG-1997; 97US-0912951.

XX PA (GERO-) GERON CORP.
XX PA (UYTE-) UNIV TECHNOLOGY CORP.
XX PI Andrews WH, Cech TR, Chapman KB, Harley C, Lingner J;
XX PI Morin GB, Nakamura T, Harley CB;
XX DR WPI; 1998-171633/16.
XX DR N-PSDB; AAV22382.
XX PT Pure and recombinant human Telomerase Reverse Transcriptase and its
XX PT variants - are useful in the diagnosis, prognosis and treatment of
XX PT cell proliferation conditions especially cancer and ageing
XX PS Disclosure; Fig 20; 387pp; English.

XX The present sequence represents a human telomerase reverse transcriptase
XX (hTERT) variant from the present invention. The present invention also
XX describes the following methods: (A) determining whether a test compound
XX is a modulator of hTERT, by detecting the change in hTERT recombinant
XX protein or polynucleotide, on administration of the compound; (B)
XX preparation of recombinant telomerase by contacting a protein
XX preparation of hTERT with a telomerase RNA component; (C) detection of
XX the hTERT RNA or protein in a sample by binding a relevant probe to the
XX sample and detecting the complex formed or in the case of RNA detection,
XX amplifying the product and correlating the presence of complex or
XX amplification product with presence of hTERT in the sample; and (D)
XX increasing the proliferation of a vertebrate cell by increasing hTERT
XX expression; and (E) the use of an agent that causes an increase in cell
XX vertebrate cell proliferation to create a medicament that inhibits
XX ageing. A protein preparation of hTERT and the polynucleotide encoding
XX hTERT can be used in the manufacture of medicaments for inhibiting the
XX effect of ageing or cancer. Inhibitors of telomerase activity can be

CC used to treat conditions that are associated with high telomerase
CC activity. A protein preparation of hTERT can also be used in the new
CC methods.
XX Sequence 807 AA;
SQ Query Match 100.0%; Score 131; DB 19; Length 807;
Best Local Similarity 100.0%; Pred. No. 2.5e-11;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 FFYVTETTFQKNRLFFYRKSWSK 24
Db 560 FFYVTETTFQKNRLFFYRKSWSK 583

Search completed: November 12, 2003, 19:47:13
Job time : 29.8868 secs

THIS PAGE BLANK (USPTO)

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 12, 2003, 19:43:50 ; Search time 11.1698 Seconds
(without alignments)
90.911 Million cell updates/sec

Title: US-08-854-050-112

Perfect score: 131

Sequence: 1 FFYVTTTFQKNRLFYRKSWSK 24

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA.*

1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*

2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*

3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*

4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*

5: /cgn2_6/ptodata/1/iaa/PTUS_COMB.pep.*

6: /cgn2_6/ptodata/1/iaa/backfiles.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	131	100.0	24	3	US-08-851-843A-112
2	131	100.0	24	3	US-08-974-549A-232
3	131	100.0	24	3	US-08-854-050-112
4	131	100.0	24	4	US-09-430-323-112
5	131	100.0	24	4	US-08-912-951-113
6	131	100.0	43	3	US-08-974-549A-72
7	131	100.0	43	4	US-08-912-951-72
8	131	100.0	48	3	US-08-974-549A-30
9	131	100.0	48	4	US-08-912-951-30
10	131	100.0	129	3	US-08-851-843A-67
11	131	100.0	129	3	US-08-974-549A-13
12	131	100.0	129	3	US-08-854-050-67
13	131	100.0	129	3	US-09-430-323-67
14	131	100.0	129	4	US-08-912-951-13
15	131	100.0	259	3	US-08-974-549A-10
16	131	100.0	259	4	US-08-912-951-10
17	131	100.0	564	3	US-08-851-843A-101
18	131	100.0	564	3	US-08-974-549A-267
19	131	100.0	564	3	US-08-854-050-101
20	131	100.0	564	4	US-09-430-323-101
21	131	100.0	807	3	US-08-974-549A-5
22	131	100.0	807	4	US-08-912-951-5
23	131	100.0	1003	3	US-08-851-843A-217
24	131	100.0	1003	3	US-08-974-549A-336
25	131	100.0	1003	3	US-08-854-050-217
26	131	100.0	1003	4	US-09-430-323-217
27	131	100.0	1132	3	US-08-851-843A-225

Sequence 2, Appli
Sequence 225, App
Sequence 225, App
Sequence 2, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 611, App
Sequence 323, App
Sequence 613, App
Sequence 325, App
Sequence 324, App
Sequence 600, App
Sequence 314, App
Sequence 604, App
Sequence 318, App
Sequence 603, App

28 131 100.0 1132 3 US-08-974-549A-2
29 131 100.0 1132 3 US-08-854-050-225
30 131 100.0 1132 4 US-09-430-323-225
31 131 100.0 1132 4 US-09-128-354-2
32 131 100.0 1132 4 US-09-675-321-2
33 131 100.0 1132 4 US-09-052-919-2
34 131 100.0 1132 4 US-08-912-951-2
35 131 100.0 1154 3 US-08-974-549A-611
36 131 100.0 1154 4 US-08-912-951-323
37 131 100.0 1189 3 US-08-974-549A-613
38 131 100.0 1189 4 US-08-912-951-325
39 131 100.0 1200 3 US-08-974-549A-612
40 131 100.0 1200 4 US-08-912-951-324
41 131 100.0 1285 3 US-08-974-549A-600
42 131 100.0 1285 4 US-08-912-951-314
43 125 95.4 515 3 US-08-974-549A-604
44 125 95.4 515 4 US-08-912-951-318
45 125 95.4 530 3 US-08-974-549A-603

ALIGNMENTS

RESULT 1
US-08-851-843A-112
; Sequence 112, Application US/08851843A
; Patent No. 6093809
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Hartley, Calvin
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: No. 6093809el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/851,843A
; FILING DATE: 06-MAY-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002930US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 112:

THIS PAGE BLANK (USPTO)

SEQUENCE CHARACTERISTICS:
LENGTH: 24 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-851-843A-112

Query Match 100.0%; Score 131; DB 3; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.3e-14;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FFYVTETTFQKNRLFFYRKSVWSK 24
Db 1 FFYVTETTFQKNRLFFYRKSVWSK 24

RESULT 2

US-08-974-549A-232
Sequence 232, Application US/08974549A
Patent No. 6166178

GENERAL INFORMATION:

APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin B.
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,549A
FILING DATE: 19-NOV-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17618

FILING DATE: 01-OCT-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-00261005
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 232:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-974-549A-232

Query Match 100.0%; Score 131; DB 3; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.3e-14;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FFYVTETTFQKNRLFFYRKSVWSK 24
Db 1 FFYVTETTFQKNRLFFYRKSVWSK 24

RESULT 3

US-08-854-050-112
Sequence 112, Application US/08854050
Patent No. 6261836

GENERAL INFORMATION:

APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin
APPLICANT: Andrews, William H.
TITLE OF INVENTION: NO. 6261836el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/854,050
FILING DATE: 09-MAY-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643

THIS PAGE BLANK (USPTO)

;
; FILING DATE: 01-OCT-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002930US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 112:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-854-050-112

Query Match 100.0%; Score 131; DB 3; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.3e-14;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FFYVTTTFQKNRLFYRKSWSK 24
Db 1 FFYVTTTFQKNRLFYRKSWSK 24

RESULT 4

US-09-430-323-112
; Sequence 112, Application US/09430323
; Patent No. 6309867

GENERAL INFORMATION:

APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin
APPLICANT: Andrews, William H.
TITLE OF INVENTION: No. 6309867el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/430,323
FILING DATE: 29-Oct-1999
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996

ATTORNEY/AGENT INFORMATION:

NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 112:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 112:
US-09-430-323-112

Query Match 100.0%; Score 131; DB 4; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.3e-14;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FFYVTTTFQKNRLFYRKSWSK 24
Db 1 FFYVTTTFQKNRLFYRKSWSK 24

RESULT 5

US-08-912-951-113
; Sequence 113, Application US/08912951
; Patent No. 6475789

GENERAL INFORMATION:

APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin
APPLICANT: Andrews, William H.
TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND THERAPEUTIC METHODS
NUMBER OF SEQUENCES: 335
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/912,951
FILING DATE: 14-AUG-1997
CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
CLASSIFICATION: 435
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
CLASSIFICATION: 435
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
CLASSIFICATION: 435
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION: 435
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

THIS PAGE BLANK (USPTO)

THIS PAGE BLANK (USPTO)

THIS PAGE BLANK (USPTO)

```

; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND
; TITLE OF INVENTION: THERAPEUTIC METHODS
; NUMBER OF SEQUENCES: 335
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/912,951
; FILING DATE: 14-AUG-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002600US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 48 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..48
; OTHER INFORMATION: /note= "motif T peptide from human TRT"
; US-08-912-951-30

```

```

Query Match 100.0%; Score 131; DB 4; Length 48;
Best Local Similarity 100.0%; Pred. No. 2.7e-14;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 1 FFYVTTTFOKNRLFFYRKSWSK 24
| | | | | | | | | | | | | | | | | |
Db 14 FFYVTTTFOKNRLFFYRKSWSK 37
| | | | | | | | | | | | | | | | | |

```

RESULT 10

```

US-08-851-843A-67
; Sequence 67, Application US/08851843A
; Patent No. 6093809
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: No. 6093809el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/851,843A
; FILING DATE: 06-MAY-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002930US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 67:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 129 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..129
; OTHER INFORMATION: /note= "TRT motifs from human"
; US-08-851-843A-67

```

```

Query Match 100.0%; Score 131; DB 3; Length 129;
Best Local Similarity 100.0%; Pred. No. 7.8e-14;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 1 FFYVTTTFOKNRLFFYRKSWSK 24
| | | | | | | | | | | | | | | | | |
Db 19 FFYVTTTFOKNRLFFYRKSWSK 42
| | | | | | | | | | | | | | | | | |

```

```

RESULT 11
US-08-974-549A-13
; Sequence 13, Application US/08974549A

```

THIS PAGE BLANK (USPTO)

THIS PAGE BLANK (USPTO)

```
;
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..129
; OTHER INFORMATION: /note= "TRT motifs from human"
US-08-854-050-67

Query Match      100.0%; Score 131; DB 3; Length 129;
Best Local Similarity 100.0%; Pred. NO. 7.8e-14;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 FFYVTETTFQKNRLFFYRKSVWSK 24
    |||||
Db 19 FFYVTETTFQKNRLFFYRKSVWSK 42
    |||||

RESULT 13
US-09-430-323-67
; Sequence 67, Application US/09430323
; Patent No. 6309867
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: No. 6309867el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/430,323
; FILING DATE: 29-Oct-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002930US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 67:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 129 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..129

;
; OTHER INFORMATION: /note= "TRT motifs from human"
; SEQUENCE DESCRIPTION: SEQ ID NO: 67:
US-09-430-323-67

Query Match      100.0%; Score 131; DB 4; Length 129;
Best Local Similarity 100.0%; Pred. NO. 7.8e-14;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 FFYVTETTFQKNRLFFYRKSVWSK 24
    |||||
Db 19 FFYVTETTFQKNRLFFYRKSVWSK 42
    |||||

RESULT 14
US-08-912-951-13
; Sequence 13, Application US/08912951
; Patent No. 6475789
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND
; NUMBER OF SEQUENCES: 335
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/912,951
; FILING DATE: 14-AUG-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002600US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
```

THIS PAGE BLANK (USPTO)

LENGTH: 129 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:

NAME/KEY: Peptide

LOCATION: 1..129

OTHER INFORMATION: /note= "TRT motifs from human"

US-08-912-951-13

Query Match 100.0%; Score 131; DB 4; Length 129;

Best Local Similarity 100.0%; Pred. No. 7.8e-14;

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 FFYVTETTFQKNRLFFYRKSWSK 24

Db 19 FFYVTETTFQKNRLFFYRKSWSK 42

RESULT 15

US-08-974-549A-10

; Sequence 10, Application US/08974549A

; Patent No. 6166178

; GENERAL INFORMATION:

; APPLICANT: Cech, Thomas R.

; APPLICANT: Lingner, Joachim

; APPLICANT: Nakamura, Toru

; APPLICANT: Chapman, Karen B.

; APPLICANT: Morin, Gregg B.

; APPLICANT: Harley, Calvin B.

; APPLICANT: Andrews, William H.

; TITLE OF INVENTION: Human Telomerase Catalytic Subunit

; NUMBER OF SEQUENCES: 727

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend and Crew LLP

; STREET: Two Embarcadero Center, Eighth Floor

; CITY: San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94111-3834

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/974,549A

; FILING DATE: 19-NOV-1997

; CLASSIFICATION: 536

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/724,643

; FILING DATE: 01-OCT-1996

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/844,419

; FILING DATE: 18-APR-1997

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/846,017

; FILING DATE: 25-APR-1997

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/851,843

; FILING DATE: 06-MAY-1997

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/854,050

; FILING DATE: 09-MAY-1997

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/911,312

; FILING DATE: 14-AUG-1997

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/912,951

; FILING DATE: 14-AUG-1997

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/915,503

; FILING DATE: 14-AUG-1997

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: WO PCT/US97/17618

; FILING DATE: 01-OCT-1997

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: WO PCT/US97/17885

; FILING DATE: 01-OCT-1997

; ATTORNEY/AGENT INFORMATION:

; NAME: Apple, Randolph Ted

; REGISTRATION NUMBER: 36,429

; REFERENCE/DOCKET NUMBER: 015389-002610US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 576-0200

; TELEFAX: (415) 576-0300

; INFORMATION FOR SEQ ID NO: 10:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 259 amino acids

; TYPE: amino acid

; STRANDEDNESS:

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; FEATURE:

; NAME/KEY: Protein

; LOCATION: 1..259

; OTHER INFORMATION: /note= "protein encoded by clone 712562"

; US-08-974-549A-10

Query Match 100.0%; Score 131; DB 3; Length 259;

Best Local Similarity 100.0%; Pred. No. 1.7e-13;

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 FFYVTETTFQKNRLFFYRKSWSK 24

Db 12 FFYVTETTFQKNRLFFYRKSWSK 35

Search completed: November 12, 2003, 19:53:26

Job time : 11.1698 secs

FILED 1967 (100-100000))

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 12, 2003, 19:47:20 ; Search time 19.1698 Seconds
(without alignments)
215.025 Million cell updates/sec

Title: US-08-854-050-112

Perfect score: 131

Sequence: 1 FFYVTTTFQKNLFFYRKSWSK 24

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 644079 seqs, 171749292 residues

Total number of hits satisfying chosen parameters: 644079

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	131	100.0	24	10	US-09-843-676-112 Sequence 112, App
2	131	100.0	24	10	US-09-766-253-112 Sequence 112, App
3	131	100.0	24	11	US-09-438-486-112 Sequence 112, App
4	131	100.0	24	15	US-10-053-758-112 Sequence 112, App
5	131	100.0	24	15	US-10-054-295-112 Sequence 112, App
6	131	100.0	24	15	US-10-054-611-112 Sequence 112, App
7	131	100.0	24	15	US-10-044-692-113 Sequence 113, App
8	131	100.0	24	15	US-10-044-539-113 Sequence 113, App
9	131	100.0	43	15	US-10-044-692-72 Sequence 72, Appl
10	131	100.0	43	15	US-10-044-539-72 Sequence 72, Appl
11	131	100.0	48	15	US-10-044-592-30 Sequence 30, Appl
12	131	100.0	48	15	US-10-044-539-30 Sequence 30, Appl
13	131	100.0	129	10	US-09-843-676-67 Sequence 67, Appl
14	131	100.0	129	10	US-09-766-253-67 Sequence 67, Appl
15	131	100.0	129	11	US-09-438-486-67 Sequence 67, Appl

16 131 100.0 129 15 US-10-053-758-67 Sequence 67, Appl
17 131 100.0 129 15 US-10-054-295-67 Sequence 67, Appl
18 131 100.0 129 15 US-10-054-611-67 Sequence 67, Appl
19 131 100.0 129 15 US-10-044-692-13 Sequence 13, Appl
20 131 100.0 129 15 US-10-044-539-13 Sequence 13, Appl
21 131 100.0 259 15 US-10-044-692-10 Sequence 10, Appl
22 131 100.0 259 15 US-10-044-539-10 Sequence 10, Appl
23 131 100.0 291 12 US-10-282-960-3 Sequence 3, Appl
24 131 100.0 437 15 US-10-294-778-2 Sequence 2, Appl
25 131 100.0 438 15 US-10-294-778-10 Sequence 10, Appl
26 131 100.0 500 12 US-10-282-960-81 Sequence 81, Appl
27 131 100.0 564 10 US-09-843-676-101 Sequence 101, App
28 131 100.0 564 10 US-09-766-253-101 Sequence 101, App
29 131 100.0 564 11 US-09-438-486-101 Sequence 101, App
30 131 100.0 564 15 US-10-053-758-101 Sequence 101, App
31 131 100.0 564 15 US-10-054-295-101 Sequence 101, App
32 131 100.0 564 15 US-10-054-611-101 Sequence 101, App
33 131 100.0 622 15 US-10-294-778-12 Sequence 12, Appl
34 131 100.0 807 15 US-10-044-692-5 Sequence 5, Appl
35 131 100.0 807 15 US-10-044-539-5 Sequence 5, Appl
36 131 100.0 1003 10 US-09-843-676-217 Sequence 217, App
37 131 100.0 1003 11 US-09-438-486-217 Sequence 217, App
38 131 100.0 1003 15 US-10-053-758-217 Sequence 217, App
39 131 100.0 1003 15 US-10-054-295-217 Sequence 217, App
40 131 100.0 1003 15 US-10-054-611-217 Sequence 217, App
41 131 100.0 1132 10 US-09-990-080-2 Sequence 2, Appl
42 131 100.0 1132 10 US-09-749-728B-31 Sequence 31, Appl
43 131 100.0 1132 10 US-09-843-676-225 Sequence 225, App
44 131 100.0 1132 10 US-09-953-052-2 Sequence 2, Appl
45 131 100.0 1132 12 US-10-295-681-57 Sequence 57, Appl

ALIGNMENTS

RESULT 1

US-09-843-676-112
; Sequence 112, Application US/09843676
; Patent No. US20020164786A1
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: NO. US20020164786A1el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/843,676
FILING DATE: 26-Apr-2001
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643

THIS PAGE BLANK (USPTO)

```
;
; FILING DATE: 01-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002930US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 112:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; MOLECULE TYPE: peptide
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 112:
US-09-843-676-112

Query Match 100.0%; Score 131; DB 10; Length 24;
Best Local Similarity 100.0%; Pred. No. 2.1e-13;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FFYVTTTFQKNRLFFYRKSWSK 24
DB 1 FFYVTTTFQKNRLFFYRKSWSK 24

RESULT 2
US-09-766-253-112
; Sequence 112, Application US/09766253
; Publication No. US20020187471A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; LINGNER, JOACHIM
; NAKAMURA, TORU
; CHAPMAN, KAREN B.
; MORIN, GREGG B.
; HARLEY, CALVIN
; ANDREWS, WILLIAM H.
; TITLE OF INVENTION: NO. US20020187471A1 Telomerase
; NUMBER OF SEQUENCES: 171
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/09/766,253
; FILING DATE: 19-Jan-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/846,017
; FILING DATE: 1997-04-25
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002920US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 112:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 amino acids
; TYPE: amino acid
; STRANDEDNESS:
```

```
;
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 112:
US-09-766-253-112

Query Match 100.0%; Score 131; DB 10; Length 24;
Best Local Similarity 100.0%; Pred. No. 2.1e-13;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FFYVTTTFQKNRLFFYRKSWSK 24
DB 1 FFYVTTTFQKNRLFFYRKSWSK 24

RESULT 3
US-09-438-486-112
; Sequence 112, Application US/09438486
; Publication No. US20030009019A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; LINGNER, JOACHIM
; NAKAMURA, TORU
; CHAPMAN, KAREN B.
; MORIN, GREGG B.
; HARLEY, CALVIN
; ANDREWS, WILLIAM H.
; TITLE OF INVENTION: NO. US20030009019A1 Telomerase
; NUMBER OF SEQUENCES: 223
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/09/438,486
; FILING DATE: 12-NOV-1999
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002931US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 112:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 amino acids
; TYPE: amino acid
; STRANDEDNESS:
```

THIS PAGE BLANK (USPTO)

TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-438-486-112

Query Match 100.0%; Score 131; DB 11; Length 24;
Best Local Similarity 100.0%; Pred. No. 2.1e-13;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FFYVTETTFQKNRLFFYRKSWSK 24
Db 1 FFYVTETTFQKNRLFFYRKSWSK 24

RESULT 4

US-10-053-758-112
Sequence 112, Application US/10053758
Publication No. US20030032075A1
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morlin, Gregg B.
Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: NO. US20030032075A1el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/053,758
FILING DATE: 18-Jan-2002
CLASSIFICATION: 536

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US

TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 112:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear

MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 112:
US-10-053-758-112

Query Match 100.0%; Score 131; DB 15; Length 24;
Best Local Similarity 100.0%; Pred. No. 2.1e-13;

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 FFYVTETTFQKNRLFFYRKSWSK 24
Db 1 FFYVTETTFQKNRLFFYRKSWSK 24

RESULT 5

US-10-054-295-112
Sequence 112, Application US/10054295
Publication No. US2003004953A1
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morlin, Gregg B.
Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: NO. US2003004953A1el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/054,295
FILING DATE: 18-Jan-2002
CLASSIFICATION: 536

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/854,050
FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996

ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 112:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 112:
US-10-054-295-112

Query Match 100.0%; Score 131; DB 15; Length 24;
Best Local Similarity 100.0%; Pred. No. 2.1e-13;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FFYVTETTFQKNRLFFYRKSWSK 24
Db 1 FFYVTETTFQKNRLFFYRKSWSK 24

RESULT 6

THIS PAGE BLANK (USPTO)

US-10-054-611-112
; Sequence 112, Application US/10054611
; Publication No. US20030059787A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin
; Andrews, William H.
; TITLE OF INVENTION: No. US20030059787A1el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/054,611
; FILING DATE: 18-Jan-2002
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/854,050
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002930US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 112:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 112:
US-10-054-611-112
Query Match 100.0%; Score 131; DB 15; Length 24;
Best Local Similarity 100.0%; Pred. No. 2.le-13;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 FFYVTTTFQKNRLFYRKSVWSK 24
Db 1 FFYVTTTFQKNRLFYRKSVWSK 24
RESULT 7
US-10-044-692-113
; Sequence 113, Application US/10044692
; Publication No. US20030096344A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin
; Andrews, William H.
; TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND
; THERAPEUTIC METHODS
; NUMBER OF SEQUENCES: 335
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/044,692
; FILING DATE: 11-Jan-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/912,951
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002600US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 113:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 113:
US-10-044-692-113
Query Match 100.0%; Score 131; DB 15; Length 24;
Best Local Similarity 100.0%; Pred. No. 2.le-13;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 FFYVTTTFQKNRLFYRKSVWSK 24
Db 1 FFYVTTTFQKNRLFYRKSVWSK 24
RESULT 8
US-10-044-539-113
; Sequence 113, Application US/10044539
; Publication No. US20030100093A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin
; Andrews, William H.

THIS PAGE BLANK (USPTO)

;; TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND
;; THERAPEUTIC METHODS
;;
;; NUMBER OF SEQUENCES: 335
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Townsend and Townsend and Crew LLP
;; STREET: Two Embarcadero Center, 8th Floor
;; CITY: San Francisco
;; STATE: California
;; COUNTRY: United States of America
;; ZIP: 94111
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/10/044,539
;; FILING DATE: 11-Jan-2002
;; CLASSIFICATION: 435
;;
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/912,951
;; FILING DATE: <Unknown>
;; FILING DATE: 09-MAY-1997
;; APPLICATION NUMBER: US 08/854,050
;; FILING DATE: 06-MAY-1997
;; APPLICATION NUMBER: US 08/851,843
;; FILING DATE: 25-APR-1997
;; APPLICATION NUMBER: US 08/846,017
;; FILING DATE: 18-APR-1997
;; APPLICATION NUMBER: US 08/844,419
;; FILING DATE: 01-OCT-1996
;;
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Apple, Randolph T.
;; REGISTRATION NUMBER: 36,429
;; REFERENCE/DOCKET NUMBER: 015389-002600US
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (415) 576-0200
;; TELEFAX: (415) 576-0300
;;
;; INFORMATION FOR SEQ ID NO: 113:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 24 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: <Unknown>
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; SEQUENCE DESCRIPTION: SEQ ID NO: 113:
US-10-044-539-113
Query Match 100.0%; Score 131; DB 15; Length 24;
Best Local Similarity 100.0%; Pred. No. 2,1e-13;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FFYVTTTFQKNRLFFYRKSVWSK 24
DB 1 FFYVTTTFQKNRLFFYRKSVWSK 24
RESULT 9
US-10-044-692-72
; Sequence 72, Application US/10044692
; Publication No. US20030096344A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin
; Andrews, William H.
; TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND
; THERAPEUTIC METHODS
; NUMBER OF SEQUENCES: 335

;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Townsend and Townsend and Crew LLP
;; STREET: Two Embarcadero Center, 8th Floor
;; CITY: San Francisco
;; STATE: California
;; COUNTRY: United States of America
;; ZIP: 94111
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/10/044,692
;; FILING DATE: 11-Jan-2002
;; CLASSIFICATION: <Unknown>
;;
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/912,951
;; FILING DATE: <Unknown>
;; FILING DATE: 09-MAY-1997
;; APPLICATION NUMBER: US 08/854,050
;; FILING DATE: 06-MAY-1997
;; APPLICATION NUMBER: US 08/851,843
;; FILING DATE: 25-APR-1997
;; APPLICATION NUMBER: US 08/846,017
;; FILING DATE: 18-APR-1997
;; APPLICATION NUMBER: US 08/844,419
;; FILING DATE: 01-OCT-1996
;;
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Apple, Randolph T.
;; REGISTRATION NUMBER: 36,429
;; REFERENCE/DOCKET NUMBER: 015389-002600US
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (415) 576-0200
;; TELEFAX: (415) 576-0300
;;
;; INFORMATION FOR SEQ ID NO: 72:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 43 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: <Unknown>
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; FEATURE:
;; NAME/KEY: Peptide
;; LOCATION: 1..43
;; OTHER INFORMATION: /note= "telomerase specific motif T
;; peptide from human TRT"
;; SEQUENCE DESCRIPTION: SEQ ID NO: 72:
US-10-044-692-72
Query Match 100.0%; Score 131; DB 15; Length 43;
Best Local Similarity 100.0%; Pred. No. 3.9e-13;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FFYVTTTFQKNRLFFYRKSVWSK 24
DB 14 FFYVTTTFQKNRLFFYRKSVWSK 37
RESULT 10
US-10-044-539-72
; Sequence 72, Application US/10044539
; Publication No. US20030100093A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin
; Andrews, William H.
; TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND

THIS PAGE BLANK (USPTO)

THIS PAGE BLANK (USPTO)

```

Morin, Gregg B.
Harley, Calvin
Andrews, William H.

TITLE OF INVENTION: NO. US20020164786A1el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/843,676
FILING DATE: 26-Apr-2001
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 67:
SEQUENCE CHARACTERISTICS:
LENGTH: 129 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..129
OTHER INFORMATION: /note= "TRT motifs from human"
SEQUENCE DESCRIPTION: SEQ ID NO: 67:
US-09-843-676-67

Query Match 100.0%; Score 131; DB 10; Length 129;
Best Local Similarity 100.0%; Pred.No.1.2e-12;
Matches 24; Conservative 0; Mismatches 0; Indels 0

Qy 1 FFYVTETTFQKNRLFYRKSVWSK 24
| | | | | | | | | | | | | | | | | | | | | |
Db 19 FFYVTETTFQKNRLFYRKSVWSK 42
| | | | | | | | | | | | | | | | | | | | | |

RESULT 14
US-09-766-253-67
Sequence 67, Application US/09766253
Publication No. US20020187471A1
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: NO. US20020187471A1el Telomerase

```

THIS PAGE BLANK (USPTO)

THIS PAGE BLANK (USPTO)

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 12, 2003, 19:43:04 ; Search time 9.35849 Seconds
(without alignments)
246.626 Million cell updates/sec

Title: US-08-854-050-112

Perfect score: 131

Sequence: 1 FFYVTTTFQKNRLFFYRKSWWSK 24

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_76:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	131	100.0	1132	2 T03844	telomerase catalyt
2	70	53.4	989	2 T03838	telomerase catalyt
3	69	52.7	1132	2 T31107	telomerase reverse
4	63	48.1	1117	2 T14891	telomerase ISC 2.7
5	55	42.0	389	2 B8462	hypothetical prote
6	52	39.7	1123	2 T51517	telomerase reverse
7	49	37.4	205	2 T51884	hypothetical prote
8	48	36.6	306	2 B30114	pril/prl2-like pro
9	47.5	36.3	345	2 A12560	hypothetical prote
10	47	35.9	791	2 A46616	cytochrome-c oxida
11	46	35.1	270	2 AH2143	hypothetical prote
12	46	35.1	277	2 E86833	transcriptional regu
13	46	35.1	363	2 F65070	hypothetical prote
14	46	35.1	396	2 G31096	probable carbamoyl
15	46	35.1	396	2 C85942	probable carbamoyl
16	46	35.1	662	2 H84984	bo-type ubiquinol
17	46	35.1	663	2 A80384	cytochrome O ubiqu
18	46	35.1	762	2 T50155	hypothetical prote
19	45.5	34.7	132	2 G84717	actin depolymerizi
20	45.5	34.7	294	2 G71276	conserved hypothet
21	45	34.4	420	2 A47649	probable inner mem
22	45	34.4	420	2 E95982	probable transport
23	45	34.4	545	2 T05510	hypothetical prote
24	45	34.4	602	2 H86468	protein f12k21.20
25	45	34.4	663	2 A85540	bo-type ubiquinol
26	45	34.4	663	2 E90689	cytochrome o ubiqu
27	45	34.4	663	2 B42226	bo-type ubiquinol
28	45	34.4	663	2 A80557	cytochrome o ubiqu
29	45	34.4	695	2 T38804	hypothetical ww do

RESULT 1
T03844
telomerase catalytic chain - human
N:Alternate names: telomerase reverse transcriptase
C:Species: Homo sapiens (man)
C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 08-Oct-1999
C:Accession: T03844
R:Nakamura, T.M.; Morin, G.B.; Chapman, K.B.; Weinrich, S.L.; Andrews, W.H.; Lingner, J.
Science 277, 955-959, 1997
A:Title: Telomerase catalytic subunit homologs from fission yeast and human.
A:Reference number: 215111; MUID:97400623; PMID:9252327
A:Accession: T03844
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-1132 <NAK>
A:Cross-references: EMBL:AF015950; NID:92330016; PIDN:AAC51672.1; PID:92330017
A:Experimental source: kidney
C:Genetics:
A:Gene: TRT
A:Map position: 5p

Query Match 100.0%; Score 131; DB 2; Length 1132;
Best Local Similarity 100.0%; Pred. No. 3.4e-12;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 FFYVTTTFQKNRLFFYRKSWWSK 24
Db 560 FFYVTTTFQKNRLFFYRKSWWSK 583

RESULT 2
T03838
telomerase catalytic chain - fission yeast (Schizosaccharomyces pombe)
N:Alternate names: telomerase reverse transcriptase 1
C:Species: Schizosaccharomyces pombe
C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 01-Dec-2000
C:Accession: T03838; T03839; T40085
R:Nakamura, T.M.; Morin, G.B.; Chapman, K.B.; Weinrich, S.L.; Andrews, W.H.; Lingner, J.
Science 277, 955-959, 1997
A:Title: Telomerase catalytic subunit homologs from fission yeast and human.
A:Reference number: 215111; MUID:97400623; PMID:9252327
A:Accession: T03838
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-989 <NAK>
A:Cross-references: EMBL:AF015783; NID:92340167; PIDN:AAC49803.1; PID:92340169
A:Experimental source: strain 92h(-)
A:Accession: T03839
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-524,526-989 <NA2>
A:Cross-references: EMBL:AF015783; NID:92340167; PIDN:AAC49802.1; PID:92340168

30 45 34.4 925 2 A72096
31 45 34.4 925 2 E81573
32 45 34.4 925 2 E86527
33 45 34.4 4196 2 T43274
34 44.5 34.0 385 2 T39826
35 44 33.6 184 2 C83911
36 44 33.6 239 2 T41951
37 44 33.6 263 2 T22536
38 44 33.6 273 2 F70158
39 44 33.6 351 2 T26918
40 44 33.6 412 2 E65146
41 44 33.6 466 2 T44650
42 44 33.6 683 2 T12123
43 44 33.6 712 2 T33028
44 43.5 33.2 445 2 AE1590
45 43.5 33.2 1237 2 T46609

ALIGNMENTS

THIS PAGE BLANK (USPTO)

THIS PAGE BLANK (USPTO)

THIS PAGE BLANK (USPTO)

A:Accession: AH2143
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-270 <KUR>
A:Cross-references: GB:BA000019; PIDN:BAB74402.1; PID:g17131796; GSPDB:GN00179
C:Experimental source: strain FCC 7120
C:Genetics:
A:Gene: ali2703
C:Superfamily: Synchocystis hypothetical protein all1774

Query Match 35.1%; Score 46; DB 2; Length 270;
Best Local Similarity 47.1%; Pred. No. 14;
Matches 8; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 2 FYVTETTFQKNRLFFYR 18
DB 61 FYIVEVQFPDDDFYR 77

RESULT 12
E86833
transcription regulator [imported] - Lactococcus lactis subsp. lactis (strain IL1403)
C:Species: Lactococcus lactis subsp. lactis
C:Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001
C:Accession: E86833
R:Boilotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarne, K.; Weissenbach, J.; Ehrlich
Genome Res. 11, 731-753, 2001
A:Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis
A:Reference number: A86625; MUID:21235186; PMID:11337471
A:Accession: E86833
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-277 <STO>
A:Cross-references: GB:AE005176; PID:g12724682; PIDN:AAK05767.1; GSPDB:GN00146
C:Experimental source: strain IL1403
C:Genetics:
A:Gene: yrb1

Query Match 35.1%; Score 46; DB 2; Length 277;
Best Local Similarity 30.4%; Pred. No. 15;
Matches 7; Conservative 6; Mismatches 10; Indels 0; Gaps 0;

QY 2 FYVTETTFQKNRLFFYRSVWSK 24
DB 146 FYLTDSFGEREIMYLMKELWGK 168

RESULT 13
F65070
hypothetical protein b2870 - Escherichia coli (strain K-12)
C:Species: Escherichia coli
C:Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 01-Mar-2002
C:Accession: F65070
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.;
A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A:Title: The complete genome sequence of Escherichia coli K-12.
A:Reference number: A64720; MUID:97426617; PMID:9278503
A:Accession: F65070
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-363 <BLAT>
A:Cross-references: GB:AE000370; GB:U00096; NID:g2367170; PIDN:AACT5908.1; PID:g1789234
A:Experimental source: strain K-12, substrain MG1655
C:Superfamily: aspartate/ornithine carbamoyltransferase homology
F:1-352/Domain: aspartate/ornithine carbamoyltransferase homology <ACT>

Query Match 35.1%; Score 46; DB 2; Length 363;
Best Local Similarity 42.1%; Pred. No. 19;
Matches 8; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 4 VTETTFQKNRLFFYRSVSW 22

THIS PAGE BLANK (USPTO)